D3. D3

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
4 January 2001 (04.01.2001)

PCT

(10) International Publication Number
WO 01/00843 A2

(51) International Patent Classification[7]: C12N 15/31, 15/61, 1/21, 9/90, C07K 14/34, C12P 13/08, C12Q 1/68

(21) International Application Number: PCT/IB00/00923

(22) International Filing Date: 23 June 2000 (23.06.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/141,031	25 June 1999 (25.06.1999)	US
199 30 476.9	1 July 1999 (01.07.1999)	DE
60/142,101	2 July 1999 (02.07.1999)	US
199 31 415.2	8 July 1999 (08.07.1999)	DE
199 31 418.7	8 July 1999 (08.07.1999)	DE
199 31 419.5	8 July 1999 (08.07.1999)	DE
199 31 420.9	8 July 1999 (08.07.1999)	DE
199 31 424.1	8 July 1999 (08.07.1999)	DE
199 31 428.4	8 July 1999 (08.07.1999)	DE
199 31 434.9	8 July 1999 (08.07.1999)	DE
199 31 435.7	8 July 1999 (08.07.1999)	DE
199 31 443.8	8 July 1999 (08.07.1999)	DE
199 31 453.5	8 July 1999 (08.07.1999)	DE
199 31 457.8	8 July 1999 (08.07.1999)	DE
199 31 465.9	8 July 1999 (08.07.1999)	DE
199 31 478.0	8 July 1999 (08.07.1999)	DE
199 31 510.8	8 July 1999 (08.07.1999)	DE
199 31 541.8	8 July 1999 (08.07.1999)	DE
199 31 573.6	8 July 1999 (08.07.1999)	DE
199 31 592.2	8 July 1999 (08.07.1999)	DE
199 31 632.5	8 July 1999 (08.07.1999)	DE
199 31 634.1	8 July 1999 (08.07.1999)	DE
199 31 636.8	8 July 1999 (08.07.1999)	DE
199 32 125.6	9 July 1999 (09.07.1999)	DE
199 32 126.4	9 July 1999 (09.07.1999)	DE
199 32 130.2	9 July 1999 (09.07.1999)	DE
199 32 186.8	9 July 1999 (09.07.1999)	DE
199 32 206.6	9 July 1999 (09.07.1999)	DE
199 32 227.9	9 July 1999 (09.07.1999)	DE
199 32 228.7	9 July 1999 (09.07.1999)	DE
199 32 229.5	9 July 1999 (09.07.1999)	DE
199 32 230.9	9 July 1999 (09.07.1999)	DE
199 32 922.2	14 July 1999 (14.07.1999)	DE
199 32 926.5	14 July 1999 (14.07.1999)	DE
199 32 928.1	14 July 1999 (14.07.1999)	DE
199 33 004.2	14 July 1999 (14.07.1999)	DE
199 33 005.0	14 July 1999 (14.07.1999)	DE
199 33 006.9	14 July 1999 (14.07.1999)	DE
60/148,613	12 August 1999 (12.08.1999)	US
199 40 764.9	27 August 1999 (27.08.1999)	DE
199 40 765.7	27 August 1999 (27.08.1999)	DE
199 40 766.5	27 August 1999 (27.08.1999)	DE
199 40 832.7	27 August 1999 (27.08.1999)	DE
199 41 378.9	31 August 1999 (31.08.1999)	DE
199 41 379.7	31 August 1999 (31.08.1999)	DE
199 41 394.0	31 August 1999 (31.08.1999)	DE
199 41 396.7	31 August 1999 (31.08.1999)	DE
199 41 380.0	31 August 1999 (31.08.1999)	DE
199 42 077.7	3 September 1999 (03.09.1999)	DE
199 42 129.3	3 September 1999 (03.09.1999)	DE
199 42 076.9	3 September 1999 (03.09.1999)	DE
199 42 079.3	3 September 1999 (03.09.1999)	DE
199 42 086.6	3 September 1999 (03.09.1999)	DE
199 42 087.4	3 September 1999 (03.09.1999)	DE
199 42 088.2	3 September 1999 (03.09.1999)	DE
199 42 095.5	3 September 1999 (03.09.1999)	DE
199 42 124.2	3 September 1999 (03.09.1999)	DE
60/187,970	9 March 2000 (09.03.2000)	US

(71) Applicant: BASF AKTIENGESELLSCHAFT [DE/DE]; D-67056 Ludwigshafen (DE).

(72) Inventors: POMPEJUS, Markus; Wenjenstr. 21, D-67251 Freinsheim (DE). KRÖGER, Burkhard; Im Waldhof 1, D-67117 Limburgerhof (DE). SCHRÖDER, Hartwig; Goethestr. 5, D-69226 Nussloch (DE). ZELDER, Oskar; Rossmarktstr. 27, D-67346 Speyer (DE). HABERHAUER, Gregor; Moselstr. 42, D-67117 Limburgerhof (DE).

(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,

[Continued on next page]

(54) Title: *CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING METABOLIC PATHWAY PROTEINS

(57) Abstract: Isolated nucleic acid molecules, designated MP nucleic acid molecules, which encode novel MP proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing MP nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated MP proteins, mutated MP proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of MP genes in this organism.

WO 01/00843 A2

IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:
— *Without international search report and to be republished upon receipt of that report.*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

CORYNEBACTERIUM GLUTAMICUM GENES ENCODING METABOLIC PATHWAY PROTEINS

Related Applications

The present application claims priority to prior filed U.S. Provisional Patent Application Serial No. 60/141031, filed June 25 , 1999, U.S. Provisional Patent Application Serial No. 60/142101, filed July 2, 1999, U.S. Provisional Patent Application Serial No. 60/148613, filed August 12, 1999, and also to U.S. Provisional Patent Application Serial No. 60/187970, filed March 9, 2000. The present application also claims priority to prior filed German Patent Application No. 19930476.9, filed July 1, 1999, German Patent Application No. 19931415.2, filed July 8, 1999, German Patent Application No. 19931418.7, filed July 8, 1999, German Patent Application No. 19931419.5, filed July 8, 1999, German Patent Application No. 19931420.9, filed July 8, 1999, German Patent Application No. 19931424.1, filed July 8, 1999, German Patent Application No. 19931428.4, filed July 8, 1999, German Patent Application No. 19931434.9, filed July 8, 1999, German Patent Application No. 19931435.7, filed July 8, 1999, German Patent Application No. 19931443.8, filed July 8, 1999, German Patent Application No. 19931453.5, filed July 8, 1999, German Patent Application No. 19931457.8, filed July 8, 1999, German Patent Application No. 19931465.9, filed July 8, 1999, German Patent Application No. 19931478.0, filed July 8, 1999, German Patent Application No. 19931510.8, filed July 8, 1999, German Patent Application No. 19931541.8, filed July 8, 1999, German Patent Application No. 19931573.6, filed July 8, 1999, German Patent Application No. 19931592.2, filed July 8, 1999, German Patent Application No. 19931632.5, filed July 8, 1999, German Patent Application No. 19931634.1, filed July 8, 1999, German Patent Application No. 19931636.8, filed July 8, 1999, German Patent Application No. 19932125.6, filed July 9, 1999, German Patent Application No. 19932126.4, filed July 9, 1999, German Patent Application No. 19932130.2, filed July 9, 1999, German Patent Application No. 19932186.8, filed July 9, 1999, German Patent Application No. 19932206.6, filed July 9, 1999, German Patent Application No. 19932227.9, filed July 9, 1999, German Patent Application No. 19932228.7, filed July 9, 1999, German Patent Application No. 19932229.5, filed July 9, 1999, German Patent Application No. 19932230.9, filed July 9, 1999, German Patent Application No. 19932922.2, filed July 14, 1999, German Patent Application No.

19932926.5, filed July 14, 1999, German Patent Application No. 19932928.1, filed July 14, 1999, German Patent Application No. 19933004.2, filed July 14, 1999, German Patent Application No. 19933005.0, filed July 14, 1999, German Patent Application No. 19933006.9, filed July 14, 1999, German Patent Application No. 19940764.9, filed August 27, 1999, German Patent Application No. 19940765.7, filed August 27, 1999, German Patent Application No. 19940766.5, filed August 27, 1999, German Patent Application No. 19940832.7, filed August 27, 1999, German Patent Application No. 19941378.9, filed August 31, 1999, German Patent Application No. 19941379.7, filed August 31, 1999, German Patent Application No. 19941380.0, filed August 31, 1999, German Patent Application No. 19941394.0, filed August 31, 1999, German Patent Application No. 19941396.7, filed August 31, 1999, German Patent Application No. 19942076.9, filed September 3, 1999, German Patent Application No. 19942077.7, filed September 3, 1999, German Patent Application No. 19942079.3, filed September 3, 1999, German Patent Application No. 19942086.6, filed September 3, 1999, German Patent Application No. 19942087.4, filed September 3, 1999, German Patent Application No. 19942088.2, filed September 3, 1999, German Patent Application No. 19942095.5, filed September 3, 1999, German Patent Application No. 19942124.2, filed September 3, 1999, and German Patent Application No. 19942129.3, filed September 3, 1999. The entire contents of all of the aforementioned applications are hereby expressly incorporated herein by this reference.

Background of the Invention

Certain products and by-products of naturally-occurring metabolic processes in cells have utility in a wide array of industries, including the food, feed, cosmetics, and pharmaceutical industries. These molecules, collectively termed 'fine chemicals', include organic acids, both proteinogenic and non-proteinogenic amino acids, nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through large-scale culture of bacteria developed to produce and secrete large quantities of a particular desired molecule. One particularly useful organism for this purpose is *Corynebacterium glutamicum*, a gram positive, nonpathogenic bacterium. Through strain selection, a number of mutant strains have

been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

Summary of the Invention

The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C. glutamicum* or related bacteria, the typing or identification of *C. glutamicum* or related bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for transformation. These novel nucleic acid molecules encode proteins, referred to herein as metabolic pathway (MP) proteins.

C. glutamicum is a gram positive, aerobic bacterium which is commonly used in industry for the large-scale production of a variety of fine chemicals, and also for the degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The MP nucleic acid molecules of the invention, therefore, can be used to identify microorganisms which can be used to produce fine chemicals, *e.g.*, by fermentation processes. Modulation of the expression of the MP nucleic acids of the invention, or modification of the sequence of the MP nucleic acid molecules of the invention, can be used to modulate the production of one or more fine chemicals from a microorganism (*e.g.*, to improve the yield or production of one or more fine chemicals from a Corynebacterium or Brevibacterium species).

The MP nucleic acids of the invention may also be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium*

diphtheriae (the causative agent of diphtheria); the detection of such organisms is of significant clinical relevance.

The MP nucleic acid molecules of the invention may also serve as reference points for mapping of the *C. glutamicum* genome, or of genomes of related organisms. Similarly, these molecules, or variants or portions thereof, may serve as markers for genetically engineered Corynebacterium or Brevibacterium species.

The MP proteins encoded by the novel nucleic acid molecules of the invention are capable of, for example, performing an enzymatic step involved in the metabolism of certain fine chemicals, including amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose. Given the availability of cloning vectors for use in *Corynebacterium glutamicum*, such as those disclosed in Sinskey *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (*e.g.*, *lactofermentum*) (Yoshihama et al, *J. Bacteriol.* 162: 591-597 (1985); Katsumata *et al.*, *J. Bacteriol.* 159: 306-311 (1984); and Santamaria *et al.*, *J. Gen. Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules of the invention may be utilized in the genetic engineering of this organism to make it a better or more efficient producer of one or more fine chemicals.

This improved production or efficiency of production of a fine chemical may be due to a direct effect of manipulation of a gene of the invention, or it may be due to an indirect effect of such manipulation. Specifically, alterations in *C. glutamicum* metabolic pathways for amino acids, vitamins, cofactors, nucleotides, and trehalose may have a direct impact on the overall production of one or more of these desired compounds from this organism. For example, optimizing the activity of a lysine biosynthetic pathway protein or decreasing the activity of a lysine degradative pathway protein may result in an increase in the yield or efficiency of production of lysine from such an engineered organism. Alterations in the proteins involved in these metabolic pathways may also have an indirect impact on the production or efficiency of production of a desired fine chemical. For example, a reaction which is in competition for an intermediate necessary for the production of a desired molecule may be eliminated, or a pathway necessary for the production of a particular intermediate for a desired compound may be optimized. Further, modulations in the biosynthesis or degradation of, for example, an amino acid, a vitamin, or a nucleotide may increase the overall

ability of the microorganism to rapidly grow and divide, thus increasing the number and/or production capacities of the microorganism in culture and thereby increasing the possible yield of the desired fine chemical.

The nucleic acid and protein molecules of the invention may be utilized to directly improve the production or efficiency of production of one or more desired fine chemicals from *Corynebacterium glutamicum*. Using recombinant genetic techniques well known in the art, one or more of the biosynthetic or degradative enzymes of the invention for amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, or trehalose may be manipulated such that its function is modulated. For example, a biosynthetic enzyme may be improved in efficiency, or its allosteric control region destroyed such that feedback inhibition of production of the compound is prevented. Similarly, a degradative enzyme may be deleted or modified by substitution, deletion, or addition such that its degradative activity is lessened for the desired compound without impairing the viability of the cell. In each case, the overall yield or rate of production of the desired fine chemical may be increased.

It is also possible that such alterations in the protein and nucleotide molecules of the invention may improve the production of other fine chemicals besides the amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose through indirect mechanisms. Metabolism of any one compound is necessarily intertwined with other biosynthetic and degradative pathways within the cell, and necessary cofactors, intermediates, or substrates in one pathway are likely supplied or limited by another such pathway. Therefore, by modulating the activity of one or more of the proteins of the invention, the production or efficiency of activity of another fine chemical biosynthetic or degradative pathway may be impacted. For example, amino acids serve as the structural units of all proteins, yet may be present intracellularly in levels which are limiting for protein synthesis; therefore, by increasing the efficiency of production or the yields of one or more amino acids within the cell, proteins, such as biosynthetic or degradative proteins, may be more readily synthesized. Likewise, an alteration in a metabolic pathway enzyme such that a particular side reaction becomes more or less favored may result in the over- or under-production of one or more compounds which are utilized as intermediates or substrates for the production of a desired fine chemical.

This invention provides novel nucleic acid molecules which encode proteins, referred to herein as metabolic pathway proteins (MP), which are capable of, for example, performing an enzymatic step involved in the metabolism of molecules important for the normal functioning of cells, such as amino acids, vitamins, cofactors, nucleotides and nucleosides, or trehalose. Nucleic acid molecules encoding an MP protein are referred to herein as MP nucleic acid molecules. In a preferred embodiment, the MP protein performs an enzymatic step related to the metabolism of one or more of the following: amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose. Examples of such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (*e.g.*, cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an MP protein or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection or amplification of MP-encoding nucleic acid (*e.g.*, DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth as the odd-numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth as an odd-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth as an even-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8....). The preferred MP proteins of the present invention also preferably possess at least one of the MP activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a

sequence having an even-numbered SEQ ID NO: in the Sequence Listing), *e.g.*, sufficiently homologous to an amino acid sequence of the invention such that the protein or portion thereof maintains an MP activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to perform an enzymatic reaction in a amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an amino acid sequence of the invention (*e.g.*, an entire amino acid sequence selected from those having an even-numbered SEQ ID NO in the Sequence Listing). In another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention (encoded by an open reading frame shown in the corresponding odd-numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (*e.g.*, an MP fusion protein) which includes a biologically active domain which is at least about 50% or more homologous to one of the amino acid sequences of the invention (*e.g.*, a sequence of one of the even-numbered SEQ ID NOs in the Sequence Listing) and is able to catalyze a reaction in a metabolic pathway for an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose, or one or more of the activities set forth in Table 1, and which also includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO in the Sequence Listing). Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* MP protein, or a biologically active portion thereof.

Another aspect of the invention pertains to vectors, *e.g.*, recombinant expression vectors, containing the nucleic acid molecules of the invention, and host cells into which such vectors have been introduced. In one embodiment, such a host cell is used to produce an MP protein by culturing the host cell in a suitable medium. The MP protein can be then isolated from the medium or the host cell.

Yet another aspect of the invention pertains to a genetically altered microorganism in which an MP gene has been introduced or altered. In one embodiment, the genome of the microorganism has been altered by introduction of a nucleic acid molecule of the invention encoding wild-type or mutated MP sequence as a transgene. In another embodiment, an endogenous MP gene within the genome of the microorganism has been altered, *e.g.*, functionally disrupted, by homologous recombination with an altered MP gene. In another embodiment, an endogenous or introduced MP gene in a microorganism has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional MP protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an MP gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the MP gene is modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

In another aspect, the invention provides a method of identifying the presence or activity of *Cornyebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth in the Sequence Listing as SEQ ID NOs 1 through 1156) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

Still another aspect of the invention pertains to an isolated MP protein or a portion, *e.g.*, a biologically active portion, thereof. In a preferred embodiment, the isolated MP protein or portion thereof can catalyze an enzymatic reaction involved in one or more pathways for the metabolism of an amino acid, a vitamin, a cofactor, a

nutraceutical, a nucleotide, a nucleoside, or trehalose. In another preferred embodiment, the isolated MP protein or portion thereof is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: in the Sequence Listing) such that the protein or portion thereof maintains the ability to catalyze an enzymatic reaction involved in one or more pathways for the metabolism of an amino acid, a vitamin, a cofactor, a nutraceutical, a nucleotide, a nucleoside, or trehalose.

The invention also provides an isolated preparation of an MP protein. In preferred embodiments, the MP protein comprises an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In another preferred embodiment, the invention pertains to an isolated full length protein which is substantially homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) (encoded by an open reading frame set forth in a corresponding odd-numbered SEQ ID NO: of the Sequence Listing). In yet another embodiment, the protein is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%, and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In other embodiments, the isolated MP protein comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and is able to catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, or has one or more of the activities set forth in Table 1.

Alternatively, the isolated MP protein can comprise an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80%, or 90%, and even more preferably at least about 95%, 96%, 97%, 98,%, or 99% or more homologous to a nucleotide sequence of one of the even-numbered SEQ ID NOs set forth in the Sequence Listing. It is also preferred that the preferred forms of MP proteins also have one or more of the MP bioactivities described herein.

The MP polypeptide, or a biologically active portion thereof, can be operatively linked to a non-MP polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the MP protein alone. In other preferred embodiments, this fusion protein, when introduced into a *C. glutamicum* pathway for the metabolism of an amino acid, vitamin, cofactor, nutraceutical, results in increased yields and/or efficiency of production of a desired fine chemical from *C. glutamicum*. In particularly preferred embodiments, integration of this fusion protein into an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway of a host cell modulates production of a desired compound from the cell.

In another aspect, the invention provides methods for screening molecules which modulate the activity of an MP protein, either by interacting with the protein itself or a substrate or binding partner of the MP protein, or by modulating the transcription or translation of an MP nucleic acid molecule of the invention.

Another aspect of the invention pertains to a method for producing a fine chemical. This method involves the culturing of a cell containing a vector directing the expression of an MP nucleic acid molecule of the invention, such that a fine chemical is produced. In a preferred embodiment, this method further includes the step of obtaining a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an MP nucleic acid. In another preferred embodiment, this method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment, the cell is from the genus *Corynebacterium* or *Brevibacterium*, or is selected from those strains set forth in Table 3.

Another aspect of the invention pertains to methods for modulating production of a molecule from a microorganism. Such methods include contacting the cell with an agent which modulates MP protein activity or MP nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated for one or more *C. glutamicum* amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathways, such that the yields or rate of production of a desired fine chemical by this microorganism is improved. The agent which modulates MP protein activity can be an agent which stimulates MP protein activity or MP nucleic acid expression.

Examples of agents which stimulate MP protein activity or MP nucleic acid expression include small molecules, active MP proteins, and nucleic acids encoding MP proteins that have been introduced into the cell. Examples of agents which inhibit MP activity or expression include small molecules, and antisense MP nucleic acid molecules.

Another aspect of the invention pertains to methods for modulating yields of a desired compound from a cell, involving the introduction of a wild-type or mutant MP gene into a cell, either maintained on a separate plasmid or integrated into the genome of the host cell. If integrated into the genome, such integration can be random, or it can take place by homologous recombination such that the native gene is replaced by the introduced copy, causing the production of the desired compound from the cell to be modulated. In a preferred embodiment, said yields are increased. In another preferred embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino acid is L-lysine.

Detailed Description of the Invention

The present invention provides MP nucleic acid and protein molecules which are involved in the metabolism of certain fine chemicals in *Corynebacterium glutamicum*, including amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose. The molecules of the invention may be utilized in the modulation of production of fine chemicals from microorganisms, such as *C. glutamicum*, either directly (*e.g.*, where modulation of the activity of a lysine biosynthesis protein has a direct impact on the production or efficiency of production of lysine from that organism), or may have an indirect impact which nonetheless results in an increase of yield or efficiency of production of the desired compound (*e.g.*, where modulation of the activity of a nucleotide biosynthesis protein has an impact on the production of an organic acid or a fatty acid from the bacterium, perhaps due to improved growth or an increased supply of necessary co-factors, energy compounds, or precursor molecules). Aspects of the invention are further explicated below.

I. Fine Chemicals

The term 'fine chemical' is art-recognized and includes molecules produced by an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described *e.g.* in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty acids (*e.g.*, arachidonic acid), diols (*e.g.*, propane diol, and butane diol), carbohydrates (*e.g.*, hyaluronic acid and trehalose), aromatic compounds (*e.g.*, aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press, (1995)), enzymes, polyketides (Cane *et al.* (1998) *Science* 282: 63-68), and all other chemicals described in Gutcho (1983) Chemicals by Fermentation, Noyes Data Corporation, ISBN: 0818805086 and references therein. The metabolism and uses of certain of these fine chemicals are further explicated below.

A. *Amino Acid Metabolism and Uses*

Amino acids comprise the basic structural units of all proteins, and as such are essential for normal cellular functioning in all organisms. The term "amino acid" is art-recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the nonproteinogenic amino acids (hundreds of which are known) are not normally found in proteins (see Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH: Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins. Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids

have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. Biochemistry, 3rd edition, pages 578-590 (1988)). The 'essential' amino acids (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

Aside from their function in protein biosynthesis, these amino acids are interesting chemicals in their own right, and many have been found to have various applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine, valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/ L-methionine are common feed additives. (Leuchtenberger, W. (1996) Amino aids – technical production and use, p. 466-502 in Rehm *et al.* (eds.) Biotechnology vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others described in Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97, VCH: Weinheim, 1985.

The biosynthesis of these natural amino acids in organisms capable of producing them, such as bacteria, has been well characterized (for review of bacterial amino acid biosynthesis and regulation thereof, see Umbarger, H.E.(1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of α-ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine are each subsequently produced from glutamate. The biosynthesis of serine is a three-

step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transferal of the side-chain β-carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase. Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.

Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of the cell (for review see Stryer, L. Biochemistry 3rd ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted amino acids into useful metabolic intermediates, amino acid production is costly in terms of energy, precursor molecules, and the enzymes necessary to synthesize them. Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own production (for overview of feedback mechanisms in amino acid biosynthetic pathways, see Stryer, L. Biochemistry, 3rd ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount of that amino acid present in the cell.

B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses

Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although

they are readily synthesized by other organisms, such as bacteria. These molecules are either bioactive substances themselves, or are precursors of biologically active substances which may serve as electron carriers or intermediates in a variety of metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other processing aids. (For an overview of the structure, activity, and industrial applications of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal functioning, but which that organism cannot synthesize by itself. The group of vitamins may encompass cofactors and nutraceutical compounds. The language "cofactor" includes nonproteinaceous compounds required for a normal enzymatic activity to occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements having health benefits in plants and animals, particularly humans. Examples of such molecules are vitamins, antioxidants, and also certain lipids (*e.g.*, polyunsaturated fatty acids).

The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley & Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press: Champaign, IL X, 374 S).

Thiamin (vitamin B_1) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B_2) is synthesized from guanosine-5'-triphosphate (GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of compounds collectively termed 'vitamin B_6' (*e.g.*, pyridoxine, pyridoxamine, pyridoxa-5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic

acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)-β-alanine) can be produced either by chemical synthesis or by fermentation. The final steps in pantothenate biosynthesis consist of the ATP-driven condensation of β-alanine and pantoic acid. The enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to β-alanine and for the condensation to panthotenic acid are known. The metabolically active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the precursors of Coenzyme A. These enzymes not only catalyze the formation of panthothante, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthenol (provitamin B_5), pantetheine (and its derivatives) and coenzyme A.

Biotin biosynthesis from the precursor molecule pimeloyl-CoA in microorganisms has been studied in detail and several of the genes involved have been identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the nifS class of proteins. Lipoic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it becomes part of the pyruvate dehydrogenase complex and the α-ketoglutarate dehydrogenase complex. The folates are a group of substances which are all derivatives of folic acid, which is turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

Corrinoids (such as the cobalamines and particularly vitamin B_{12}) and porphyrines belong to a group of chemicals characterized by a tetrapyrole ring system. The biosynthesis of vitamin B_{12} is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-scale culture of microorganisms, such as riboflavin, Vitamin B_6, pantothenate, and

biotin. Only Vitamin B_{12} is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses

Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language "purine" or "pyrimidine" includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term "nucleotide" includes the basic structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language "nucleoside" includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are nucleotides which do not form nucleic acid molecules, but rather serve as energy stores (*i.e.*, AMP) or as coenzymes (*i.e.*, FAD and NAD).

Several publications have described the use of these chemicals for these medical indications, by influencing purine and/or pyrimidine metabolism (*e.g.* Christopherson, R.I. and Lyons, S.D. (1990) "Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents." *Med. Res. Reviews* 10: 505-548). Studies of enzymes involved in purine and pyrimidine metabolism have been focused on the development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) "Enzymes in nucleotide synthesis." *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (*e.g.*, thiamine, S-adenosyl-methionine, folates, or riboflavin), as energy carriers for the cell (*e.g.*, ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (*e.g.*, IMP or GMP) or for several medicinal applications (see, for example, Kuninaka, A. (1996) Nucleotides and

Related Compounds in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, p. 561-612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.

The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) "*de novo* purine nucleotide biosynthesis", in: Progress in Nucleic Acid Research and Molecular Biology, vol. 42, Academic Press:, p. 259-287; and Michal, G. (1999) "Nucleotides and Nucleosides", Chapter 8 in: Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, Wiley: New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell. Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP). The deoxy- forms of all of these nucleotides are produced in a one step reduction reaction from the diphosphate ribose form of the nucleotide to the diphosphate deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

D. Trehalose Metabolism and Uses

Trehalose consists of two glucose molecules, bound in α, α-1,1 linkage. It is commonly used in the food industry as a sweetener, an additive for dried or frozen foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto *et al.*, (1998) U.S. Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and Shiosaka, M. (1997) J. Japan 172: 97-102). Trehalose is produced by enzymes from

many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.

II. Elements and Methods of the Invention

The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as MP nucleic acid and protein molecules, which play a role in or function in one or more cellular metabolic pathways. In one embodiment, the MP molecules catalyze an enzymatic reaction involving one or more amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathways. In a preferred embodiment, the activity of the MP molecules of the present invention in one or more *C. glutamicum* metabolic pathways for amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides or trehalose has an impact on the production of a desired fine chemical by this organism. In a particularly preferred embodiment, the MP molecules of the invention are modulated in activity, such that the *C. glutamicum* metabolic pathways in which the MP proteins of the invention are involved are modulated in efficiency or output, which either directly or indirectly modulates the production or efficiency of production of a desired fine chemical by *C. glutamicum*.

The language, “MP protein” or “MP polypeptide” includes proteins which play a role in, *e.g.*, catalyze an enzymatic reaction, in one or more amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside or trehalose metabolic pathways. Examples of MP proteins include those encoded by the MP genes set forth in Table 1 and by the odd-numbered SEQ ID NOs. The terms “MP gene” or “MP nucleic acid sequence” include nucleic acid sequences encoding an MP protein, which consist of a coding region and also corresponding untranslated 5’ and 3’ sequence regions. Examples of MP genes include those set forth in Table 1. The terms “production” or “productivity” are art-recognized and include the concentration of the fermentation product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (*e.g.*, kg product per hour per liter). The term “efficiency of production” includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term “yield” or “product/carbon yield” is art-recognized and includes

the efficiency of the conversion of the carbon source into the product (*i.e.*, fine chemical). This is generally written as, for example, kg product per kg carbon source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms "biosynthesis" or a "biosynthetic pathway" are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the breakdown of a compound, preferably an organic compound, by a cell to degradation products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The language "metabolism" is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (*e.g.*, the metabolism of an amino acid such as glycine) comprises the overall biosynthetic, modification, and degradation pathways in the cell related to this compound.

In another embodiment, the MP molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*. Using recombinant genetic techniques, one or more of the biosynthetic or degradative enzymes of the invention for amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, or trehalose may be manipulated such that its function is modulated. For example, a biosynthetic enzyme may be improved in efficiency, or its allosteric control region destroyed such that feedback inhibition of production of the compound is prevented. Similarly, a degradative enzyme may be deleted or modified by substitution, deletion, or addition such that its degradative activity is lessened for the desired compound without impairing the viability of the cell. In each case, the overall yield or rate of production of one of these desired fine chemicals may be increased.

It is also possible that such alterations in the protein and nucleotide molecules of the invention may improve the production of other fine chemicals besides the amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose. Metabolism of any one compound is necessarily intertwined with other biosynthetic and

degradative pathways within the cell, and necessary cofactors, intermediates, or substrates in one pathway are likely supplied or limited by another such pathway. Therefore, by modulating the activity of one or more of the proteins of the invention, the production or efficiency of activity of another fine chemical biosynthetic or degradative pathway may be impacted. For example, amino acids serve as the structural units of all proteins, yet may be present intracellularly in levels which are limiting for protein synthesis; therefore, by increasing the efficiency of production or the yields of one or more amino acids within the cell, proteins, such as biosynthetic or degradative proteins, may be more readily synthesized. Likewise, an alteration in a metabolic pathway enzyme such that a particular side reaction becomes more or less favored may result in the over- or under-production of one or more compounds which are utilized as intermediates or substrates for the production of a desired fine chemical.

The isolated nucleic acid sequences of the invention are contained within the genome of a *Corynebacterium glutamicum* strain available through the American Type Culture Collection, given designation ATCC 13032. The nucleotide sequence of the isolated *C. glutamicum* MP DNAs and the predicted amino acid sequences of the *C. glutamicum* MP proteins are shown in the Sequence Listing as odd-numbered SEQ ID NOs and even-numbered SEQ ID NOs, respectively. Computational analyses were performed which classified and/or identified these nucleotide sequences as sequences which encode metabolic pathway proteins.

The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of the invention (*e.g.*, the sequence of an even-numbered SEQ ID NO of the Sequence Listing). As used herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, *e.g.*, the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence.

The MP protein or a biologically active portion or fragment thereof of the invention can catalyze an enzymatic reaction in one or more amino acid, vitamin,

cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathways, or have one or more of the activities set forth in Table 1.

Various aspects of the invention are described in further detail in the following subsections:

A. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules that encode MP polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or amplification of MP-encoding nucleic acid (*e.g.*, MP DNA). As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA) and RNA molecules (*e.g.*, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides of sequence upstream from the 5' end of the coding region and at least about 20 nucleotides of sequence downstream from the 3'end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated MP nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (e.g, a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having a nucleotide sequence of an odd-numbered SEQ ID NO of the Sequence Listing, or a portion thereof, can be isolated using standard molecular biology techniques and the

sequence information provided herein. For example, a *C. glutamicum* MP DNA can be isolated from a *C. glutamicum* library using all or portion of one of the odd-numbered SEQ ID NO sequences of the Sequence Listing as a hybridization probe and standard hybridization techniques (*e.g.*, as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory,* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989). Moreover, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (*e.g.*, an odd-numbered SEQ ID NO:) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence (*e.g.*, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (*e.g.*, an odd-numbered SEQ ID NO of the Sequence Listing) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence). For example, mRNA can be isolated from normal endothelial cells (*e.g.*, by the guanidinium-thiocyanate extraction procedure of Chirgwin *et al.* (1979) *Biochemistry* 18: 5294-5299) and DNA can be prepared using reverse transcriptase (*e.g.*, Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL). Synthetic oligonucleotide primers for polymerase chain reaction amplification can be designed based upon one of the nucleotide sequences shown in the Sequence Listing. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to an MP nucleotide sequence can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in the Sequence Listing. The nucleic acid sequences of the invention, as set forth in the Sequence Listing, correspond to the *Corynebacterium glutamicum* MP DNAs of the invention. This DNA comprises sequences encoding MP proteins (*i.e.*, the "coding region", indicated in each odd-numbered SEQ ID NO: sequence in the Sequence Listing), as well as 5' untranslated

sequences and 3' untranslated sequences, also indicated in each odd-numbered SEQ ID NO: in the Sequence Listing. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the nucleic acid sequences of the Sequence Listing.

For the purposes of this application, it will be understood that each of the nucleic acid and amino acid sequences set forth in the Sequence Listing has an identifying RXA, RXN, RXS, or RXC number having the designation "RXA", "RXN", "RXS", or "RXC" followed by 5 digits (*i.e.*, RXA00007, RXN00023, RXS00116, or RXC00128). Each of the nucleic acid sequences comprises up to three parts: a 5' upstream region, a coding region, and a downstream region. Each of these three regions is identified by the same RXA, RXN, RXS, or RXC designation to eliminate confusion. The recitation "one of the odd-numbered sequences of the Sequence Listing", then, refers to any of the nucleic acid sequences in the Sequence Listing, which may also be distinguished by their differing RXA, RXN, RXS, or RXC designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is also set forth in the Sequence Listing, as an even-numbered SEQ ID NO: immediately following the corresponding nucleic acid sequence . For example, the coding region for RXA02229 is set forth in SEQ ID NO:1, while the amino acid sequence which it encodes is set forth as SEQ ID NO:2. The sequences of the nucleic acid molecules of the invention are identified by the same RXA, RXN, RXS, or RXC designations as the amino acid molecules which they encode, such that they can be readily correlated. For example, the amino acid sequences designated RXA02229, RX00351, RXS02970, and RXC02390 are translations of the coding regions of the nucleotide sequences of nucleic acid molecules RXA02229, RX00351, RXS02970, and RXC02390, respectively. The correspondence between the RXA, RXN, RXS, and RXC nucleotide and amino acid sequences of the invention and their assigned SEQ ID NOs is set forth in Table 1.

Several of the genes of the invention are "F-designated genes". An F-designated gene includes those genes set forth in Table 1 which have an 'F' in front of the RXA, RXN, RXS, or RXC designation. For example, SEQ ID NO:5, designated, as indicated on Table 1, as "F RXA01009", is an F-designated gene, as are SEQ ID NOs: 73, 75, and 77 (designated on Table 1 as "F RXA00007", "F RXA00364", and "F RXA00367", respectively).

In one embodiment, the nucleic acid molecules of the present invention are not intended to include *C. glutamicum* those compiled in Table 2. In the case of the dapD gene, a sequence for this gene was published in Wehrmann, A., *et al.* (1998) *J. Bacteriol.* 180(12): 3159-3165. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences of the invention is one which is sufficiently complementary to one of the nucleotide sequences shown in the Sequence Listing (*e.g.*, the sequence of an odd-numbered SEQ ID NO:) such that it can hybridize to one of the nucleotide sequences of the invention, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. Ranges and identity values intermediate to the above-recited ranges, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to one of the nucleotide sequences of the invention, or a portion thereof.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of the sequence of one of the odd-numbered SEQ ID NOs

of the Sequence Listing, for example a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of an MP protein. The nucleotide sequences determined from the cloning of the MP genes from *C. glutamicum* allows for the generation of probes and primers designed for use in identifying and/or cloning MP homologues in other cell types and organisms, as well as MP homologues from other *Corynebacteria* or related species. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one of the nucleotide sequences of the invention (*e.g.*, a sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing), an anti-sense sequence of one of these sequences, or naturally occurring mutants thereof. Primers based on a nucleotide sequence of the invention can be used in PCR reactions to clone MP homologues. Probes based on the MP nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, *e.g.* the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an MP protein, such as by measuring a level of an MP-encoding nucleic acid in a sample of cells from a subject *e.g.*, detecting MP mRNA levels or determining whether a genomic MP gene has been mutated or deleted.

In one embodiment, the nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO of the Sequence Listing) such that the protein or portion thereof maintains the ability to catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway. As used herein, the language "sufficiently homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or equivalent (*e.g.*, an amino acid residue which has a similar side chain as an amino acid residue in a sequence of one of the even-numbered SEQ ID NOs of the Sequence Listing) amino acid residues to an amino acid sequence of the invention such that the

protein or portion thereof is able to catalyze an enzymatic reaction in a *C. glutamicum* amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside or trehalose metabolic pathway. Protein members of such metabolic pathways, as described herein, function to catalyze the biosynthesis or degradation of one or more of: amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, or trehalose. Examples of such activities are also described herein. Thus, "the function of an MP protein" contributes to the overall functioning of one or more such metabolic pathway and contributes, either directly or indirectly, to the yield, production, and/or efficiency of production of one or more fine chemicals. Examples of MP protein activities are set forth in Table 1.

In another embodiment, the protein is at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing).

Portions of proteins encoded by the MP nucleic acid molecules of the invention are preferably biologically active portions of one of the MP proteins. As used herein, the term "biologically active portion of an MP protein" is intended to include a portion, *e.g.*, a domain/motif, of an MP protein that catalyzes an enzymatic reaction in one or more *C. glutamicum* amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathways, or has an activity as set forth in Table 1. To determine whether an MP protein or a biologically active portion thereof can catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, an assay of enzymatic activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as detailed in Example 8 of the Exemplification.

Additional nucleic acid fragments encoding biologically active portions of an MP protein can be prepared by isolating a portion of one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing), expressing the encoded portion of the MP protein or peptide (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the MP protein or peptide.

The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing) (and portions thereof) due to degeneracy of the genetic code and thus encode the same MP protein as that encoded by the nucleotide sequences of the invention. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in the Sequence Listing (*e.g.*, an even-numbered SEQ ID NO:). In a still further embodiment, the nucleic acid molecule of the invention encodes a full length *C. glutamicum* protein which is substantially homologous to an amino acid sequence of the invention (encoded by an open reading frame shown in an odd-numbered SEQ ID NO: of the Sequence Listing).

It will be understood by one of ordinary skill in the art that in one embodiment the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Tables 2 or 4 which were available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the invention which is greater than that of a sequence of the prior art (*e.g.*, a Genbank sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 40% identical to the nucleotide sequence designated RXA00115 (SEQ ID NO:185), a nucleotide sequence which is greater than and/or at least % identical to the nucleotide sequence designated RXA00131 (SEQ ID NO:991), and a nucleotide sequence which is greater than and/or at least 39% identical to the nucleotide sequence designated RXA00219 (SEQ ID NO:345). One of ordinary skill in the art would be able to calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4 for each of the three top hits for the given sequence, and by subtracting the highest GAP-calculated percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino acid sequences having percent identities greater than the lower threshold so calculated (*e.g.*, at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%,

74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more identical) are also encompassed by the invention.

In addition to the *C. glutamicum* MP nucleotide sequences set forth in the Sequence Listing as odd-numbered SEQ ID NOs, it will be appreciated by one of ordinary skill in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of MP proteins may exist within a population (*e.g.*, the *C. glutamicum* population). Such genetic polymorphism in the MP gene may exist among individuals within a population due to natural variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an MP protein, preferably a *C. glutamicum* MP protein. Such natural variations can typically result in 1-5% variance in the nucleotide sequence of the MP gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in MP that are the result of natural variation and that do not alter the functional activity of MP proteins are intended to be within the scope of the invention.

Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* MP DNA of the invention can be isolated based on their homology to the *C. glutamicum* MP nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of an odd-numbered SEQ ID NO: of the Sequence Listing. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or more nucleotides in length. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to one of ordinary skill in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6.

A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a nucleotide sequence of the invention corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C. glutamicum* MP protein.

In addition to naturally-occurring variants of the MP sequence that may exist in the population, one of ordinary skill in the art will further appreciate that changes can be introduced by mutation into a nucleotide sequence of the invention, thereby leading to changes in the amino acid sequence of the encoded MP protein, without altering the functional ability of the MP protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a nucleotide sequence of the invention. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the MP proteins (*e.g.*, an even-numbered SEQ ID NO: of the Sequence Listing) without altering the activity of said MP protein, whereas an "essential" amino acid residue is required for MP protein activity. Other amino acid residues, however, (*e.g.*, those that are not conserved or only semi-conserved in the domain having MP activity) may not be essential for activity and thus are likely to be amenable to alteration without altering MP activity.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding MP proteins that contain changes in amino acid residues that are not essential for MP activity. Such MP proteins differ in amino acid sequence from a sequence of an even-numbered SEQ ID NO: of the Sequence Listing yet retain at least one of the MP activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of the invention and is capable of catalyzing an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, or has one or more activities set forth in Table 1. Preferably, the protein encoded by the nucleic

acid molecule is at least about 50-60% homologous to the amino acid sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, more preferably at least about 60-70% homologous to one of these sequences, even more preferably at least about 70-80%, 80-90%, 90-95% homologous to one of these sequences, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the amino acid sequences of the invention.

To determine the percent homology of two amino acid sequences (*e.g.*, one of the amino acid sequences of the invention and a mutant form thereof) or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence (*e.g.*, one of the amino acid sequences of the invention) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (*e.g.*, a mutant form of the amino acid sequence), then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % homology = # of identical positions/total # of positions x 100).

An isolated nucleic acid molecule encoding an MP protein homologous to a protein sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of the invention such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one of the nucleotide sequences of the invention by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic

acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an MP protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an MP coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an MP activity described herein to identify mutants that retain MP activity. Following mutagenesis of the nucleotide sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, the encoded protein can be expressed recombinantly and the activity of the protein can be determined using, for example, assays described herein (see Example 8 of the Exemplification).

In addition to the nucleic acid molecules encoding MP proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded DNA molecule or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire MP coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an MP protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (*e.g.*, the entire coding region of SEQ ID NO. 1 (RXA02229) comprises nucleotides 1 to 825). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding MP. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding MP disclosed herein (*e.g.*, the sequences set forth as odd-numbered SEQ ID NOs in the Sequence Listing), antisense

nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of MP mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of MP mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of MP mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5- oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an MCT protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids. Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave MP mRNA transcripts to thereby inhibit translation of MP mRNA. A ribozyme having specificity for an MP-encoding nucleic acid can be designed based upon the nucleotide sequence of an MP DNA disclosed herein (*i.e.*, SEQ ID NO: 1 (RXA02229). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an MP-encoding mRNA. See, *e.g.*, Cech *et al.*

U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No. 5,116,742. Alternatively, MP mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

Alternatively, MP gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an MP nucleotide sequence (*e.g.*, an MP promoter and/or enhancers) to form triple helical structures that prevent transcription of an MP gene in target cells. See generally, Helene, C. (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher, L.J. (1992) *Bioassays* 14(12):807-15.

B. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an MP protein (or a portion thereof). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, repressor binding sites, activator binding sites, enhancers and other expression control elements (*e.g.*, terminators, polyadenylation signals, or other elements of mRNA secondary structure). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells. Preferred regulatory sequences are, for example, promoters such as cos-, tac-, trp-, tet-, trp-tet-, lpp-, lac-, lpp-lac-, $lacI^q$-, T7-, T5-, T3-, gal-, trc-, ara-, SP6-, arny, SPO2, λ-P_R- or λ P_L, which are used preferably in bacteria. Additional regulatory sequences are, for example, promoters from yeasts and fungi, such as ADC1, MFα, AC, P-60, CYC1, GAPDH, TEF, rp28, ADH, promoters from plants such as CaMV/35S, SSU, OCS, lib4, usp, STLS1, B33, nos or ubiquitin- or phaseolin-promoters. It is also possible to use artificial promoters. It will be appreciated by one of ordinary skill in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, MP proteins, mutant forms of MP proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of MP proteins in prokaryotic or eukaryotic cells. For example, MP genes can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus

expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.* (1992) "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: More Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge), algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* –mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants" *Plant Cell Rep.*: 583-586), or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein but also to the C-terminus or fused within suitable regions in the proteins. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the MP protein is cloned into a pGEX expression vector to create a vector encoding a fusion protein comprising, from

the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin. Recombinant MP protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315) pLG338, pACYC184, pBR322, pUC18, pUC19, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-III113-B1, λgt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89; and Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York IBSN 0 444 904018). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter. For transformation of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming Streptomyces, while plasmids pUB110, pC194, or pBD214 are suited for transformation of Bacillus species. Several plasmids of use in the transfer of genetic information into Corynebacterium include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York IBSN 0 444 904018).

One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada *et al.* (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the MP protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*, (1987) *Embo J.* 6:229-234), , 2 μ, pAG-1, Yep6, Yep13, pEMBLYe23, pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J.F. Peberdy, *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge, and Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York (IBSN 0 444 904018).

Alternatively, the MP proteins of the invention can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.* (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In another embodiment, the MP proteins of the invention may be expressed in unicellular plant cells (such as algae) or in plant cells from higher plants (*e.g.*, the spermatophytes, such as crop plants). Examples of plant expression vectors include those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHlac+, pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York IBSN 0 444 904018).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both

prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory,* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α-fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to MP mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell

type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. *et al.*, Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, an MP protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those of ordinary skill in the art. Microorganisms related to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection", "conjugation" and "transduction" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, linear DNA or RNA (*e.g.*, a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (*e.g.*, a plasmid, phage, phasmid, phagemid, transposon or other DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, natural competence, chemical-mediated transfer, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory,* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these

integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding an MP protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

To create a homologous recombinant microorganism, a vector is prepared which contains at least a portion of an MP gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the MP gene. Preferably, this MP gene is a *Corynebacterium glutamicum* MP gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source. In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous MP gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous MP gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous MP protein). In the homologous recombination vector, the altered portion of the MP gene is flanked at its 5' and 3' ends by additional nucleic acid of the MP gene to allow for homologous recombination to occur between the exogenous MP gene carried by the vector and an endogenous MP gene in a microorganism. The additional flanking MP nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see *e.g.*, Thomas, K.R., and Capecchi, M.R. (1987) Cell 51: 503 for a description of homologous recombination vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and cells in which the introduced MP gene has homologously recombined with the endogenous MP gene are selected, using art-known techniques.

In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene.

For example, inclusion of an MP gene on a vector placing it under control of the lac operon permits expression of the MP gene only in the presence of IPTG. Such regulatory systems are well known in the art.

In another embodiment, an endogenous MP gene in a host cell is disrupted (*e.g.*, by homologous recombination or other genetic means known in the art) such that expression of its protein product does not occur. In another embodiment, an endogenous or introduced MP gene in a host cell has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional MP protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an MP gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the MP gene is modulated. One of ordinary skill in the art will appreciate that host cells containing more than one of the described MP gene and protein modifications may be readily produced using the methods of the invention, and are meant to be included in the present invention.

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) an MP protein. Accordingly, the invention further provides methods for producing MP proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding an MP protein has been introduced, or into which genome has been introduced a gene encoding a wild-type or altered MP protein) in a suitable medium until MP protein is produced. In another embodiment, the method further comprises isolating MP proteins from the medium or the host cell.

C. Isolated MP Proteins

Another aspect of the invention pertains to isolated MP proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of MP protein in which the protein is separated from cellular components of the cells in which

it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of MP protein having less than about 30% (by dry weight) of non-MP protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-MP protein, still more preferably less than about 10% of non-MP protein, and most preferably less than about 5% non-MP protein. When the MP protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of MP protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of MP protein having less than about 30% (by dry weight) of chemical precursors or non-MP chemicals, more preferably less than about 20% chemical precursors or non-MP chemicals, still more preferably less than about 10% chemical precursors or non-MP chemicals, and most preferably less than about 5% chemical precursors or non-MP chemicals. In preferred embodiments, isolated proteins or biologically active portions thereof lack contaminating proteins from the same organism from which the MP protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* MP protein in a microorganism such as *C. glutamicum*.

An isolated MP protein or a portion thereof of the invention can catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, or has one or more of the activities set forth in Table 1. In preferred embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) such that the protein or portion thereof maintains the ability to catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway. The portion of the protein is preferably a biologically active portion as described herein. In another preferred embodiment, an MP protein of

the invention has an amino acid sequence set forth as an even-numbered SEQ ID NO: of the Sequence Listing. In yet another preferred embodiment, the MP protein has an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing). In still another preferred embodiment, the MP protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to one of the nucleic acid sequences of the invention, or a portion thereof. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. The preferred MP proteins of the present invention also preferably possess at least one of the MP activities described herein. For example, a preferred MP protein of the present invention includes an amino acid sequence encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of the invention, and which can catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, or which has one or more of the activities set forth in Table 1.

In other embodiments, the MP protein is substantially homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and retains the functional activity of the protein of one of the amino acid sequences of the invention yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in another embodiment, the MP protein is a protein which comprises an amino acid sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%,

78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention and which has at least one of the MP activities described herein. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In another embodiment, the invention pertains to a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention.

Biologically active portions of an MP protein include peptides comprising amino acid sequences derived from the amino acid sequence of an MP protein, *e.g.*, an amino acid sequence of an even-numbered SEQ ID NO: of the Sequence Listing or the amino acid sequence of a protein homologous to an MP protein, which include fewer amino acids than a full length MP protein or the full length protein which is homologous to an MP protein, and exhibit at least one activity of an MP protein. Typically, biologically active portions (peptides, *e.g.*, peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of an MP protein. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an MP protein include one or more selected domains/motifs or portions thereof having biological activity.

MP proteins are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described above), the expression vector is introduced into a host cell (as described above) and the MP protein is expressed in the host cell. The MP protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Alternative to recombinant expression, an MP protein, polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native MP protein can be isolated from cells (*e.g.*, endothelial

cells), for example using an anti-MP antibody, which can be produced by standard techniques utilizing an MP protein or fragment thereof of this invention.

The invention also provides MP chimeric or fusion proteins. As used herein, an MP "chimeric protein" or "fusion protein" comprises an MP polypeptide operatively linked to a non-MP polypeptide. An "MP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to MP, whereas a "non-MP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to the MP protein, *e.g.*, a protein which is different from the MP protein and which is derived from the same or a different organism. Within the fusion protein, the term "operatively linked" is intended to indicate that the MP polypeptide and the non-MP polypeptide are fused in-frame to each other. The non-MP polypeptide can be fused to the N-terminus or C-terminus of the MP polypeptide. For example, in one embodiment the fusion protein is a GST-MP fusion protein in which the MP sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant MP proteins. In another embodiment, the fusion protein is an MP protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of an MP protein can be increased through use of a heterologous signal sequence.

Preferably, an MP chimeric or fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel *et al.* John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An MP-

encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the MP protein.

Homologues of the MP protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the MP protein. As used herein, the term "homologue" refers to a variant form of the MP protein which acts as an agonist or antagonist of the activity of the MP protein. An agonist of the MP protein can retain substantially the same, or a subset, of the biological activities of the MP protein. An antagonist of the MP protein can inhibit one or more of the activities of the naturally occurring form of the MP protein, by, for example, competitively binding to a downstream or upstream member of the MP cascade which includes the MP protein. Thus, the *C. glutamicum* MP protein and homologues thereof of the present invention may modulate the activity of one or more metabolic pathways in which MP proteins play a role in this microorganism.

In an alternative embodiment, homologues of the MP protein can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the MP protein for MP protein agonist or antagonist activity. In one embodiment, a variegated library of MP variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of MP variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential MP sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of MP sequences therein. There are a variety of methods which can be used to produce libraries of potential MP homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential MP sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, S.A. (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477.

In addition, libraries of fragments of the MP protein coding can be used to generate a variegated population of MP fragments for screening and subsequent selection of homologues of an MP protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an MP coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the MP protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of MP homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify MP homologues (Arkin and Yourvan (1992) *PNAS* 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

In another embodiment, cell based assays can be exploited to analyze a variegated MP library, using methods well known in the art.

D. Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of *C. glutamicum* and related organisms; mapping of genomes of organisms related to *C. glutamicum*; identification and localization of *C.*

glutamicum sequences of interest; evolutionary studies; determination of MP protein regions required for function; modulation of an MP protein activity; modulation of the activity of an MP pathway; and modulation of cellular production of a desired compound, such as a fine chemical.

The MP nucleic acid molecules of the invention have a variety of uses. First, they may be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof. Also, they may be used to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is not pathogenic to humans, it is related to species which are human pathogens, such as *Corynebacterium diphtheriae*. *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli secrete toxin which is disseminated through this lesion to distal susceptible tissues of the body. Degenerative changes brought about by the inhibition of protein synthesis in these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and spleen, result in the systemic pathology of the disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and the independent states of the former Soviet Union. An ongoing epidemic of diphtheria in the latter two regions has resulted in at least 5,000 deaths since 1990.

In one embodiment, the invention provides a method of identifying the presence or activity of *Cornyebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth as odd-numbered or even-numbered SEQ ID NOs, respectively, in the Sequence Listing) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules in *C. glutamicum*

are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

The nucleic acid and protein molecules of the invention may also serve as markers for specific regions of the genome. This has utility not only in the mapping of the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated with the DNA-binding protein. Those which bind the protein may be additionally probed with the nucleic acid molecules of the invention, preferably with readily detectable labels; binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *C. glutamicum*, and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds. Further, the nucleic acid molecules of the invention may be sufficiently homologous to the sequences of related species such that these nucleic acid molecules may serve as markers for the construction of a genomic map in related bacteria, such as *Brevibacterium lactofermentum*.

The MP nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The metabolic processes in which the molecules of the invention participate are utilized by a wide variety of prokaryotic and eukaryotic cells; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the enzyme. This type of determination is of value for protein engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

Manipulation of the MP nucleic acid molecules of the invention may result in the production of MP proteins having functional differences from the wild-type MP proteins. These proteins may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

The invention also provides methods for screening molecules which modulate the activity of an MP protein, either by interacting with the protein itself or a substrate or binding partner of the MP protein, or by modulating the transcription or translation of an MP nucleic acid molecule of the invention. In such methods, a microorganism expressing one or more MP proteins of the invention is contacted with one or more test compounds, and the effect of each test compound on the activity or level of expression of the MP protein is assessed.

When the desired fine chemical to be isolated from large-scale fermentative culture of *C. glutamicum* is an amino acid, a vitamin, a cofactor, a nutraceutical, a nucleotide, a nucleoside, or trehalose, modulation of the activity or efficiency of activity of one or more of the proteins of the invention by recombinant genetic mechanisms may directly impact the production of one of these fine chemicals. For example, in the case of an enzyme in a biosynthetic pathway for a desired amino acid, improvement in efficiency or activity of the enzyme (including the presence of multiple copies of the gene) should lead to an increased production or efficiency of production of that desired amino acid. In the case of an enzyme in a biosynthetic pathway for an amino acid whose synthesis is in competition with the synthesis of a desired amino acid, any decrease in the efficiency or activity of this enzyme (including deletion of the gene) should result in an increase in production or efficiency of production of the desired amino acid, due to decreased competition for intermediate compounds and/or energy. In the case of an enzyme in a degradation pathway for a desired amino acid, any decrease in efficiency or activity of the enzyme should result in a greater yield or efficiency of production of the desired product due to a decrease in its degradation. Lastly, mutagenesis of an enzyme involved in the biosynthesis of a desired amino acid such that this enzyme is no longer is capable of feedback inhibition should result in increased yields or efficiency of production of the desired amino acid. The same should apply to the biosynthetic and degradative enzymes of the invention involved in the metabolism of vitamins, cofactors, nutraceuticals, nucleotides, nucleosides and trehalose.

Similarly, when the desired fine chemical is not one of the aforementioned compounds, the modulation of activity of one of the proteins of the invention may still impact the yield and/or efficiency of production of the compound from large-scale culture of *C. glutamicum*. The metabolic pathways of any organism are closely

interconnected; the intermediate used by one pathway is often supplied by a different pathway. Enzyme expression and function may be regulated based on the cellular levels of a compound from a different metabolic process, and the cellular levels of molecules necessary for basic growth, such as amino acids and nucleotides, may critically affect the viability of the microorganism in large-scale culture. Thus, modulation of an amino acid biosynthesis enzyme, for example, such that it is no longer responsive to feedback inhibition or such that it is improved in efficiency or turnover may result in increased cellular levels of one or more amino acids. In turn, this increased pool of amino acids provides not only an increased supply of molecules necessary for protein synthesis, but also of molecules which are utilized as intermediates and precursors in a number of other biosynthetic pathways. If a particular amino acid had been limiting in the cell, its increased production might increase the ability of the cell to perform numerous other metabolic reactions, as well as enabling the cell to more efficiently produce proteins of all kinds, possibly increasing the overall growth rate or survival ability of the cell in large scale culture. Increased viability improves the number of cells capable of producing the desired fine chemical in fermentative culture, thereby increasing the yield of this compound. Similar processes are possible by the modulation of activity of a degradative enzyme of the invention such that the enzyme no longer catalyzes, or catalyzes less efficiently, the degradation of a cellular compound which is important for the biosynthesis of a desired compound, or which will enable the cell to grow and reproduce more efficiently in large-scale culture. It should be emphasized that optimizing the degradative activity or decreasing the biosynthetic activity of certain molecules of the invention may also have a beneficial effect on the production of certain fine chemicals from *C. glutamicum*. For example, by decreasing the efficiency of activity of a biosynthetic enzyme in a pathway which competes with the biosynthetic pathway of a desired compound for one or more intermediates, more of those intermediates should be available for conversion to the desired product. A similar situation may call for the improvement of degradative ability or efficiency of one or more proteins of the invention.

This aforementioned list of mutagenesis strategies for MP proteins to result in increased yields of a desired compound is not meant to be limiting; variations on these mutagenesis strategies will be readily apparent to one of ordinary skill in the art. By

these mechanisms, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated MP nucleic acid and protein molecules such that the yield, production, and/or efficiency of production of a desired compound is improved. This desired compound may be any natural product of *C. glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do not naturally occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patent applications, patents, published patent applications, Tables, and the sequence listing cited throughout this application are hereby incorporated by reference.

TABLE 1: Included Genes

Lysine biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1	2	RXA02229	GR00653	2793	3617	DIAMINOPIMELATE EPIMERASE (EC 5.1.1.7)
3	4	RXS02970				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
5	6	F RXA01009	GR00287	4714	5943	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
7	8	RXC02390				MEMBRANE SPANNING PROTEIN INVOLVED IN LYSINE METABOLISM
9	10	RXC01796				MEMBRANE ASSOCIATED PROTEIN INVOLVED IN LYSINE METABOLISM
11	12	RXC01207				CYTOSOLIC PROTEIN INVOLVED IN METABOLISM OF LYSINE AND THREONINE
13	14	RXC00657				TRANSCRIPTIONAL REGULATOR INVOLVED IN LYSINE METABOLISM
15	16	RXC00552				CYTOSOLIC PROTEIN INVOLVED IN LYSINE METABOLISM

Trehalose

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
17	18	RXN00351	VV0135	37078	38532	ALPHA,ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-FORMING) 56 KD SUBUNIT (EC 2.4.1.15)
19	20	F RXA00351	GR00066	1486	2931	ALPHA,ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-FORMING) 56 KD SUBUNIT (EC 2.4.1.15)
21	22	RXA00873	GR00241	3	758	trehalose synthase (EC 2.4.1.-)
23	24	RXA00891	GR00243	1005	4	trehalose synthase (EC 2.4.1.-)

Lysine biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
25	26	RXA00534	GR00137	4758	3496	ASPARTOKINASE ALPHA AND BETA SUBUNITS (EC 2.7.2.4)
27	28	RXA00533	GR00137	3469	2438	ASPARTATE-SEMIALDEHYDE DEHYDROGENASE (EC 1.2.1.11)
29	30	RXA02843	GR00842	543	4	2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (EC 2.3.1.117)
31	32	RXA02022	GR00613	2063	3169	SUCCINYL-DIAMINOPIMELATE DESUCCINYLASE (EC 3.5.1.18)
33	34	RXA00044	GR00007	3458	4393	DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52)
35	36	RXA00863	GR00236	896	1639	DIHYDRODIPICOLINATE REDUCTASE (EC 1.3.1.26)
37	38	RXA00864	GR00236	1694	2443	probable 2,3-dihydrodipicolinate N-C6-lyase (cyclizing) (EC 4.3.3.-) - Corynebacterium glutamicum
39	40	RXA02843	GR00842	543	4	2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (EC 2.3.1.117)
41	42	RXN00355	VV0135	31980	30961	MESO-DIAMINOPIMELATE D-DEHYDROGENASE
43	44	F RXA00352	GR00068	861	4	MESO-DIAMINOPIMELATE D-DEHYDROGENASE (EC 1.4.1.16)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
45	46	RXA00972	GR00274	3	1379	DIAMINOPIMELATE DECARBOXYLASE (EC 4.1.1.20)
47	48	RXA02653	GR00752	5237	7234	DIAMINOPIMELATE DECARBOXYLASE (EC 4.1.1.20)
49	50	RXA01393	GR00408	4249	3380	LYSINE EXPORT REGULATOR PROTEIN
51	52	RXA00241	GR00036	5443	6945	L-LYSINE TRANSPORT PROTEIN
53	54	RXA01394	GR00408	4320	5018	LYSINE EXPORTER PROTEIN
55	56	RXA00865	GR00236	2647	3549	DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52)
57	58	RXS02021				2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (EC 2.3.1.117)
59	60	RXS02157				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
61	62	RXC00733				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN LYSINE METABOLISM
63	64	RXC00861				PROTEIN INVOLVED IN LYSINE METABOLISM
65	66	RXC00866				ZN-DEPENDENT HYDROLASE INVOLVED IN LYSINE METABOLISM
67	68	RXC02095				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN LYSINE METABOLISM
69	70	RXC03185				PROTEIN INVOLVED IN LYSINE METABOLISM

Glutamate and glutamine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
71	72	RXN00367	VV0196	9744	14273	GLUTAMATE SYNTHASE [NADH] PRECURSOR (EC 1.4.1.14)
73	74	F RXA00007	GR00001	7107	8912	GLUTAMATE SYNTHASE (NADPH) LARGE CHAIN PRECURSOR (EC 1.4.1.13)
75	76	F RXA00364	GR00074	1296	4	GLUTAMATE SYNTHASE (NADPH) LARGE CHAIN PRECURSOR (EC 1.4.1.13)
77	78	F RXA00367	GR00075	1806	964	GLUTAMATE SYNTHASE (NADPH) LARGE CHAIN PRECURSOR (EC 1.4.1.13)
79	80	RXN00076	VV0154	2752	4122	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
81	82	F RXA00075	GR00012	2757	3419	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
83	84	RXN00198	VV0181	7916	7368	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
85	86	F RXA00198	GR00031	2	283	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
87	88	RXN00365	VV0196	14607	15233	GLUTAMATE SYNTHASE [NADPH] SMALL CHAIN (EC 1.4.1.13)
89	90	F RXA00365	GR00075	630	4	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
91	92	RXA00366	GR00075	961	605	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
93	94	RXA02072	GR00628	1259	2599	NADP-SPECIFIC GLUTAMATE DEHYDROGENASE (EC 1.4.1.4)
95	96	RXA00323	GR00057	3855	5192	GLUTAMINE SYNTHETASE (EC 6.3.1.2)
97	98	RXA00335	GR00057	19180	17750	GLUTAMINE SYNTHETASE (EC 6.3.1.2)
99	100	RXA00324	GR00057	5262	8396	GLUTAMATE-AMMONIA-LIGASE ADENYLYLTRANSFERASE (EC 2.7.7.42)
101	102	RXN03176	VV0332	2	862	GLUTAMINASE (EC 3.5.1.2)
103	104	F RXA02879	GR10017	2	862	GLUTAMINASE (EC 3.5.1.2)
105	106	RXA00278	GR00043	2612	1581	GLUTAMINE-BINDING PROTEIN PRECURSOR
107	108	RXA00727	GR00193	614	1525	GLUTAMINE-BINDING PERIPLASMIC PROTEIN PRECURSOR

Table 1 (continued)

Alanine and Aspartate and Asparagine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
109	110	RXA02139	GR00639	6739	4901	ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING) (EC 6.3.5.4)
111	112	RXN00116	VV0100	26974	25814	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
113	114	F RXA00116	GR00018	510	4	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
115	116	RXN00618	VV0135	10288	9182	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
117	118	F RXA00618	GR00163	213	746	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
119	120	F RXA00627	GR00164	854	1138	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
121	122	RXA02550	GR00729	1585	275	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
123	124	RXA02193	GR00645	1942	365	ASPARTATE AMMONIA-LYASE (EC 4.3.1.1)
125	126	RXA02432	GR00708	2669	1695	L-ASPARAGINASE (EC 3.5.1.1)
127	128	RXN03003	VV0138	680	6	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
129	130	RXN00508	VV0086	4701	5783	ALANINE RACEMASE (EC 5.1.1.1)
131	132	RXN00636	VV0135	20972	19944	ALANINE RACEMASE, BIOSYNTHETIC (EC 5.1.1.1)

beta-Alanine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
133	134	RXA02536	GR00726	8581	7826	BETA-UREIDOPROPIONASE (EC 3.5.1.6)
135	136	RXS00870				METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE (ACYLATING) (EC 1.2.1.27)
137	138	RXS02299				ASPARTATE 1-DECARBOXYLASE PRECURSOR (EC 4.1.1.11)

Glycine and serine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
139	140	RXA01561	GR00435	1113	2042	L-SERINE DEHYDRATASE (EC 4.2.1.13)
141	142	RXA01850	GR00525	481	1827	L-SERINE DEHYDRATASE (EC 4.2.1.13)
143	144	RXA00580	GR00156	7343	6042	SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1)
145	146	RXA01821	GR00515	10253	9876	SARCOSINE OXIDASE (EC 1.5.3.1)
147	148	RXN02263	VV0202	11783	12160	SARCOSINE OXIDASE (EC 1.5.3.1)
149	150	F RXA02263	GR00654	33454	33813	SARCOSINE OXIDASE (EC 1.5.3.1)
151	152	RXA02176	GR00641	11454	12581	PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52)
153	154	RXN02758	GR00766	5082	4648	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
155	156	F RXA02479	GR00717	393	4	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
157	158	F RXA02758	GR00766	5082	4648	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
159	160	F RXA02759	GR00768	5330	5220	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
161	162	RXA02501	GR00720	15041	13977	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
163	164	RXN03105	VV0074	15857	15423	SARCOSINE OXIDASE (EC 1.5.3.1)
165	166	RXS01130				D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
167	168	RXS03112				D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)

Table 1 (continued)

Threonine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
169	170	RXN00969	VV0149	12053	13387	HOMOSERINE DEHYDROGENASE (EC 1.1.1.3)
171	172	F RXA00974	GR00274	2623	3015	HOMOSERINE DEHYDROGENASE (EC 1.1.1.3)
173	174	RXA00970	GR00273	161	1087	HOMOSERINE KINASE (EC 2.7.1.39)
175	176	RXA00330	GR00057	12968	14410	THREONINE SYNTHASE (EC 4.2.99.2)
177	178	RXN00403	VV0086	70041	68911	HOMOSERINE O-ACETYLTRANSFERASE
179	180	F RXA00403	GR00088	723	1832	HOMOSERINE O-ACETYLTRANSFERASE (EC 2.3.1.11)
181	182	RXC01207				CYTOSOLIC PROTEIN INVOLVED IN METABOLISM OF LYSINE AND THREONINE
183	184	RXC00152				MEMBRANE ASSOCIATED PROTEIN INVOLVED IN THREONINE METABOLISM

Metabolism of methionine and S-adenosyl methionine

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
185	186	RXA00115	GR00017	5359	4313	HOMOSERINE O-ACETYLTRANSFERASE (EC 2.3.1.31)
187	188	RXN00403	VV0086	70041	68911	HOMOSERINE O-ACETYLTRANSFERASE
189	190	F RXA00403	GR00088	723	1832	HOMOSERINE O-ACETYLTRANSFERASE (EC 2.3.1.11)
191	192	RXS03158				CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
193	194	F RXA00254	GR00038	2404	1811	CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
195	196	RXA02532	GR00726	3085	2039	CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
197	198	RXS03159				CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
199	200	F RXA02768	GR00770	1919	2521	CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
201	202	RXA00216	GR00032	16286	15297	5-methyltetrahydrofolate-homocysteine methyltransferase (methionine synthetase)
203	204	RXN00402	VV0086	70787	70188	O-ACETYLHOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYLSERINE SULFHYDRYLASE (EC 4.2.99.8)
205	206	F RXA00402	GR00088	1	576	O-ACETYLHOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYLSERINE SULFHYDRYLASE (EC 4.2.99.8)
207	208	RXA00405	GR00089	3289	3801	O-ACETYLHOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYLSERINE SULFHYDRYLASE (EC 4.2.99.8)
209	210	RXA02197	GR00645	4552	4025	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
211	212	RXN02198	VV0302	9228	11726	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
213	214	F RXA02198	GR00646	2483	6	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
215	216	RXN03074	VV0042	2238	1741	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
217	218	F RXA02906	GR10044	1142	645	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
219	220	RXN00132	VV0124	3612	5045	ADENOSYLHOMOCYSTEINASE (EC 3.3.1.1)
221	222	F RXA00132	GR00020	7728	7624	ADENOSYLHOMOCYSTEINASE (EC 3.3.1.1)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
223	224	F RXA01371	GR00398	2339	3634	ADENOSYLHOMOCYSTEINASE (EC 3.3.1.1)
225	226	RXN02085				5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
227	228	F RXA02085	GR00629	3496	5295	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
229	230	F RXA02086	GR00629	5252	5731	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
231	232	RXN02648				5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
233	234	F RXA02648	GR00751	5254	4730	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
235	236	F RXA02658	GR00752	14764	15447	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
237	238	RXC02238				PROTEIN INVOLVED IN METABOLISM OF S-ADENOSYLMETHIONINE, PURINES AND PANTOTHENATE
239	240	RXC00128				EXPORTED PROTEIN INVOLVED IN METABOLISM OF PYRIDIMES AND ADENOSYLHOMOCYSTEINE

S-adenosyl methionine (SAM) Biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
241	242	RXA02240	GR00654	7160	8380	S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6)

Cysteine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
243	244	RXA00780	GR00206	1689	2234	SERINE ACETYLTRANSFERASE (EC 2.3.1.30)
245	246	RXA00779	GR00206	550	1482	CYSTEINE SYNTHASE (EC 4.2.99.8)
247	248	RXN00402	VV0086	70787	70188	O-ACETYLHOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYLSERINE SULFHYDRYLASE (EC 4.2.99.8)
249	250	F RXA00402	GR00088	1	576	O-ACETYLHOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYLSERINE SULFHYDRYLASE (EC 4.2.99.8)
251	252	RXS00405				O-ACETYLHOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYLSERINE SULFHYDRYLASE (EC 4.2.99.8)
253	254	RXC00164				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN CYSTEINE METABOLISM
255	256	RXC01191				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN CYSTEINE METABOLISM

Table 1 (continued)

Valine, leucine and isoleucine

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
257	258	RXA02646	GR00751	3856	2588	THREONINE DEHYDRATASE BIOSYNTHETIC (EC 4.2.1.16)
259	260	RXA00766	GR00204	5091	4249	BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE (EC 2.6.1.42)
261	262	RXN01690	VV0246	1296	196	BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE (EC 2.6.1.42)
263	264	F RXA01690	GR00473	1248	196	BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE (EC 2.6.1.42)
265	266	RXN01026	VV0143	9171	7513	3-ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT (EC 4.2.1.33)
267	268	F RXA01026	GR00294	1	1602	3-ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT (EC 4.2.1.33)
269	270	RXN01127	VV0157	4491	3472	3-ISOPROPYLMALATE DEHYDROGENASE (EC 1.1.1.85)
271	272	F RXA01132	GR00315	1349	1651	3-ISOPROPYLMALATE DEHYDROGENASE (EC 1.1.1.85)
273	274	RXN00536	VV0219	6128	7498	2-ISOPROPYLMALATE SYNTHASE (EC 4.1.3.12)
275	276	F RXA00536	GR00137	6128	7360	2-ISOPROPYLMALATE SYNTHASE (EC 4.1.3.1)
277	278	RXN02965	VV0143	7711	7121	3-ISOPROPYLMALATE DEHYDRATASE SMALL SUBUNIT (EC 4.2.1.33)
279	280	RXN01929	VV0127	47590	48402	3-METHYL-2-OXOBUTANOATE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.11) / DECARBOXYLASE (EC 4.1.1.44)
281	282	F RXA01929	GR00555	2766	1960	3-METHYL-2-OXOBUTANOATE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.11)
283	284	RXN01420	VV0122	15584	14643	4"-MYCAROSYL ISOVALERYL-COA TRANSFERASE (EC 2.-.-.-)
285	286	RXS01145				KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86)
287	288	F RXA01145	GR00321	1075	1530	KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86)

Arginine and proline metabolism

Enzymes of proline biosynthesis:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
289	290	RXA02375	GR00689	1449	223	GLUTAMATE 5-KINASE (EC 2.7.2.11)
291	292	RXN02382	VV0213	5162	3867	GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41)
293	294	F RXA02378	GR00690	624	16	GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41)
295	296	F RXA02382	GR00691	2493	1894	GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41)
297	298	RXA02499	GR00720	11883	12692	PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2)
299	300	RXS02157				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
301	302	RXS02262				ORNITHINE CYCLODEAMINASE (EC 4.3.1.12)
303	304	RXS02970				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
305	306	F RXA01009	GR00287	4714	5943	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)

Table 1 (continued)

Enzymes of proline degradation:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
307	308	RXN00023	VV0127	68158	64703	PROLINE DEHYDROGENASE (EC 1.5.99.8) / DELTA-1- PYRROLINE-5-CARBOXYLATE DEHYDROGENASE (EC 1.5.1.12)
309	310	F RXA00023	GR00003	2	454	PROLINE DEHYDROGENASE (EC 1.5.99.8) / DELTA-1- PYRROLINE-5-CARBOXYLATE DEHYDROGENASE (EC 1.5.1.12)
311	312	F RXA02284	GR00660	3028	5	PROLINE DEHYDROGENASE (EC 1.5.99.8) / DELTA-1- PYRROLINE-5-CARBOXYLATE DEHYDROGENASE (EC 1.5.1.12)
313	314	RXC02498				PROTEIN INVOLVED IN PROLINE METABOLISM

Synthesis of 3-Hydoxy-proline:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
315	316	RXA01491	GR00423	5337	4687	DNA FOR L-PROLINE 3-HYDROXYLASE, COMPLETE CDS

Enzymes of ornithine, arginine and spermidine metabolism:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
317	318	RXA02155	GR00640	1913	3076	GLUTAMATE N-ACETYLTRANSFERASE (EC 2.3.1.35) / AMINO-ACID ACETYLTRANSFERASE (EC 2.3.1.1)
319	320	RXA02156	GR00640	3125	4075	ACETYLGLUTAMATE KINASE (EC 2.7.2.8)
321	322	RXN02153	VV0122	14106	13327	N-ACETYL-GAMMA-GLUTAMYL-PHOSPHATE REDUCTASE (EC 1.2.1.38)
323	324	F RXA02153	GR00640	757	1536	N-ACETYLGLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE
325	326	RXA02154	GR00640	1536	1826	N-ACETYLGLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE
327	328	RXA02157	GR00640	4079	5251	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
329	330	RXS02970				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
331	332	F RXA01009	GR00287	4714	5943	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
333	334	RXA02158	GR00640	5268	6224	ORNITHINE CARBAMOYLTRANSFERASE (EC 2.1.3.3)
335	336	RXA02160	GR00640	6914	8116	ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5)
337	338	RXN02162	VV0122	6683	5253	ARGININOSUCCINATE LYASE (EC 4.3.2.1)
339	340	F RXA02161	GR00640	8180	8962	ARGININOSUCCINATE LYASE (EC 4.3.2.1)
341	342	F RXA02162	GR00640	8949	9611	ARGININOSUCCINATE LYASE (EC 4.3.2.1)
343	344	RXA02262	GR00654	32291	33436	ORNITHINE CYCLODEAMINASE (EC 4.3.1.12)
345	346	RXA00219	GR00032	19289	20230	SPERMIDINE SYNTHASE (EC 2.5.1.16)
347	348	RXA01508	GR00424	12652	14190	SPERMIDINE SYNTHASE (EC 2.5.1.16)
349	350	RXA01757	GR00498	2942	2142	PUTRESCINE OXIDASE (EC 1.4.3.10)
351	352	RXA02159	GR00640	6231	6743	ARGININE HYDROXIMATE RESISTANCE PROTEIN
353	354	RXN02154	VV0122	13327	13037	N-ACETYL-GAMMA-GLUTAMYL-PHOSPHATE REDUCTASE (EC 1.2.1.38)
355	356	RXS00147				CARBAMOYL-PHOSPHATE SYNTHASE SMALL CHAIN (EC 6.3.5.5)
357	358	RXS00905				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
359	360	RXS00906				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
361	362	RXS00907				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
363	364	RXS02001				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
365	366	RXS02101				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
367	368	RXS02234				CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN (EC 6.3.5.5)
369	370	F RXA02234	GR00654	1	3198	CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN (EC 6.3.5.5)
371	372	RXS02565				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
373	374	RXS02937				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)

Histidine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
375	376	RXA02194	GR00645	2897	2055	ATP PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.17)
377	378	RXA02195	GR00645	3186	2917	PHOSPHORIBOSYL-ATP PYROPHOSPHOHYDROLASE (EC 3.6.1.31)
379	380	RXA01097	GR00306	4726	4373	PHOSPHORIBOSYL-AMP CYCLOHYDROLASE (EC 3.5.4.19)
381	382	RXA01100	GR00306	7072	6335	PHOSPHORIBOSYLFORMIMINO-5-AMINOIMIDAZOLE CARBOXAMIDE RIBOTIDE ISOMERASE (EC 5.3.1.16)
383	384	RXA01101	GR00306	7726	7094	AMIDOTRANSFERASE HISH (EC 2.4.2.-)
385	386	RXN01657	VV0010	39950	39351	AMIDOTRANSFERASE HISH (EC 2.4.2.-)
387	388	F RXA01657	GR00460	2444	2944	AMIDOTRANSFERASE HISH (EC 2.4.2.-)
389	390	RXA01098	GR00306	5499	4726	HISF PROTEIN
391	392	RXN01104	VV0059	7037	6432	IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE (EC 4.2.1.19)
393	394	F RXA01104	GR00306	10927	10322	IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE (EC 4.2.1.19) / HISTIDINOL-PHOSPHATASE (EC 3.1.3.15)
395	396	RXN00446	VV0112	24181	23318	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
397	398	F RXA00446	GR00108	4	525	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
399	400	RXA01105	GR00306	12044	10947	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
401	402	RXA01106	GR00306	13378	12053	HISTIDINOL DEHYDROGENASE (EC 1.1.1.23)
403	404	RXC00930				PROTEIN INVOLVED IN HISTIDINE METABOLISM
405	406	RXC01096				PROTEIN INVOLVED IN HISTIDINE METABOLISM
407	408	RXC01656				PROTEIN INVOLVED IN HISTIDINE METABOLISM
409	410	RXC01158				MEMBRANE SPANNING PROTEIN INVOLVED IN HISTIDINE METABOLISM

Metabolism of aromatic amino acids

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
411	412	RXA02458	GR00712	3056	4345	3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE (EC 2.5.1.19)
413	414	RXA02790	GR00777	5806	6948	4-AMINO-4-DEOXYCHORISMATE LYASE (EC 4.-.-.-)
415	416	RXN00954	VV0247	3197	2577	ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.18)
417	418	F RXA00954	GR00263	3	590	ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.18)
419	420	RXN00957	VV0208	1211	2764	ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27)
421	422	F RXA00957	GR00264	3	1130	ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
423	424	RXA02687	GR00754	11306	12250	CHORISMATE MUTASE (EC 5.4.99.5) / PREPHENATE DEHYDRATASE (EC 4.2.1.51)
425	426	RXN01698	VV0134	11507	12736	CHORISMATE SYNTHASE (EC 4.6.1.4)
427	428	F RXA01698	GR00477	2	991	CHORISMATE SYNTHASE (EC 4.6.1.4)
429	430	RXA01095	GR00306	3603	2821	INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE (EC 4.1.1.48)
431	432	RXA00955	GR00263	586	2007	INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE (EC 4.1.1.48) / N-(5'-PHOSPHO-RIBOSYL)ANTHRANILATE ISOMERASE (EC 5.3.1.24)
433	434	RXA02814	GR00795	598	128	ISOCHORISMATE MUTASE
435	436	RXA00229	GR00033	1715	936	SHIKIMATE 5-DEHYDROGENASE (EC 1.1.1.25)
437	438	RXA02093	GR00629	12444	13247	SHIKIMATE 5-DEHYDROGENASE (EC 1.1.1.25)
439	440	RXA02791	GR00777	6968	7795	SHIKIMATE 5-DEHYDROGENASE (EC 1.1.1.25)
441	442	RXA01699	GR00477	984	1553	SHIKIMATE KINASE (EC 2.7.1.71)
443	444	RXA00952	GR00262	97	936	TRYPTOPHAN SYNTHASE ALPHA CHAIN (EC 4.2.1.20)
445	446	RXN00956	VV0247	1140	4	TRYPTOPHAN SYNTHASE BETA CHAIN (EC 4.2.1.20)
447	448	F RXA00956	GR00263	2027	3157	TRYPTOPHAN SYNTHASE BETA CHAIN (EC 4.2.1.20)
449	450	RXA00064	GR00010	2499	3776	TYROSINE AMINOTRANSFERASE (EC 2.6.1.5)
451	452	RXN00448	VV0112	33959	32940	PREPHENATE DEHYDROGENASE (EC 1.3.1.12)
453	454	F RXA00448	GR00109	3	668	PREPHENATE DEHYDROGENASE (EC 1.3.1.12)
455	456	F RXA00452	GR00110	854	1099	PREPHENATE DEHYDROGENASE (EC 1.3.1.12)
457	458	RXA00584	GR00156	11384	10260	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE (EC 4.1.2.15)
459	460	RXA00579	GR00156	5946	4087	PARA-AMINOBENZOATE SYNTHASE COMPONENT I (EC 4.1.3.-)
461	462	RXA00958	GR00264	1130	1753	PARA-AMINOBENZOATE SYNTHASE GLUTAMINE AMIDOTRANSFERASE COMPONENT II (EC 4.1.3.-) / ANTHRANILATE SYNTHASE COMPONENT II (EC 4.1.3.27)
463	464	RXN03007	VV0208	3410	3778	ANTHRANILATE SYNTHASE COMPONENT II (EC 4.1.3.27)
465	466	RXN02918	VV0086	25447	25887	TRYPTOPHAN SYNTHASE BETA CHAIN (EC 4.2.1.20)
467	468	RXN01116	VV0182	7497	6886	3-OXOADIPATE COA-TRANSFERASE SUBUNIT B (EC 2.8.3.6)
469	470	RXN01115	VV0182	10347	11099	3-OXOADIPATE ENOL-LACTONE HYDROLASE (EC 3.1.1.24) / 4-CARBOXYMUCONOLACTONE
471	472	RXS00116				ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
473	474	F RXA00116	GR00018	510	4	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
475	476	RXS00391				O-SUCCINYLBENZOIC ACID--COA LIGASE (EC 6.2.1.26)
477	478	RXS00393				1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE (EC 2.5.-.-)
479	480	F RXA00393	GR00086	4030	4911	1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE (EC 2.5.-.-)
481	482	RXS00446				HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
483	484	F RXA00446	GR00108	4	525	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
485	486	RXS00618				ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
487	488	F RXA00618	GR00163	213	746	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
489	490	F RXA00627	GR00164	854	1138	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
491	492	RXS01105				HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
493	494	RXS02315				2-SUCCINYL-6-HYDROXY-2,4-CYCLOHEXADIENE-1-CARBOXYLATE SYNTHASE / 2-OXOGLUTARATE DECARBOXYLASE (EC 4.1.1.71)
495	496	RXS02550				ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
497	498	RXS02319				NAPHTHOATE SYNTHASE (EC 4.1.3.36)
499	500	RXS02908				O-SUCCINYLBENZOIC ACID--COA LIGASE (EC 6.2.1.26)
501	502	RXS03003				ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
503	504	RXS03026				3-DEHYDROQUINATE DEHYDRATASE (EC 4.2.1.10)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
505	506	RXS03074				S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
507	508	RXC01434				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS AND RIBOFLAVIN
509	510	RXC02080				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS
511	512	RXC02789				CYTOSOLIC PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS
513	514	RXC02295				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS

Aminobutyrate metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
515	516	RXN03063	VV0035	666	1697	4-aminobutyrate aminotransferase (EC 2.6.1.19)
517	518	RXN02970	VV0021	4714	6081	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
519	520	F RXA01009	GR00287	4714	5943	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)

Vitamins, vitamin-like substances (cofactors), nutraceuticals

Thiamine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
521	522	RXA01551	GR00431	2945	4819	THIAMIN BIOSYNTHESIS PROTEIN THIC
523	524	RXA01019	GR00291	6	995	THIAMIN-MONOPHOSPHATE KINASE (EC 2.7.4.16)
525	526	RXA01352	GR00393	609	4	THIAMIN-PHOSPHATE PYROPHOSPHORYLASE (EC 2.5.1.3)
527	528	RXA01381	GR00403	3206	2286	THIF PROTEIN
529	530	RXA01360	GR00394	162	4	THIG PROTEIN
531	532	RXA01361	GR00394	983	378	THIG PROTEIN
533	534	RXA01208	GR00348	229	1032	HYDROXYETHYLTHIAZOLE KINASE (EC 2.7.1.50)
535	536	RXA00838	GR00227	1532	633	APBA PROTEIN
537	538	RXA02400	GR00699	1988	2557	THIAMIN BIOSYNTHESIS PROTEIN X
539	540	RXN01209	VV0270	1019	2446	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
541	542	F RXA01209	GR00348	1019	2446	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
543	544	RXN01413	VV0050	27306	27905	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
545	546	RXN01617	VV0050	22187	22858	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
547	548	F RXA01617	GR00451	2	616	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
549	550	RXS01807				PYRIDOXINE KINASE (EC 2.7.1.35)
551	552	RXC01021				CYTOSOLIC KINASE INVOLVED IN METABOLISM OF SUGARS AND THIAMIN

Table 1 (continued)

Riboflavin metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
553	554	RXN02246	VV0130	4388	5371	diaminohydroxyphosphoribosylaminopyrimidine deaminase (EC 3.5.4.26) / 5-amino-6-(5-phosphoribosylamino)uracil reductase (EC 1.1.1.193)
555	556	F RXA02246	GR00654	14299	15282	RIBG PROTEIN riboflavin-specific deaminase [EC:3.5.4.-]
557	558	RXA02247	GR00654	15286	15918	RIBOFLAVIN SYNTHASE ALPHA CHAIN (EC 2.5.1.9)
559	560	RXN02248	VV0130	6021	7286	GTP CYCLOHYDROLASE II (EC 3.5.4.25) / 3,4-DIHYDROXY-2-BUTANONE 4-PHOSPHATE SYNTHASE
561	562	F RXA02248	GR00654	15932	17197	RIBA PROTEIN - GTP cyclohydrolase II [EC:3.5.4.25]
563	564	RXN02249	VV0130	7301	7777	6,7-DIMETHYL-8-RIBITYLLUMAZINE SYNTHASE (EC 2.5.1.9)
565	566	F RXA02249	GR00654	17212	17688	RIBH PROTEIN - 6,7-dimethyl-8-ribityllumazine synthase (dmrl synthase, lumazine synthase, riboflavin synthase beta chain) [EC:2.5.1.9]
567	568	RXA02250	GR00654	17778	18356	RIBX PROTEIN
569	570	RXA01489	GR00423	3410	2388	RIBOFLAVIN KINASE (EC 2.7.1.26) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2)
571	572	RXA02135	GR00639	2809	1736	NICOTINATE-NUCLEOTIDE--DIMETHYLBENZIMIDAZOLE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.21)
573	574	RXA01489	GR00423	3410	2388	RIBOFLAVIN KINASE (EC 2.7.1.26) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2)
575	576	RXN01712	VV0191	8993	8298	RIBOFLAVIN-SPECIFIC DEAMINASE (EC 3.5.4.-)
577	578	F RXA01712	GR00484	2652	2152	RIBOFLAVIN-SPECIFIC DEAMINASE (EC 3.5.4.-)
579	580	RXN02384	VV0213	1386	679	ALPHA-RIBAZOLE-5'-PHOSPHATE PHOSPHATASE (EC 3.1.3.-)
581	582	RXN01560	VV0319	767	438	RIBOFLAVIN-SPECIFIC DEAMINASE (EC 3.5.4.-)
583	584	RXN00667	VV0109	1363	350	DRAP DEAMINASE
585	586	RXC01711				MEMBRANE SPANNING PROTEIN INVOLVED IN RIBOFLAVIN METABOLISM
587	588	RXC02380				PROTEIN INVOLVED IN RIBOFLAVIN METABOLISM
589	590	F RXA02380	GR00691	709	56	Predicted nucleotidyltransferases
591	592	RXC02921				CYTOSOLIC PROTEIN INVOLVED IN METABOLISM OF RIBOFLAVIN AND LIPIDS
593	594	RXC01434				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS AND RIBOFLAVIN

Vitamin B6 metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
595	596	RXA01807	GR00509	7868	7077	PYRIDOXINE KINASE (EC 2.7.1.35), pyridoxal/pyridoxine/pyridoxamine kinase

Table 1 (continued)

Nicotinate (nicotinic acid), nicotinamide, NAD and NADP

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
597	598	RXN02754	VV0084	22564	23901	NICOTINATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.11)
599	600	F RXA02405	GR00701	774	4	NICOTINATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.11)
601	602	F RXA02754	GR00766	3	488	NICOTINATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.11)
603	604	RXA02112	GR00632	5600	6436	NICOTINATE-NUCLEOTIDE PYROPHOSPHORYLASE (CARBOXYLATING) (EC 2.4.2.19)
605	606	RXA02111	GR00632	4310	5593	QUINOLINATE SYNTHETASE A

NAD Biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
607	608	RXA01073	GR00300	1274	2104	NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1)
609	610	RXN02754	VV0084	22564	23901	NICOTINATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.11)

Pantothenate and Coenzyme A (CoA) biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
611	612	RXA02299	GR00662	10452	10859	ASPARTATE 1-DECARBOXYLASE PRECURSOR (EC 4.1.1.11)
613	614	RXA01928	GR00555	1957	1121	PANTOATE--BETA-ALANINE LIGASE (EC 6.3.2.1)
615	616	RXN01929	VV0127	47590	48402	3-METHYL-2-OXOBUTANOATE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.11) / DECARBOXYLASE (EC 4.1.1.44)
617	618	F RXA01929	GR00555	2766	1960	3-METHYL-2-OXOBUTANOATE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.11)
619	620	RXA01521	GR00424	25167	25964	PANTOATE--BETA-ALANINE LIGASE (EC 6.3.2.1)
621	622	RXS01145				KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86)
623	624	F RXA01145	GR00321	1075	1530	KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86)
625	626	RXA02239	GR00654	5784	7049	DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN
627	628	RXA00581	GR00156	7572	8540	PANTOTHENATE KINASE (EC 2.7.1.33)
629	630	RXS00838				2-DEHYDROPANTOATE 2-REDUCTASE (EC 1.1.1.169)
631	632	RXC02238				PROTEIN INVOLVED IN METABOLISM OF S-ADENOSYLMETHIONINE, PURINES AND PANTOTHENATE

Biotin metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
633	634	RXN03058	VV0028	8272	8754	BIOTIN SYNTHESIS PROTEIN BIOC

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
635	636	F RXA02903	GR10040	11532	12014	BIOTIN SYNTHESIS PROTEIN BIOC
637	638	RXA00166	GR00025	3650	4309	BIOTIN SYNTHESIS PROTEIN BIOC
639	640	RXA00633	GR00166	3556	2288	ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (EC 2.6.1.62)
641	642	RXA00632	GR00166	2281	1610	DETHIOBIOTIN SYNTHETASE (EC 6.3.3.3)
643	644	RXA00295	GR00047	3407	4408	BIOTIN SYNTHASE (EC 2.8.1.6)
645	646	RXA00223	GR00032	23967	22879	NIFS PROTEIN
647	648	RXN00262	VV0123	16681	15608	NIFS PROTEIN
649	650	F RXA00262	GR00040	79	897	NIFS PROTEIN
651	652	RXN00435	VV0112	10037	11209	NIFS PROTEIN
653	654	F RXA00435	GR00100	3563	2949	NIFS PROTEIN
655	656	F RXA02801	GR00782	438	4	NIFS PROTEIN
657	658	RXA02516	GR00723	1724	2986	NIFS PROTEIN
659	660	RXA02517	GR00723	2989	3435	NIFU PROTEIN

Lipoic Acid

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
661	662	RXA01747	GR00495	2506	3549	LIPOIC ACID SYNTHETASE
663	664	RXA01746	GR00495	1614	2366	LIPOATE-PROTEIN LIGASE B (EC 6.-.-.-)
665	666	RXA02106	GR00632	472	1527	LIPOATE-PROTEIN LIGASE A (EC 6.-.-.-)
667	668	RXS01183				DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT (E2) OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61)
669	670	RXS01260				LIPOAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)
671	672	RXS01261				LIPOAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)

Folate biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
673	674	RXA02717	GR00758	18281	17400	5,10-METHYLENETETRAHYDROFOLATE REDUCTASE (EC 1.7.99.5)
675	676	RXN02027	VV0296	503	1003	5-FORMYLTETRAHYDROFOLATE CYCLO-LIGASE (EC 6.3.3.2)
677	678	F RXA02027	GR00616	500	6	5-FORMYLTETRAHYDROFOLATE CYCLO-LIGASE (EC 6.3.3.2)
679	680	RXA00106	GR00014	17469	17924	DIHYDROFOLATE REDUCTASE (EC 1.5.1.3)
681	682	RXN01321	VV0082	8868	9788	FORMYLTETRAHYDROFOLATE DEFORMYLASE (EC 3.5.1.10)
683	684	F RXA01321	GR00384	23	559	FORMYLTETRAHYDROFOLATE DEFORMYLASE (EC 3.5.1.10)
685	686	RXA00461	GR00116	428	1279	METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9)
687	688	RXA01514	GR00424	20922	21509	GTP CYCLOHYDROLASE I (EC 3.5.4.16)
689	690	RXA01516	GR00424	22360	22749	DIHYDRONEOPTERIN ALDOLASE (EC 4.1.2.25)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
691	692	RXA01515	GR00424	21513	22364	DIHYDROPTEROATE SYNTHASE (EC 2.5.1.15)
693	694	RXA02024	GR00613	4026	4784	DIHYDROPTEROATE SYNTHASE (EC 2.5.1.15)
695	696	RXA00106	GR00014	17469	17924	DIHYDROFOLATE REDUCTASE (EC 1.5.1.3)
697	698	RXA00989	GR00280	2903	1371	FOLYLPOLYGLUTAMATE SYNTHASE (EC 6.3.2.17)
699	700	RXA01517	GR00424	22752	23228	2-AMINO-4-HYDROXY-6-HYDROXYMETHYLDIHYDROPTERIDINE PYROPHOSPHOKINASE (EC 2.7.6.3)
701	702	RXA00579	GR00156	5946	4087	PARA-AMINOBENZOATE SYNTHASE COMPONENT I (EC 4.1.3.-)
703	704	RXA00958	GR00264	1130	1753	PARA-AMINOBENZOATE SYNTHASE GLUTAMINE AMIDOTRANSFERASE COMPONENT II (EC 4.1.3.-) / ANTHRANILATE SYNTHASE COMPONENT II (EC 4.1.3.27)
705	706	RXA02790	GR00777	5806	6948	4-AMINO-4-DEOXYCHORISMATE LYASE (EC 4.-.-.-)
707	708	RXA00106	GR00014	17469	17924	DIHYDROFOLATE REDUCTASE (EC 1.5.1.3)
709	710	RXN02198	VV0302	9228	11726	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
711	712	F RXA02198	GR00646	2483	6	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
713	714	RXN02085	VV0126	8483	10717	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE
715	716	F RXA02085	GR00629	3496	5295	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
717	718	F RXA02086	GR00629	5252	5731	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
719	720	RXN02648				5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
721	722	F RXA02648	GR00751	5254	4730	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
723	724	F RXA02658	GR00752	14764	15447	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
725	726	RXS02197				5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
727	728	RXC00988				PROTEIN INVOLVED IN FOLATE METABOLISM
729	730	RXC01518				MEMBRANE SPANNING PROTEIN INVOLVED IN FOLATE METABOLISM
731	732	RXC01942				ATP-BINDING PROTEIN INVOLVED IN FOLATE METABOLISM

Molybdopterin Metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
733	734	RXN02802	VV0112	17369	16299	MOLYBDOPTERIN BIOSYNTHESIS MOEB PROTEIN
735	736	F RXA02802	GR00783	7	474	MOLYBDOPTERIN BIOSYNTHESIS MOEB PROTEIN
737	738	F RXA00438	GR00103	362	796	MOLYBDOPTERIN BIOSYNTHESIS MOEB PROTEIN
739	740	RXN00437	VV0112	17824	17369	MOLYBDOPTERIN (MPT) CONVERTING FACTOR, SUBUNIT 2
741	742	F RXA00437	GR00103	3	362	MOLYBDOPTERIN (MPT) CONVERTING FACTOR, SUBUNIT 2
743	744	RXN00439	VV0112	18742	18275	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN
745	746	F RXA00439	GR00104	2	196	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN
747	748	F RXA00442	GR00105	830	1087	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
749	750	RXA00440	GR00104	196	654	MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN CB
751	752	RXN00441	VV0112	19942	18779	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN
753	754	F RXA00441	GR00105	2	793	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN
755	756	RXN02085				5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
757	758	F RXA02085	GR00629	3496	5295	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
759	760	F RXA02086	GR00629	5252	5731	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
761	762	RXN02648				5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
763	764	F RXA02648	GR00751	5254	4730	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
765	766	F RXA02658	GR00752	14764	15447	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
767	768	RXA01516	GR00424	22360	22749	DIHYDRONEOPTERIN ALDOLASE (EC 4.1.2.25)
769	770	RXA01515	GR00424	21513	22364	DIHYDROPTEROATE SYNTHASE (EC 2.5.1.15)
771	772	RXA02024	GR00613	4026	4784	DIHYDROPTEROATE SYNTHASE (EC 2.5.1.15)
773	774	RXA01719	GR00488	1264	704	MOLYBDOPTERIN-GUANINE DINUCLEOTIDE BIOSYNTHESIS PROTEIN A
775	776	RXA01720	GR00488	2476	1268	MOLYBDOPTERIN BIOSYNTHESIS MOEA PROTEIN
777	778	RXS03223				MOLYBDOPTERIN BIOSYNTHESIS MOEA PROTEIN
779	780	F RXA01970	GR00568	2	1207	MOLYBDOPTERIN BIOSYNTHESIS MOEA PROTEIN
781	782	RXA02629	GR00748	1274	690	MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN
783	784	RXA02318	GR00665	9684	9962	(D90909) pterin-4a-carbinolamine dehydratase [Synechocystis sp.]
785	786	RXA01517	GR00424	22752	23228	2-AMINO-4-HYDROXY-6-HYDROXYMETHYLDIHYDROPTERIDINE PYROPHOSPHOKINASE (EC 2.7.6.3)
787	788	RXN01304	VV0148	4449	4934	MOLYBDOPTERIN BIOSYNTHESIS MOG PROTEIN
789	790	RXS02556				FLAVOHEMOPROTEIN / DIHYDROPTERIDINE REDUCTASE (EC 1.6.99.7)
791	792	RXS02560				OXYGEN-INSENSITIVE NAD(P)H NITROREDUCTASE (EC 1.-.-.-) / DIHYDROPTERIDINE REDUCTASE (EC1.6.99.7)

Vitamin B_{12}, porphyrins and heme metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
793	794	RXA00382	GR00082	2752	1451	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE (EC 5.4.3.8)
795	796	RXA00156	GR00023	10509	9400	FERROCHELATASE (EC 4.99.1.1)
797	798	RXA00624	GR00163	7910	8596	FERROCHELATASE (EC 4.99.1.1)
799	800	RXA00306	GR00051	2206	1274	HEMK PROTEIN
801	802	RXA00884	GR00242	10137	11276	OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.-.-.-)
803	804	RXN02503	VV0007	22456	22854	PORPHOBILINOGEN DEAMINASE (EC 4.3.1.8)
805	806	F RXA02503	GR00720	16906	17340	PORPHOBILINOGEN DEAMINASE (EC 4.3.1.8)
807	808	RXA00377	GR00081	1427	306	UROPORPHYRINOGEN DECARBOXYLASE (EC 4.1.1.37)
809	810	RXN02504	VV0007	22805	23362	PORPHOBILINOGEN DEAMINASE (EC 4.3.1.8)
811	812	F RXA02504	GR00720	17379	17816	PORPHOBILINOGEN DEAMINASE (EC 4.3.1.8)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
813	814	RXN01162	VV0088	1849	524	PRECORRIN-6Y METHYLASE (EC 2.1.1.-)
815	816	F RXA01162	GR00330	1248	4	PRECORRIN-6Y METHYLASE (EC 2.1.1.-)
817	818	RXA01692	GR00474	1498	749	UROPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107)
819	820	RXN00371	VV0226	4180	5973	UROPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107) / UROPORPHYRINOGEN-III SYNTHASE (EC 4.2.1.75)
821	822	F RXA00371	GR00078	929	6	UROPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107) / UROPORPHYRINOGEN-III SYNTHASE (EC 4.2.1.75)
823	824	F RXA00374	GR00079	1102	371	UROPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107) / UROPORPHYRINOGEN-III SYNTHASE (EC 4.2.1.75)
825	826	RXN00383	VV0223	4206	2863	PROTOPORPHYRINOGEN OXIDASE (EC 1.3.3.4)
827	828	F RXA00376	GR00081	287	6	PROTOPORPHYRINOGEN OXIDASE (EC 1.3.3.4)
829	830	F RXA00383	GR00082	3876	2863	PROTOPORPHYRINOGEN OXIDASE (EC 1.3.3.4)
831	832	RXA01253	GR00365	2536	1787	COBYRIC ACID SYNTHASE
833	834	RXA02134	GR00639	1721	801	COBALAMIN (5'-PHOSPHATE) SYNTHASE
835	836	RXA02135	GR00639	2809	1736	NICOTINATE-NUCLEOTIDE--DIMETHYLBENZIMIDAZOLE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.21)
837	838	RXA02136	GR00639	3362	2841	COBINAMIDE KINASE / COBINAMIDE PHOSPHATE GUANYLYLTRANSFERASE
839	840	RXN03114	VV0088	1	552	COBG PROTEIN (EC 1.-.-.-)
841	842	RXN01810	VV0082	1739	663	HEMIN-BINDING PERIPLASMIC PROTEIN HMUT PRECURSOR
843	844	RXS03205				HEMK PROTEIN
845	846	F RXA00306				HEMK PROTEIN
847	848	RXC01715				CYTOSOLIC PROTEIN INVOLVED IN PORPHYRIN METABOLISM

Vitamin C precursors

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
849	850	RXN00420	VV0112	2511	1048	L-GULONOLACTONE OXIDASE (EC 1.1.3.8)
851	852	F RXA00420	GR00096	2	541	L-GULONOLACTONE OXIDASE (EC 1.1.3.8)
853	854	F RXA00426	GR00097	1737	2258	L-GULONOLACTONE OXIDASE (EC 1.1.3.8)
855	856	RXN00708	VV0005	4678	3872	2,5-DIKETO-D-GLUCONIC ACID REDUCTASE (EC 1.1.1.-)
857	858	F RXA00708	GR00185	2030	1359	2,5-DIKETO-D-GLUCONIC ACID REDUCTASE (EC 1.1.1.-)
859	860	RXA02373	GR00688	1540	626	2,5-DIKETO-D-GLUCONIC ACID REDUCTASE (EC 1.1.1.-)
861	862	RXS00389				oxoglutarate semialdehyde dehydrogenase (EC 1.2.1.-)
863	864	RXS00419				ACETOACETYL-COA REDUCTASE (EC 1.1.1.36)
865	866	RXC00416				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF VITAMIN C PRECURSORS
867	868	RXC02206				OXIDOREDUCTASE INVOLVED IN METABOLISM OF VITAMIN C PRECURSORS

Vitamin K2

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
869	870	RXS03074				S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
871	872	F RXA02906	GR10044	1142	645	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
873	874	RXA02315	GR00665	8011	6383	2-SUCCINYL-6-HYDROXY-2,4-CYCLOHEXADIENE-1-CARBOXYLATE SYNTHASE /2-OXOGLUTARATE DECARBOXYLASE (EC 4.1.1.71)
875	876	RXA02319	GR00665	9977	10933	NAPHTHOATE SYNTHASE (EC 4.1.3.36)
877	878	RXS00393				1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE (EC 2.5.-.-)
879	880	F RXA00393	GR00086	4030	4911	1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE (EC 2.5.-.-)
881	882	RXA00391	GR00086	2031	2750	O-SUCCINYLBENZOIC ACID--COA LIGASE (EC 6.2.1.26)
883	884	RXS02908				O-SUCCINYLBENZOIC ACID--COA LIGASE (EC 6.2.1.26)

Ubiquinone biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
885	886	RXA00997	GR00283	2389	1808	3-DEMETHYLUBIQUINONE-9 3-METHYLTRANSFERASE (EC 2.1.1.64)
887	888	RXA02189	GR00642	986	249	3-DEMETHYLUBIQUINONE-9 3-METHYLTRANSFERASE (EC 2.1.1.64)
889	890	RXA02311	GR00665	3073	2384	3-DEMETHYLUBIQUINONE-9 3-METHYLTRANSFERASE (EC 2.1.1.64)
891	892	RXN02912	VV0135	13299	12547	UBIQUINONE/MENAQUINONE BIOSYNTHESIS METHLYTRANSFERASE UBIE (EC 2.1.1.-)
893	894	RXS00998				COMA OPERON PROTEIN 2

Purines and Pyrimidines and other Nucleotides

Regulation of purine and pyrimidine biosynthesis pathways

Purine metabolism

Purine Biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
895	896	RXA01215	GR00352	1187	213	RIBOSE-PHOSPHATE PYROPHOSPHOKINASE, PRPP synthetase (EC 2.7.6.1)
897	898	RXN00558	VV0103	8235	9581	AMIDOPHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.14)
899	900	F RXA00558	GR00148	61	501	AMIDOPHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.14)
901	902	RXN00626	VV0135	11624	10362	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (EC 6.3.4.13)
903	904	F RXA00629	GR00165	1450	1713	PHOSPHORIBOSYLAMINE-GLYCINE LIGASE (EC 6.3.4.13)
905	906	F RXA00626	GR00164	1	780	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE, GARS (EC 6.3.4.13)
907	908	RXA02623	GR00746	4875	4285	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (EC 6.3.4.13) / PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE (EC 6.3.3.1) / PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE (EC 2.1.2.2)
909	910	RXA01442	GR00418	10277	9054	PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE 2 (EC 2.1.2.-)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
911	912	RXN00537	VV0103	3351	5636	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
913	914	F RXA02805	GR00786	54	638	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
915	916	F RXA00537	GR00138	23	697	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
917	918	F RXA00561	GR00150	2	280	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
919	920	RXA00541	GR00139	2269	2937	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
921	922	RXA00620	GR00163	3049	3939	PHOSPHORIBOSYLAMIDOIMIDAZOLE-SUCCINOCARBOXAMIDE SYNTHASE (EC 6.3.2.6)
923	924	RXN00770	VV0103	9614	10783	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE (EC 6.3.3.1)
925	926	F RXA00557	GR00147	15	818	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE (EC 6.3.3.1)
927	928	F RXA00770	GR00204	7809	7495	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE (EC 6.3.3.1)
929	930	RXN02345	VV0078	4788	5984	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE ATPASE SUBUNIT (EC 4.1.1.21)
931	932	F RXA02345	GR00676	1534	725	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE ATPASE SUBUNIT (EC 4.1.1.21)
933	934	RXN02350	VV0078	8369	8863	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE CATALYTIC SUBUNIT (EC 4.1.1.21)
935	936	F RXA02346	GR00677	127	5	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE CATALYTIC SUBUNIT (EC 4.1.1.21)
937	938	F RXA02350	GR00678	1120	911	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE CATALYTIC SUBUNIT (EC 4.1.1.21)
939	940	RXA01087	GR00304	498	1373	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE (EC 4.1.1.21)
941	942	RXA00619	GR00163	793	2220	ADENYLOSUCCINATE LYASE (EC 4.3.2.2)
943	944	RXA02622	GR00746	4274	2715	PHOSPHORIBOSYLAMINOIMIDAZOLECARBOXAMIDE FORMYLTRANSFERASE (EC 2.1.2.3) / IMP CYCLOHYDROLASE (EC 3.5.4.10)

GMP, GDP, AMP and ADP synthesis, from inosine-5'-monophosphate (IMP)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
945	946	RXN00488	VV0086	19066	20583	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
947	948	F RXA00492	GR00122	1171	1644	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
949	950	F RXA00488	GR00121	1	534	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
951	952	RXA02469	GR00715	1927	497	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
953	954	RXN00487	VV0086	23734	25302	GMP SYNTHASE [GLUTAMINE-HYDROLYZING] (EC 6.3.5.2)
955	956	F RXA00487	GR00120	712	2097	GMP SYNTHASE (EC 6.3.4.1)
957	958	RXA02237	GR00654	4577	5146	GUANYLATE KINASE (EC 2.7.4.8)
959	960	RXA01446	GR00418	17765	16476	ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4)
961	962	RXA00619	GR00163	793	2220	ADENYLOSUCCINATE LYASE (EC 4.3.2.2)
963	964	RXA00688	GR00179	10443	10985	ADENYLATE KINASE (EC 2.7.4.3)
965	966	RXA00266	GR00040	3769	3362	NUCLEOSIDE DIPHOSPHATE KINASE (EC 2.7.4.6)

Table 1 (continued)

GMP/AMP degrading activities

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
967	968	RXA00489	GR00121	654	1775	GMP REDUCTASE (EC 1.6.6.8)
969	970	RXN02281	VV0152	1893	3323	AMP NUCLEOSIDASE (EC 3.2.2.4)
971	972	F RXA02281	GR00659	1101	34	AMP NUCLEOSIDASE (EC 3.2.2.4)

Pyrimidine metabolism

Pyrimidine biosynthesis de novo:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
973	974	RXA00147	GR00022	9722	10900	CARBAMOYL-PHOSPHATE SYNTHASE SMALL CHAIN (EC 6.3.5.5)
975	976	RXA00145	GR00022	7258	8193	ASPARTATE CARBAMOYLTRANSFERASE CATALYTIC CHAIN (EC 2.1.3.2)
977	978	RXA00146	GR00022	8249	9589	DIHYDROOROTASE (EC 3.5.2.3)
979	980	RXA02208	GR00647	2	1003	DIHYDROOROTATE DEHYDROGENASE (EC 1.3.3.1)
981	982	RXA01660	GR00462	591	1142	OROTATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.10)
983	984	RXA02235	GR00654	3207	4040	OROTIDINE 5'-PHOSPHATE DECARBOXYLASE (EC 4.1.1.23)
985	986	RXN01892	VV0150	3020	3748	URIDYLATE KINASE (EC 2.7.4.-)
987	988	F RXA01892	GR00542	47	775	URIDYLATE KINASE (EC 2.7.4.-)
989	990	RXA00105	GR00014	16672	17346	THYMIDYLATE SYNTHASE (EC 2.1.1.45)
991	992	RXA00131	GR00020	7621	7013	THYMIDYLATE KINASE (EC 2.7.4.9)
993	994	RXA00266	GR00040	3769	3362	NUCLEOSIDE DIPHOSPHATE KINASE (EC 2.7.4.6)
995	996	RXA00718	GR00188	4576	5283	CYTIDYLATE KINASE (EC 2.7.4.14)
997	998	RXA01599	GR00447	8780	10441	CTP SYNTHASE (EC 6.3.4.2)
999	1000	RXN02234	VV0134	24708	28046	CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN (EC 6.3.5.5)
1001	1002	F RXA02234	GR00654	1	3198	CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN (EC 6.3.5.5)
1003	1004	RXN00450	VV0112	34491	34814	CYTOSINE DEAMINASE (EC 3.5.4.1)
1005	1006	F RXA00450	GR00110	322	5	CYTOSINE DEAMINASE (EC 3.5.4.1)
1007	1008	RXN02272	VV0020	15566	16810	CYTOSINE DEAMINASE (EC 3.5.4.1)
1009	1010	F RXA02272	GR00655	6691	7935	CREATININE DEAMINASE (EC 3.5.4.21)
1011	1012	RXN03004	VV0237	1862	2341	DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13)
1013	1014	RXN03137	VV0129	9680	9579	THYMIDYLATE SYNTHASE (EC 2.1.1.45)
1015	1016	RXN03171	VV0328	568	1080	URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9)
1017	1018	F RXA02857	GR10003	570	1082	URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9)

Table 1 (continued)

Purine and pyrimidine base, nucleoside and nucleotide salvage, interconversion, reduction and degradation:

Purines:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1019	1020	RXA02771	GR00772	1329	1883	ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7)
1021	1022	RXA01512	GR00424	17633	18232	HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8)
1023	1024	RXA02031	GR00618	3820	3347	XANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.22)
1025	1026	RXA00981	GR00276	3388	4017	GTP PYROPHOSPHOKINASE (EC 2.7.6.5)
1027	1028	RXN02772	VV0171	2045	1011	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
1029	1030	F RXA02772	GR00772	1962	2741	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
1031	1032	F RXA02773	GR00772	2741	2902	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
1033	1034	RXA01835	GR00517	3147	3677	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
1035	1036	RXA01483	GR00422	19511	18240	DEOXYGUANOSINETRIPHOSPHATE TRIPHOSPHOHYDROLASE (EC 3.1.5.1)
1037	1038	RXN01027	VV0143	5761	6768	DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
1039	1040	F RXA01024	GR00293	661	5	DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
1041	1042	F RXA01027	GR00294	2580	2347	DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
1043	1044	RXA01528	GR00425	5653	5126	DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
1045	1046	RXA00072	GR00012	446	6	PHOSPHOADENOSINE PHOSPHOSULFATE REDUCTASE (EC 1.8.99.4)
1047	1048	RXA01878	GR00537	1239	2117	DIMETHYLADENOSINE TRANSFERASE (EC 2.1.1.-)
1049	1050	RXN02281	VV0152	1893	3323	AMP NUCLEOSIDASE (EC 3.2.2.4)
1051	1052	F RXA02281	GR00659	1101	34	AMP NUCLEOSIDASE (EC 3.2.2.4)
1053	1054	RXN01240	VV0090	30442	29420	GTP PYROPHOSPHOKINASE (EC 2.7.6.5)
1055	1056	RXN02008	VV0171	1138	5	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)

Pyrimdine and purine metabolism:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1057	1058	RXN01940	VV0120	10268	9333	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (EC 3.2.2.1)
1059	1060	F RXA01940	GR00557	3	581	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (EC 3.2.2.1)
1061	1062	RXA02559	GR00731	5418	6320	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (EC 3.2.2.1)
1063	1064	RXA02497	GR00720	10059	10985	EXOPOLYPHOSPHATASE (EC 3.6.1.11)
1065	1066	RXN01079	VV0084	38084	35982	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA CHAIN (EC 1.17.4.1)
1067	1068	F RXA01079	GR00301	693	4	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA CHAIN (EC 1.17.4.1)
1069	1070	F RXA01084	GR00302	3402	2062	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA CHAIN (EC 1.17.4.1)
1071	1072	RXN01920	VV0084	32843	31842	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE 2 BETA CHAIN (EC 1.17.4.1)
1073	1074	F RXA01920	GR00550	1321	908	RIBONUCLEOTIDE REDUCTASE SUBUNIT R2F
1075	1076	RXA01080	GR00301	1240	797	NRDI PROTEIN
1077	1078	RXA00867	GR00237	1	627	POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8)
1079	1080	RXA01416	GR00413	2	631	POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8)
1081	1082	RXA01486	GR00423	660	4	POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1083	1084	RXA01678	GR00467	7162	7689	2',3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE (EC 3.1.4.16)
1085	1086	RXA01679	GR00467	7729	8964	2',3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE (EC 3.1.4.16)
1087	1088	RXN01488	VV0139	39842	40789	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (EC 3.2.2.1)
1089	1090	RXC00540				CYTOSOLIC PROTEIN INVOLVED IN PURINE METABOLISM
1091	1092	RXC00560				PROTEIN INVOLVED IN PURINE METABOLISM
1093	1094	RXC01088				CYTOSOLIC PROTEIN INVOLVED IN PURINE METABOLISM
1095	1096	RXC02624				MEMBRANE SPANNING PROTEIN INVOLVED IN PURINE METABOLISM
1097	1098	RXC02665				PROTEIN INVOLVED IN PURINE METABOLISM
1099	1100	RXC02770				LIPOPROTEIN INVOLVED IN PURINE METABOLISM
1101	1102	RXC02238				PROTEIN INVOLVED IN METABOLISM OF S-ADENOSYLMETHIONINE, PURINES AND PANTOTHENATE
1103	1104	RXC01946				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN PURINE METABOLISM

Pyrimdines:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1105	1106	RXN03171	VV0328	568	1080	URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9)
1107	1108	F RXA02857	GR10003	570	1082	URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9)
1109	1110	RXN00450	VV0112	34491	34814	CYTOSINE DEAMINASE (EC 3.5.4.1)
1111	1112	F RXA00450	GR00110	322	5	CYTOSINE DEAMINASE (EC 3.5.4.1)
1113	1114	RXA00465	GR00117	337	828	CYTOSINE DEAMINASE (EC 3.5.4.1)
1115	1116	RXA00717	GR00188	3617	4576	RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70)
1117	1118	RXA01894	GR00542	1622	2476	PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.41)
1119	1120	RXA02536	GR00726	8581	7826	BETA-UREIDOPROPIONASE (EC 3.5.1.6)
1121	1122	RXN01209	VV0270	1019	2446	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
1123	1124	F RXA01209	GR00348	1019	2446	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
1125	1126	RXN01617	VV0050	22187	22858	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
1127	1128	F RXA01617	GR00451	2	616	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
1129	1130	RXC01600				CYTOSOLIC PROTEIN INVOLVED IN PYRIMIDINE METABOLISM
1131	1132	RXC01622				CYTOSOLIC PROTEIN INVOLVED IN PYRIMIDINE METABOLISM
1133	1134	RXC00128				EXPORTED PROTEIN INVOLVED IN METABOLISM OF PYRIDIMES AND ADENOSYLHOMOCYSTEINE
1135	1136	RXC01709				CYTOSOLIC PROTEIN INVOLVED IN PYRIMIDINE METABOLISM
1137	1138	RXC02207				EXPORTED PROTEIN INVOLVED IN PYRIMIDINE METABOLISM

Table 1 (continued)

Sugars

Trehalose

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1139	1140	RXA00347	GR00065	246	1013	TREHALOSE-PHOSPHATASE (EC 3.1.3.12)
1141	1142	RXN01239	VV0090	32921	30489	maltooligosyltrehalose synthase
1143	1144	F RXA01239	GR00358	5147	7579	maltooligosyltrehalose synthase
1145	1146	RXA02645	GR00751	714	2543	maltooligosyltrehalose trehalohydrolase
1147	1148	RXN02355	VV0051	735	4	TREHALOSE/MALTOSE BINDING PROTEIN
1149	1150	RXN02909	VV0135	38532	39017	Hypothetical Trehalose-Binding Protein
1151	1152	RXS00349				Hypothetical Trehalose Transport Protein
1153	1154	RXS03183				TREHALOSE/MALTOSE BINDING PROTEIN
1155	1156	RXC00874				TRANSMEBRANE PROTEIN INVOLVED IN TREHALOSE METABOLISM

TABLE 2 – Excluded Genes

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvat corboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-aminino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," *Biochem. Biophys. Res. Commun.*, 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," *Appl. Microbiol. Biotechnol.*, 51(2):223-228 (1999)
AB018530	dtsR		Kimura, E. et al. "Molecular cloning of a novel gene, dtsR, which rescues the detergent sensitivity of a mutant derived from *Brevibacterium lactofermentum*," *Biosci. Biotechnol. Biochem.*, 60(10):1565-1570 (1996)
AB018531	dtsR1; dtsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkt	transketolase	
AB024708	gltB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamolytransferase	
AF036932	aroD	3-dehydroquinate dehydratase	
AF038548	pyc	Pyruvate carboxylase	

Table 2 (continued)

AF038651	dciAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the Corynebacterium glutamicum rel gene in (p)ppGpp metabolism," *Microbiology,* 144:1853-1862 (1998)
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in Corynebacterium glutamicum," *Mol. Cells.,* 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinate synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the Corynebacterium glutamicum panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in Escherichia coli," *Appl. Environ. Microbiol.,* 65(4)1530-1539 (1999)
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinate synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		

Table 2 (continued)

AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," *J. Bacteriol.*, 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete[i])	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with Corynebacterium glutamicum," *J. Bacteriol.*, 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY, glnB, glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzmye); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in Corynebacterium glutamicum; Isolation of genes involved in biochemical characterization of corresponding proteins," *FEMS Microbiol.*, 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol aceteyl transferase	
AJ224946	mqo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from Corynebacterium glutamicum," *Eur. J. Biochem.*, 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of Corynebacterium glutamicum: The channel is formed by a low molecular mass polypeptide," *Biochemistry*, 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes et al."Isolation and characterization of IS31831, a transposable element from Corynebacterium glutamicum," *Mol. Microbiol.*, 11(4):739-746 (1994)
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the Corynebacterium glutamicum (Brevibacterium lactofermentum AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," *Microbiology*, 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-thereonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-thereonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87

Table 2 (continued)

E01377		Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937		Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040		Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041		Desthiobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307		Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376		Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377		Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484		Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108		Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112		Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93
E05776		Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779		Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110		Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111		Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146		Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825		Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94

Table 2 (continued)

E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membraneous protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08649		Aspartase	Kohama, K. et al "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-trypophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97

Table 2 (continued)

E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L01508	IlvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," *J. Bacteriol.*, 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," *FEMS Microbiol. Lett.*, 107:223-230 (1993)
L09232	IlvB; ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase	Keilhauer, C. et al. "Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," *J. Bacteriol.*, 175(17):5595-5603 (1993)
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in Escherichia coli and homology to enzymes II from enteric bacteria," *PNAS USA*, 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," *FEMS Microbiol. Lett.*, 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum," *J. Microbiol. Biotechnol.*, 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from Corynebacterium glutamicum," *Appl. Environ. Microbiol.*, 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	
L35906	dtxr	Diphtheria toxin repressor	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the Corynebacterium diphtheriae dtxR from Brevibacterium lactofermentum," *J. Bacteriol.*, 177(2):465-467 (1995)
M13774		Prephenate dehydratase	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the Corynebacterium glutamicum pheA gene," *J. Bacteriol.*, 167:695-702 (1986)
M16175	5S rRNA		Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 56 rRNA sequences," *J. Bacteriol.*, 169:1801-1806 (1987)
M16663	trpE	Anthranilate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," *Gene*, 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3'end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," *Gene*, 52:191-200 (1987)

Table 2 (continued)

M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of Corynebacterium glutamicum ATCC13032," *Gene*, 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," *J. Gen. Microbiol.*, 138:1167-1175 (1992)
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," *J. Gen. Microbiol.*, 138:1167-1175 (1992)
M89931	aecD; brnQ; yhbw	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbw	Rossol, I. et al. "The Corynebacterium glutamicum aecD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," *J. Bacteriol.*, 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in Corynebacterium glutamicum ATCC 13032 is directed by the brnQ gene product," *Arch. Microbiol.*, 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of Corynebacterium glutamicum: identification of a mutation in the trp leader sequence," *Appl. Environ. Microbiol.*, 59(3):791-799 (1993)
U11545	trpD	Anthranilate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the Corynebacterium glutamicum ATCC 21850 tpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cglIM; cglIR; clglIR	Putative type II 5-cytosoine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from Corynebacterium glutamicum ATCC 13032 and analysis of its role in intergeneric conjugation with Escherichia coli," *J. Bacteriol.*, 176(23):7309-7319 (1994); Schafer, A. et al. "The Corynebacterium glutamicum cglIM gene encoding a 5-cytosine in an McrBC-deficient Escherichia coli strain," *Gene*, 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," *J. Bacteriol.*, 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," *J. Bacteriol.*, 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?;gamma glutamyl kinase;similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," *J. Bacteriol.*, 178(15):4412-4419 (1996)

Table 2 (continued)

U31281	bioB	Biotin synthase	Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of Methylobacillus flagellatum and Corynebacterium glutamicum," *Gene,* 175:15-22 (1996)
U35023	thtR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A Corynebacterium glutamicum gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," *Arch. Microbiol.,* 166(2);76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A Corynebacterium glutamicum gene conferring multidrug resistance in the heterologous host Escherichia coli," *J. Bacteriol.,* 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'5''-aminoglycoside phosphotransferase	
U89648		Corynebacterium glutamicum unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the Brevibacterium lactofermentum tryptophan operon," *Nucleic Acids Res.,* 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the lysA gene of Corynebacterium glutamicum and possible mechanisms for modulation of its expression," *Mol. Gen. Genet.,* 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of Corynebacterium glutamicum: Molecular cloning, nucleotide sequence, and expression," *Mol. Gen. Genet.,* 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," *Plant. Mol. Biol.,* 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the Corynebacterium glutamicum fda gene: structural comparison of C. glutamicum fructose-1, 6-biphosphate aldolase to class I and class II aldolases," *Mol. Microbiol.,*
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the dapA gene from Corynebacterium glutamicum," *Nucleic Acids Res.,* 18(21):6421 (1990)
X54223		AttB-related site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum , and the attP site of lambdacorynephage," *FEMS. Microbiol, Lett.,* 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the Corynebacterium glutamicum lysA gene," *Mol. Microbiol.,* 4(11):1819-1830 (1990)

Table 2 (continued)

X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component 1	Heery, D.M. et al. "Nucleotide sequence of the Corynebacterium glutamicum trpE gene," *Nucleic Acids Res.*, 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the Corynebacterium glutamicum threonine synthase gene," *Mol. Microbiol.*, 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum , and the attP site of lambdacorynephage," *FEMS. Microbiol, Lett.*, 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from Corynebacterium glutamicum," *Mol. Microbiol.*, 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspertate beta-semialdehyde dehydrogenase gene asd in Corynebacterium glutamicum," *Mol. Gen. Genet.*, 224(3):317-324 (1990)
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a Corynebacterium glutamicum gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomeras," *J. Bacteriol.*, 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the Corynebacterium glutamicum gdh gene encoding glutamate dehydrogenase," *Mol. Microbiol.*, 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the Corynebacterium glutamicum lysI gene involved in lysine uptake," *Mol. Microbiol.*, 5(12):2995-3005 (1991)
X66078	cop1	Ps1 protein	Joliff, G. et al. "Cloning and nucleotide sequence of the csp1 gene encoding PS1, one of the two major secreted proteins of Corynebacterium glutamicum: The deduced N-terminal region of PS1 is similar to the Mycobacterium antigen 85 complex," *Mol. Microbiol.*, 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the Corynebacterium glutamicum gltA gene encoding citrate synthase," *Microbiol.*, 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	
X69103	csp2	Surface layer protein PS2	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in Corynebacterium glutamicum," *Mol. Microbiol.*, 9(1):97-109 (1993)
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a Corynebacterium glutamicum IS3-related insertion sequence and phylogenetic analysis," *Mol. Microbiol.*, 14(3):571-581 (1994)

Table 2 (continued)

X70959	leuA	Isopropylmalate synthase	Patek, M. et al. "Leucine synthesis in Corynebacterium glutamicum: enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," *Appl. Environ. Microbiol.*, 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the Corynebacterium glutamicum icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," *J. Bacteriol.*, 177(3):774-782 (1995)
X72855	GDHA	Glutamate dehydrogenase (NADP+)	
X75083, X70584	mtrA	5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of Corynebacterium glutamicum encoding resistance to 5-methyltryptophan," *Biochem. Biophys. Res. Commun.*, 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of Corynebacterium glutamicum and Brevibacterium lactofermentum," *Appl. Microbiol. Biotechnol.*, 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from Corynebacterium glutamicum and biochemical analysis of the enzyme," *J. Bacteriol.*, 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," *Antonie Van Leeuwenhoek*, 64:285-305 (1993)
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," *Antonie Van Leeuwenhoek*, 64:285-305 (1993)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from Corynebacterium glutamicum," *DNA Seq.*, 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from Corynebacterium glutamicum pta-ack operon encoding phosphotransacetylase: sequence analysis," *Microbiology*, 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera Rhodococcus and Norcardia and evidence for the evolutionary origin of the genus Norcardia from within the radiation of Rhodococcus species," *Microbiol.*, 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronemeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of Corynebacterium glutamicum," *J. Bacteriol.*, 177(5):1152-1158 (1995)
X81379	dapE	Succinyldiaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of Corynebacterium glutamicum complementing dapE of Escherichia coli," *Microbiology*, 40:3349-56 (1994)

Table 2 (continued)

X82061	16S rDNA	16S ribosomal RNA	Ruimy, R. et al. "Phylogeny of the genus Corynebacterium deduced from analyses of small-subunit ribosomal DNA sequences," *Int. J. Syst. Bacteriol.*, 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," *J. Bacteriol.*, 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," *J. Bacteriol.*, 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus Corynebacterium based on 16S rRNA gene sequences," *Int. J. Syst. Bacteriol.*, 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann et al. "Functional analysis of sequences adjacent to dapE of C. glutamicum proline reveals the presence of aroP, which encodes the aromatic amino acid transporter," *J. Bacteriol.*, 177(20):5991-5993 (1995)
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in Corynebacterium glutamicum: enzyme evolution in the early steps of the arginine pathway," *Microbiology*, 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the Corynebacterium glutamicum pta-ack operon encoding phosphotransacetylase and acetate kinase," *Microbiology*, 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting "Arthrobacter aureus C70," *J. Bacteriol.*, 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)

Table 2 (continued)

X90360		Promoter fragment F22	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90361		Promoter fragment F34	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90362		Promoter fragment F37	Patek, M. et al. "Promoters from C. glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90363		Promoter fragment F45	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90364		Promoter fragment F64	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90365		Promoter fragment F75	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90366		Promoter fragment PF101	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90367		Promoter fragment PF104	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90368		Promoter fragment PF109	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X93513	amt	Ammonium transport system	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of Corynebacterium glutamicum," *J. Biol. Chem.,* 271(10):5398-5403 (1996)
X93514	betP	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the Corynebacterium glutamicum betP gene, encoding the transport system for the compatible solute glycine betaine," *J. Bacteriol.,* 178(17):5229-5234 (1996)
X95649	orf4		Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of Corynebacterium glutamicum, encoding two enzymes involved in L-lysine synthesis," *Biotechnol. Lett.,* 19:1113-1117 (1997)
X96471	lysE; lysG	Lysine exporter protein; Lysine export regulator protein	Vrljic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from Corynebacterium glutamicum," *Mol. Microbiol.,* 22(5):815-826 (1996)

Table 2 (continued)

X96580	panB; panC; xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahm, H. et al. "D-pantothenate synthesis in Corynebacterium glutamicum and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," *Appl. Environ. Microbiol.*, 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer Brevibacterium lactofermentum (Corynebacterium glutamicum ATCC 13869)," *Gene,* 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the Brevibacterium lactofermentum," *Nucleic Acids Res.*, 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from Corynebacterium glutamicum," *Nucleic Acids Res.*, 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the Brevibacterium lactofermentum," *Nucleic Acids Res.*, 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the Corynebacterium glutamicum hom-thrB operon," *Mol. Microbiol.*, 2(1):63-72 (1988)
Y08964	murC; ftsQ/divD; ftsZ	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from Brevibacterium lactofermentum," *Mol. Gen. Genet.*, 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of Corynebacterium glutamicumproline and characterization of a low-affinity uptake system for compatible solutes," *Arch. Microbiol.*, 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from Corynebacterium glutamicum: characterization, expression and inactivation of the pyc gene," *Microbiology*, 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from Corynebacterium glutamicum," *Appl. Microbiol. Biotechnol.*, 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of corynephage Phi-16: The construction of an integration vector," *Microbiol.*, 145:539-548 (1999)
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," *J. Bacteriol.*, 180(22):6005-6012 (1998)

Table 2 (continued)

Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of Corynebacterium glutamicum glnA gene encoding glutamine synthetase I," *FEMS Microbiol. Lett.*, 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site Corynephage 304L	Moreau, S. et al. "Analysis of the integration functions of φ304L: An integrase module among corynephages," *Virology*, 255(1):150-159 (1999)
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in Brevibacterium lactofermentum: Regulation of argS-lysA cluster expression by arginine," *J. Bacteriol.*,175(22):7356-7362 (1993)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of Brevibacterium lactofermentum encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," *J. Bacteriol.*, 175(9):2743-2749 (1993)
Z29563	thrC	Threonine synthase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," *Appl. Environ. Microbiol.*, 60(7)2209-2219 (1994)
Z46753	16S rDNA	Gene for 16S ribosomal RNA	
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB," *J. Bacteriol.*, 178(2):550-553 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al "The galE gene encoding the UDP-galactose 4-epimerase of Brevibacterium lactofermentum is coupled transcriptionally to the dmdR gene," *Gene*, 177:103-107 (1996)
Z49824	orf1; sigB	?; SigB sigma factor	Oguiza, J.A. et al "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB," *J. Bacteriol.*, 178(2):550-553 (1996)
Z66534		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of Brevibacterium lactofermentum ATCC 13869," *Gene*, 170(1):91-94 (1996)

[1] A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

TABLE 3: Corynebacterium and Brevibacterium Strains Which May be Used in the Practice of the Invention

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	ammoniagenes	21054							
Brevibacterium	ammoniagenes	19350							
Brevibacterium	ammoniagenes	19351							
Brevibacterium	ammoniagenes	19352							
Brevibacterium	ammoniagenes	19353							
Brevibacterium	ammoniagenes	19354							
Brevibacterium	ammoniagenes	19355							
Brevibacterium	ammoniagenes	19356							
Brevibacterium	ammoniagenes	21055							
Brevibacterium	ammoniagenes	21077							
Brevibacterium	ammoniagenes	21553							
Brevibacterium	ammoniagenes	21580							
Brevibacterium	ammoniagenes	39101							
Brevibacterium	butanicum	21196							
Brevibacterium	divaricatum	21792	P928						
Brevibacterium	flavum	21474							
Brevibacterium	flavum	21129							
Brevibacterium	flavum	21518							
Brevibacterium	flavum			B11474					
Brevibacterium	flavum			B11472					
Brevibacterium	flavum	21127							
Brevibacterium	flavum	21128							
Brevibacterium	flavum	21427							
Brevibacterium	flavum	21475							
Brevibacterium	flavum	21517							
Brevibacterium	flavum	21528							
Brevibacterium	flavum	21529							
Brevibacterium	flavum			B11477					
Brevibacterium	flavum			B11478					
Brevibacterium	flavum	21127							
Brevibacterium	flavum			B11474					
Brevibacterium	healii	15527							
Brevibacterium	ketoglutamicum	21004							
Brevibacterium	ketoglutamicum	21089							
Brevibacterium	ketosoreductum	21914							
Brevibacterium	lactofermentum				70				
Brevibacterium	lactofermentum				74				
Brevibacterium	lactofermentum				77				
Brevibacterium	lactofermentum	21798							
Brevibacterium	lactofermentum	21799							
Brevibacterium	lactofermentum	21800							
Brevibacterium	lactofermentum	21801							
Brevibacterium	lactofermentum			B11470					
Brevibacterium	lactofermentum			B11471					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	21420							
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	31269							
Brevibacterium	linens	9174							
Brevibacterium	linens	19391							
Brevibacterium	linens	8377							
Brevibacterium	paraffinolyticum					11160			
Brevibacterium	spec.						717.73		
Brevibacterium	spec.						717.73		
Brevibacterium	spec.	14604							
Brevibacterium	spec.	21860							
Brevibacterium	spec.	21864							
Brevibacterium	spec.	21865							
Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetoacidophilum	21476							
Corynebacterium	acetoacidophilum	13870							
Corynebacterium	acetoglutamicum			B11473					
Corynebacterium	acetoglutamicum			B11475					
Corynebacterium	acetoglutamicum	15806							
Corynebacterium	acetoglutamicum	21491							
Corynebacterium	acetoglutamicum	31270							
Corynebacterium	acetophilum			B3671					
Corynebacterium	ammoniagenes	6872						2399	
Corynebacterium	ammoniagenes	15511							
Corynebacterium	fujiokense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							
Corynebacterium	glutamicum	21514							
Corynebacterium	glutamicum	21516							
Corynebacterium	glutamicum	21299							

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum	21300							
Corynebacterium	glutamicum	39684							
Corynebacterium	glutamicum	21488							
Corynebacterium	glutamicum	21649							
Corynebacterium	glutamicum	21650							
Corynebacterium	glutamicum	19223							
Corynebacterium	glutamicum	13869							
Corynebacterium	glutamicum	21157							
Corynebacterium	glutamicum	21158							
Corynebacterium	glutamicum	21159							
Corynebacterium	glutamicum	21355							
Corynebacterium	glutamicum	31808							
Corynebacterium	glutamicum	21674							
Corynebacterium	glutamicum	21562							
Corynebacterium	glutamicum	21563							
Corynebacterium	glutamicum	21564							
Corynebacterium	glutamicum	21565							
Corynebacterium	glutamicum	21566							
Corynebacterium	glutamicum	21567							
Corynebacterium	glutamicum	21568							
Corynebacterium	glutamicum	21569							
Corynebacterium	glutamicum	21570							
Corynebacterium	glutamicum	21571							
Corynebacterium	glutamicum	21572							
Corynebacterium	glutamicum	21573							
Corynebacterium	glutamicum	21579							
Corynebacterium	glutamicum	19049							
Corynebacterium	glutamicum	19050							
Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum			B8183					
Corynebacterium	glutamicum			B8182					
Corynebacterium	glutamicum			B12416					
Corynebacterium	glutamicum			B12417					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum			B12418					
Corynebacterium	glutamicum			B11476					
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium		P973						
Corynebacterium	nitrilophilus	21419				11594			
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	15954							20145
Corynebacterium	spec.	21857							
Corynebacterium	spec.	21862							
Corynebacterium	spec.	21863							

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4^{th} edn), World federation for culture collections world data center on microorganisms, Saimata, Japen.

Table 4: Alignment Results

ID #	length (NT)	Genbank Hit	Length	Accession	Name of Genbank Hit	Source of Genbank Hit	% homology (GAP)	Date of Deposit
rxa00023	3579	GB_EST33:AI776129	483	AI776129	EST257217 tomato resistant, Cornell Lycopersicon esculentum cDNA clone cLER17D3, mRNA sequence.	Lycopersicon esculentum	40,956	29-Jun-99
		GB_EST33:AI776129	483	AI776129	EST257217 tomato resistant, Cornell Lycopersicon esculentum cDNA clone cLER17D3, mRNA sequence.	Lycopersicon esculentum	40,956	29-Jun-99
rxa00044	1059	EM_PAT:E11760	6911	E11760	Base sequence of sucrase gene.	Corynebacterium glutamicum	42,979	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:I26124	6911	I26124	Sequence 4 from patent US 5556776.	Unknown.	42,979	07-OCT-1998
		GB_BA2:ECOUW89	176195	U00006	E. coli chromosomal region from 89.2 to 92.8 minutes.	Escherichia coli	39,097	17-DEC-1993
rxa00064	1401	GB_PAT:E16763	2517	E16763	gDNA encoding aspartate transferase (AAT).	Corynebacterium glutamicum	95,429	28-Jul-99
		GB_HTG2:AC007892	134257	AC007892	Drosophila melanogaster chromosome 3 clone BACR02O03 (D797) RPCI-98 02.O.3 map 99B-99B strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 113 unordered pieces.	Drosophila melanogaster	31,111	2-Aug-99
		GB_HTG2:AC007892	134257	AC007892	Drosophila melanogaster chromosome 3 clone BACR02O03 (D797) RPCI-98 02.O.3 map 99B-99B strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 113 unordered pieces.	Drosophila melanogaster	31,111	2-Aug-99
rxa00072								
rxa00105	798	GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	37,753	17-Jun-98
		GB_BA1:ECU29581	71128	U29581	Escherichia coli K-12 genome; approximately 63 to 64 minutes.	Escherichia coli	35,669	14-Jan-97
		GB_BA2:AE000366	10405	AE000366	Escherichia coli K-12 MG1655 section 256 of 400 of the complete genome.	Escherichia coli	35,669	12-Nov-98
rxa00106	579	GB_EST15:AA494237	367	AA494237	ng83f04.s1 NCI_CGAP_Pr6 Homo sapiens cDNA clone IMAGE:941407 similar to SW:DYR_LACCA P00381 DIHYDROFOLATE REDUCTASE ;, mRNA sequence.	Homo sapiens	42,896	20-Aug-97
		GB_BA2:AF161327	2021	AF161327	Corynebacterium diphtheriae histidine kinase ChrS (chrS) and response regulator ChrA (chrA) genes, complete cds.	Corynebacterium diphtheriae	40,210	9-Sep-99
		GB_PAT:AR041189	654	AR041189	Sequence 4 from patent US 5811286.	Unknown.	41,176	29-Sep-99
rxa00115	1170	GB_PR4:AC007110	148336	AC007110	Homo sapiens chromosome 17, clone hRPK.472_J_18, complete sequence.	Homo sapiens	36,783	30-MAR-1999
		GB_HTG3:AC008537	170030	AC008537	Homo sapiens chromosome 19 clone CIT-HSPC_490E21, *** SEQUENCING IN PROGRESS ***, 93 unordered pieces.	Homo sapiens	40,296	2-Sep-99
		GB_HTG3:AC008537	170030	AC008537	Homo sapiens chromosome 19 clone CIT-HSPC_490E21, *** SEQUENCING IN PROGRESS ***, 93 unordered pieces.	Homo sapiens	40,296	2-Sep-99

Table 4 (continued)

rxa00116	1284	GB_BA2:AF062345	16458	AF062345	Caulobacter crescentus Sst1 (sst1), S-layer protein subunit (rsaA), ABC transporter (rsaD), membrane forming unit (rsaE), putative GDP-mannose-4,6-dehydratase (lpsA), putative acetyltransferase (lpsB), putative perosamine synthetase (lpsC), putative mannosyltransferase (lpsD), putative mannosyltransferase (lpsE), outer membrane protein (rsaF), and putative perosamine transferase (lpsE) genes, complete cds.	Caulobacter crescentus	36,235	19-OCT-1999
		GB_PAT:I18647	3300	I18647	Sequence 6 from patent US 5500353.	Unknown.	36,821	07-OCT-1996
		GB_GSS13:AQ446197	751	AQ446197	nbxb0062D16r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0062D16r, genomic survey sequence.	Oryza sativa	38,124	8-Apr-99
rxa00131	732	GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	Mycobacterium tuberculosis	43,571	17-Jun-98
		GB_BA1:SAR7932	15176	AJ007932	Streptomyces argillaceus mithramycin biosynthetic genes.	Streptomyces argillaceus	41,116	15-Jun-99
		GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	Mycobacterium tuberculosis	39,726	17-Jun-98
rxa00132	1557	GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	Mycobacterium tuberculosis	36,788	17-Jun-98
		GB_IN2:TVU40872	1882	U40872	Trichomonas vaginalis S-adenosyl-L-homocysteine hydrolase gene, complete cds.	Trichomonas vaginalis	61,914	31-OCT-1996
		GB_HTG6:AC010706	169265	AC010706	Drosophila melanogaster chromosome X clone BACR36D15 (D887) RPCI-98 36.D.15 map 13C-13E strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 74 unordered pieces.	Drosophila melanogaster	51,325	22-Nov-99
rxa00145	1059	GB_BA1:MTCY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	63,365	18-Jun-98
		GB_BA1:PSEPYRBX	2273	L19649	Pseudomonas aeruginosa aspartate transcarbamoylase (pyrB) and dihydroorotase-like (pyrX) genes, complete cds's.	Pseudomonas aeruginosa	56,080	26-Jul-93
		GB_BA1:LLPYRBDNA	1468	X84262	L.leichmannii pyrB gene.	Lactobacillus leichmannii	47,514	29-Apr-97
rxa00146	1464	GB_BA1:MTCY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	60,714	18-Jun-98
		GB_BA1:MTCY154	13935	Z98209	Mycobacterium tuberculosis H37Rv complete genome; segment 121/162.	Mycobacterium tuberculosis	39,229	17-Jun-98
		GB_BA1:MSGY154	40221	AD000002	Mycobacterium tuberculosis sequence from clone y154.	Mycobacterium tuberculosis	36,618	03-DEC-1996
rxa00147	1302	GB_BA1:MTCY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	61,527	18-Jun-98
		GB_BA1:MSGB937CS	38914	L78820	Mycobacterium leprae cosmid B937 DNA sequence.	Mycobacterium leprae	59,538	15-Jun-96
		GB_BA1:PAU81259	7285	U81259	Pseudomonas aeruginosa dihydrodipicolinate reductase (dapB) gene, partial cds, carbamoylphosphate synthetase small subunit (carA) and carbamoylphosphate synthetase large subunit (carB) genes, complete cds, and FtsJ homolog (ftsJ) gene, partial cds.	Pseudomonas aeruginosa	55,396	23-DEC-1996
rxa00156	1233	GB_BA1:SC9B10	33320	AL009204	Streptomyces coelicolor cosmid 9B10.	Streptomyces coelicolor	52,666	10-Feb-99

Table 4 (continued)

		GB_BA2:AF002133	15437	AF002133	Mycobacterium avium strain GIR10 transcriptional regulator (mav81) gene, partial cds, aconitase (acn), invasin 1 (inv1), invasin 2 (inv2), transcriptional regulator (moxR), ketoacyl-reductase (fabG), enoyl-reductase (inhA) and ferrochelatase (mav272) genes, complete cds.	Mycobacterium avium	54,191	26-MAR-1998
		GB_BA1:D85417	7984	D85417	Propionibacterium freudenreichii hemY, hemH, hemB, hemX, hemR and hemL genes, complete cds.	Propionibacterium freudenreichii	46,667	6-Feb-99
rxa00166	783	GB_HTG3:AC008167	174223	AC008167	Homo sapiens clone NH0172O13, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.	Homo sapiens	37,451	21-Aug-99
		GB_HTG3:AC008167	174223	AC008167	Homo sapiens clone NH0172O13, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.	Homo sapiens	37,451	21-Aug-99
		GB_HTG4:AC010118	80605	AC010118	Drosophila melanogaster chromosome 3L/62B1 clone RPCI98-10D15, *** SEQUENCING IN PROGRESS ***, 51 unordered pieces.	Drosophila melanogaster	38,627	16-OCT-1999
rxa00198	672	GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	92,113	13-MAR-1999
		GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	93,702	13-MAR-1999
		GB_EST24:AI232702	528	AI232702	EST229390 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone RKICF35 3' end, mRNA sequence.	Rattus sp.	34,221	31-Jan-99
rxa00216	1113	GB_HTG2:HSDJ850E9	117353	AL121758	Homo sapiens chromosome 20 clone RP5-850E9, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	37,965	03-DEC-1999
		GB_HTG2:HSDJ850E9	117353	AL121758	Homo sapiens chromosome 20 clone RP5-850E9, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	37,965	03-DEC-1999
		GB_PR2:CNS01DSA	159400	AL121766	Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-412H8 of RPCI-11 library from chromosome 14 of Homo sapiens (Human), complete sequence.	Homo sapiens	38,796	11-Nov-99
rxa00219	1065	GB_HTG2:AC005079_0	110000	AC005079	Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	38,227	22-Nov-98
		GB_HTG2:AC005079_1	110000	AC005079	Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	38,227	22-Nov-98
		GB_HTG2:AC005079_1	110000	AC005079	Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	38,227	22-Nov-98
rxa00223	1212	GB_BA1:PPEA3NIF	19771	X99694	Plasmid pEA3 nitrogen fixation genes.	Enterobacter agglomerans	48,826	2-Aug-96
		GB_BA2:AF128444	2477	AF128444	Rhodobacter capsulatus molybdenum cofactor biosynthetic gene cluster, partial sequence.	Rhodobacter capsulatus	40,135	22-MAR-1999
		GB_HTG4:AC010111	138938	AC010111	Drosophila melanogaster chromosome 3L/70C1 clone RPCI98-9B18, *** SEQUENCING IN PROGRESS ***, 64 unordered pieces.	Drosophila melanogaster	39,527	16-OCT-1999
rxa00229	803	GB_BA2:AF124518	1758	AF124518	Corynebacterium glutamicum 3-dehydroquinase (aroD) and shikimate dehydrogenase (aroE) genes, complete cds.	Corynebacterium glutamicum	98,237	18-MAY-1999
		GB_PR3:AC004593	150221	AC004593	Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence.	Homo sapiens	36,616	18-Apr-98
		GB_HTG2:AC006907	188972	AC006907	Caenorhabditis elegans clone Y76B12, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces.	Caenorhabditis elegans	37,095	26-Feb-99
rxa00241	1626	GB_BA1:CGLYSI	4232	X60312	C.glutamicum lysI gene for L-lysine permease.	Corynebacterium glutamicum	100,000	30-Jan-92

Table 4 (continued)

		GB_HTG1:PFMAL13P1	192581	AL049180	Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Plasmodium falciparum	34,947	11-Aug-99
		GB_HTG1:PFMAL13P1	192581	AL049180	Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Plasmodium falciparum	34,947	11-Aug-99
rxa00262	1197	GB_IN2:EHU89655	3219	U89655	Entamoeba histolytica unconventional myosin IB mRNA, complete cds.	Entamoeba histolytica	36,496	23-MAY-1997
		GB_IN2:EHU89655	3219	U89655	Entamoeba histolytica unconventional myosin IB mRNA, complete cds.	Entamoeba histolytica	37,544	23-MAY-1997
rxa00266	531	GB_RO:AF016190	2939	AF016190	Mus musculus connexin-36 (Cx36) gene, complete cds.	Mus musculus	41,856	9-Feb-99
		EM_PAT:E09719	3505	E09719	DNA encoding precursor protein of alkaline cellulase.	Bacillus sp.	34,741	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:E02133	3494	E02133	gDNA encoding alkaline cellulase.	Bacillus sp.	34,741	29-Sep-97
rxa00278	1155	GB_IN1:CELK05F6	36912	AF040653	Caenorhabditis elegans cosmid K05F6.	Caenorhabditis elegans	36,943	6-Jan-98
		GB_BA1:CGU43535	2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds.	Corynebacterium glutamicum	36,658	9-Apr-97
		GB_RO:RNU30789	3510	U30789	Rattus norvegicus clone N27 mRNA.	Rattus norvegicus	38,190	20-Aug-96
rxa00295	1125	GB_BA2:CGU31281	1614	U31281	Corynebacterium glutamicum biotin synthase (bioB) gene, complete cds.	Corynebacterium glutamicum	99,111	21-Nov-96
		GB_BA1:BRLBIOBA	1647	D14084	Brevibacterium flavum gene for biotin synthetase, complete cds.	Corynebacterium glutamicum	98,489	3-Feb-99
		GB_PAT:E03937	1005	E03937	DNA sequence encoding Brevibacterium flavum biotin-synthase.	Corynebacterium glutamicum	98,207	29-Sep-97
rxa00323	1461	GB_BA1:MTCY427	38110	Z70692	Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.	Mycobacterium tuberculosis	35,615	24-Jun-99
		GB_BA1:MSGB32CS	36404	L78818	Mycobacterium leprae cosmid B32 DNA sequence.	Mycobacterium leprae	60,917	15-Jun-96
		GB_BA1:MTCY427	38110	Z70692	Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.	Mycobacterium tuberculosis	44,606	24-Jun-99
rxa00324	3258	GB_BA1:MSGB32CS	36404	L78818	Mycobacterium leprae cosmid B32 DNA sequence.	Mycobacterium leprae	52,516	15-Jun-96
		GB_BA1:MTCY427	38110	Z70692	Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.	Mycobacterium tuberculosis	38,079	24-Jun-99
		GB_OM:BOVELA	3242	J02717	Bovine elastin a mRNA, complete cds.	Bos taurus	39,351	27-Apr-93
rxa00330	1566	GB_BA1:CGTHRC	3120	X56037	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2).	Corynebacterium glutamicum	99,808	17-Jun-97
		GB_PAT:I09078	3146	I09078	Sequence 4 from Patent WO 8809819.	Unknown.	99,617	02-DEC-1994
		GB_BA1:BLTHRESYN	1892	Z29563	Brevibacterium lactofermentum; ATCC 13869;; DNA (genomic);.	Corynebacterium glutamicum	99,170	20-Sep-95
rxa00335	1554	GB_BA1:CGGLNA	3686	Y13221	Corynebacterium glutamicum glnA gene.	Corynebacterium glutamicum	100,000	28-Aug-97

Table 4 (continued)

		GB_BA2:AF005635	1690	AF005635	Corynebacterium glutamicum glutamine synthetase (glnA) gene, complete cds.	Corynebacterium glutamicum	98,906	14-Jun-99
		GB_BA1:MSGB27CS	38793	L78817	Mycobacterium leprae cosmid B27 DNA sequence.	Mycobacterium leprae	66,345	15-Jun-96
rxa00347	891	GB_EST27:AI455217	624	AI455217	LD21828.3prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD21828 3prime, mRNA sequence.	Drosophila melanogaster	34,510	09-MAR-1999
		GB_BA2:SSU30252	2891	U30252	Synechococcus PCC7942 nucleoside diphosphate kinase and ORF2 protein genes, complete cds, ORF1 protein gene, partial cds, and neutral site I for vector use.	Synechococcus PCC7942	37,084	29-OCT-1999
		GB_EST21:AA911262	581	AA911262	oe75a02.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1417418 3' similar to gb:A18757 UROKINASE PLASMINOGEN ACTIVATOR SURFACE RECEPTOR, GPI-ANCHORED (HUMAN);, mRNA sequence.	Homo sapiens	37,500	21-Apr-98
rxa00351	1578	GB_BA1:MLU15187	36138	U15187	Mycobacterium leprae cosmid L296.	Mycobacterium leprae	52,972	09-MAR-1995
		GB_IN2:AC004373	72722	AC004373	Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.	Drosophila melanogaster	46,341	17-Jul-98
		GB_IN2:AF145653	3197	AF145653	Drosophila melanogaster clone GH08860 BcDNA.GH08860 (BcDNA.GH08860) mRNA, complete cds.	Drosophila melanogaster	49,471	14-Jun-99
rxa00365	727	GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	96,556	13-MAR-1999
		GB_BA1:MTCY1A6	37751	Z83864	Mycobacterium tuberculosis H37Rv complete genome; segment 159/162.	Mycobacterium tuberculosis	39,496	17-Jun-98
		GB_BA1:SC3A3	15901	AL109849	Streptomyces coelicolor cosmid 3A3.	Streptomyces coelicolor A3(2)	37,946	16-Aug-99
rxa00366	480	GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	99,374	13-MAR-1999
		GB_BA1:MTCY1A6	37751	Z83864	Mycobacterium tuberculosis H37Rv complete genome; segment 159/162.	Mycobacterium tuberculosis	41,333	17-Jun-98
		GB_BA1:SC3A3	15901	AL109849	Streptomyces coelicolor cosmid 3A3.	Streptomyces coelicolor A3(2)	37,554	16-Aug-99
rxa00367	4653	GB_BA1:AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	99,312	13-MAR-1999
		GB_BA1:MTCY1A6	37751	Z83864	Mycobacterium tuberculosis H37Rv complete genome; segment 159/162.	Mycobacterium tuberculosis	36,971	17-Jun-98
		GB_BA1:SC3A3	15901	AL109849	Streptomyces coelicolor cosmid 3A3.	Streptomyces coelicolor A3(2)	37,905	16-Aug-99
rxa00371	1917	GB_VI:SBVORFS	7568	M89923	Sugarcane bacilliform virus ORF 1,2,and 3 DNA, complete cds.	Sugarcane bacilliform virus	35,843	12-Jun-93
		GB_EST37:AI967505	380	AI967505	Ljirnpest03-215-c10 Ljimp Lambda HybriZap two-hybrid library Lotus japonicus cDNA clone LP215-03-c10 5' similar to 60S ribosomal protein L39, mRNA sequence.	Lotus japonicus	42,593	24-Aug-99
		GB_IN1:CELK09H9	37881	AF043700	Caenorhabditis elegans cosmid K09H9.	Caenorhabditis elegans	34,295	22-Jan-98

Table 4 (continued)

rxa00377	1245	GB_BA1:CCU13664	1678	U13664	Caulobacter crescentus uroporphyrinogen decarboxylase homolog (hemE) gene, partial cds.	Caulobacter crescentus	36,832	24-MAR-1995
		GB_PL1:ANSDGENE	1299	Y08866	A.nidulans sD gene.	Emericella nidulans	39,603	17-OCT-1996
		GB_GSS4:AQ730303	483	AQ730303	HS_5505_B1_C04_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1081 Col=7 Row=F, genomic survey sequence.	Homo sapiens	36,728	15-Jul-99
rxa00382	1425	GB_BA1:PAHEML	4444	X82072	P.aeruginosa hemL gene.	Pseudomonas aeruginosa	54,175	18-DEC-1995
		GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	61,143	17-Jun-98
		GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	61,143	03-DEC-1996
rxa00383	1467	GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	43,981	27-Aug-99
		GB_HTG2:AC006269	167171	AC006269	Homo sapiens chromosome 17 clone hRPK.515_E_23 map 17, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.	Homo sapiens	35,444	10-Jun-99
		GB_HTG2:AC007638	178053	AC007638	Homo sapiens chromosome 17 clone hRPK.515_O_17 map 17, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces.	Homo sapiens	34,821	22-MAY-1999
rxa00391	843	GB_EST38:AW017053	613	AW017053	EST272398 Schistosoma mansoni male, Phil LoVerde/Joe Merrick Schistosoma mansoni cDNA clone SMMAS14 5' end, mRNA sequence.	Schistosoma mansoni	40,472	10-Sep-99
		GB_PAT:AR065852	32207	AR065852	Sequence 20 from patent US 5849564.	Unknown.	38,586	29-Sep-99
		GB_VI:AF148805	28559	AF148805	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamidine synthase, and LAMP (LAMP) genes, complete cds.	Kaposi's sarcoma-associated herpesvirus	38,509	2-Aug-99
rxa00393	1017	GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	36,308	17-Jun-98
		GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	39,282	03-DEC-1996
		GB_BA1:MLB1306	7762	Y13803	Mycobacterium leprae cosmid B1306 DNA.	Mycobacterium leprae	39,228	24-Jun-97
rxa00402	623	GB_BA2:AF052652	2096	AF052652	Corynebacterium glutamicum homoserine O-acetyltransferase (metA) gene, complete cds.	Corynebacterium glutamicum	99,672	19-MAR-1998
		GB_BA2:AF109162	4514	AF109162	Corynebacterium diphtheriae heme uptake locus, complete sequence.	Corynebacterium diphtheriae	40,830	8-Jun-99
		GB_BA2:AF092918	20758	AF092918	Pseudomonas alcaligenes outer membrane Xcp-secretion system gene cluster.	Pseudomonas alcaligenes	50,161	06-DEC-1998
rxa00403	1254	GB_BA2:AF052652	2096	AF052652	Corynebacterium glutamicum homoserine O-acetyltransferase (metA) gene, complete cds.	Corynebacterium glutamicum	99,920	19-MAR-1998
		GB_BA1:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	52,898	23-Jun-99
		GB_EST23:AI111288	750	AI111288	SWOvAMCAQ02A05SK Onchocerca volvulus adult male cDNA (SAW98MLW-OvAM) Onchocerca volvulus cDNA clone SWOvAMCAQ02A05 5', mRNA sequence.	Onchocerca volvulus	37,565	31-Aug-98

Table 4 (continued)

rxa00405	613	GB_BA1:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	57,259	23-Jun-99
		GB_PR4:AC005145	143678	AC005145	Homo sapiens Xp22-166-169 GSHB-523A23 (Genome Systems Human BAC library) complete sequence.	Homo sapiens	34,179	08-DEC-1998
		GB_BA1:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	40,169	23-Jun-99
rxa00420	1587	GB_BA1:MTY13D12	37085	Z80343	Mycobacterium tuberculosis H37Rv complete genome; segment 156/162.	Mycobacterium tuberculosis	62,031	17-Jun-98
		GB_BA1:MSGY126	37164	AD000012	Mycobacterium tuberculosis sequence from clone y126.	Mycobacterium tuberculosis	61,902	10-DEC-1996
		GB_BA1:MSGB971CS	37566	L78821	Mycobacterium leprae cosmid B971 DNA sequence.	Mycobacterium leprae	39,651	15-Jun-96
rxa00435	1296	GB_BA1:AFACBBTZ	2760	M68904	Alcaligenes eutrophus chromsomal transketolase (cbbTc) and phosphoglycolate phosphatase (cbbZc) genes, complete cds.	Ralstonia eutropha	38,677	27-Jul-94
		GB_HTG4:AC009541	169583	AC009541	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces.	Homo sapiens	36,335	12-OCT-1999
		GB_HTG4:AC009541	169583	AC009541	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces.	Homo sapiens	36,335	12-OCT-1999
rxa00437	579	GB_PR4:AC005951	155450	AC005951	Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.	Homo sapiens	31,738	18-Nov-98
		GB_BA1:SC2A11	22789	AL031184	Streptomyces coelicolor cosmid 2A11.	Streptomyces coelicolor	43,262	5-Aug-98
		GB_PR4:AC005951	155450	AC005951	Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.	Homo sapiens	37,647	18-Nov-98
rxa00439	591	GB_BA1:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	37,088	23-Jun-99
		GB_PL2:AF167358	1022	AF167358	Rumex acetosa expansin (EXP3) gene, partial cds.	Rumex acetosa	46,538	17-Aug-99
		GB_HTG3:AC009120	269445	AC009120	Homo sapiens chromosome 16 clone RPCI-11_484E3, *** SEQUENCING IN PROGRESS ***, 34 unordered pieces.	Homo sapiens	43,276	3-Aug-99
rxa00440	582	GB_BA2:SKZ86111	7860	Z86111	Streptomyces lividans rpsP, trmD, rplS, sipW, sipX, sipY, sipZ, mutT genes and 4 open reading frames.	Streptomyces lividans	43,080	27-OCT-1999
		GB_BA1:SC2E1	38962	AL023797	Streptomyces coelicolor cosmid 2E1.	Streptomyces coelicolor	42,931	4-Jun-98
		GB_BA1:SC2E1	38962	AL023797	Streptomyces coelicolor cosmid 2E1.	Streptomyces coelicolor	38,702	4-Jun-98
rxa00441	1287	GB_PR2:HS173D1	117338	AL031984	Human DNA sequence from clone 173D1 on chromosome 1p36.21-36.33.Contains ESTs, STSs and GSSs, complete sequence.	Homo sapiens	38,027	23-Nov-99
		GB_HTG2:HSDJ719K3	267114	AL109931	Homo sapiens chromosome X clone RP4-719K3 map q21.1-21.31, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	34,521	03-DEC-1999
		GB_HTG2:HSDJ719K3	267114	AL109931	Homo sapiens chromosome X clone RP4-719K3 map q21.1-21.31, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	34,521	03-DEC-1999
rxa00446	987	GB_BA1:SCD78	36224	AL034355	Streptomyces coelicolor cosmid D78.	Streptomyces coelicolor	56,410	26-Nov-98
		GB_HTG4:AC009367	226055	AC009367	Drosophila melanogaster chromosome 3L/76A2 clone RPCI98-48B15, *** SEQUENCING IN PROGRESS ***, 44 unordered pieces.	Drosophila melanogaster	34,959	16-OCT-1999
		GB_HTG4:AC009367	226055	AC009367	Drosophila melanogaster chromosome 3L/76A2 clone RPCI98-48B15, *** SEQUENCING IN PROGRESS ***, 44 unordered pieces.	Drosophila melanogaster	34,959	16-OCT-1999

Table 4 (continued)

rxa00448	1143	GB_PR3:AC003670	88945	AC003670	Homo sapiens 12q13.1 PAC RPCI1-130F5 (Roswell Park Cancer Institute Human PAC library) complete sequence.	Homo sapiens	35,682	9-Jun-98
		GB_HTG2:AF029367	148676	AF029367	Homo sapiens chromosome 12 clone RPCI-1 130F5 map 12q13.1, *** SEQUENCING IN PROGRESS ***, 156 unordered pieces.	Homo sapiens	31,373	18-OCT-1997
		GB_HTG2:AF029367	148676	AF029367	Homo sapiens chromosome 12 clone RPCI-1 130F5 map 12q13.1, *** SEQUENCING IN PROGRESS ***, 156 unordered pieces.	Homo sapiens	31,373	18-OCT-1997
rxa00450	424	GB_HTG2:AC007824	133361	AC007824	Drosophila melanogaster chromosome 3 clone BACR02L16 (D715) RPCI-98 02.L.16 map 89E-90A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 91 unordered pieces.	Drosophila melanogaster	40,000	2-Aug-99
		GB_HTG2:AC007824	133361	AC007824	Drosophila melanogaster chromosome 3 clone BACR02L16 (D715) RPCI-98 02.L.16 map 89E-90A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 91 unordered pieces.	Drosophila melanogaster	40,000	2-Aug-99
		GB_EST35:AI818057	412	AI818057	wk14a08.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2412278 3' similar to gb:Y00764 UBIQUINOL-CYTOCHROME C REDUCTASE 11 KD PROTEIN (HUMAN);, mRNA sequence.	Homo sapiens	35,714	24-Aug-99
rxa00461	975	GB_BA1:MLCB1779	43254	Z98271	Mycobacterium leprae cosmid B1779.	Mycobacterium leprae	39,308	8-Aug-97
		GB_IN1:DMC86E4	29352	AL021086	Drosophila melanogaster cosmid clone 86E4.	Drosophila melanogaster	37,487	27-Apr-99
		GB_GSS15:AQ640325	467	AQ640325	927P1-2H3.TP 927P1 Trypanosoma brucei genomic clone 927P1-2H3, genomic survey sequence.	Trypanosoma brucei	38,116	8-Jul-99
rxa00465								
rxa00487	1692	GB_BA1:BAGUAA	3866	Y10499	B.ammoniagenes guaA gene.	Corynebacterium ammoniagenes	74,259	8-Jan-98
		GB_BA2:U00015	42325	U00015	Mycobacterium leprae cosmid B1620.	Mycobacterium leprae	37,248	01-MAR-1994
		GB_BA1:MTCY78	33818	Z77165	Mycobacterium tuberculosis H37Rv complete genome; segment 145/162.	Mycobacterium tuberculosis	39,725	17-Jun-98
rxa00488	1641	GB_BA1:MTCY78	33818	Z77165	Mycobacterium tuberculosis H37Rv complete genome; segment 145/162.	Mycobacterium tuberculosis	39,451	17-Jun-98
		GB_BA2:U00015	42325	U00015	Mycobacterium leprae cosmid B1620.	Mycobacterium leprae	39,178	01-MAR-1994
		GB_BA1:SCAJ10601	4692	AJ010601	Streptomyces coelicolor A3(2) DNA for whiD and whiK loci.	Streptomyces coelicolor	60,835	17-Sep-98
rxa00489	1245	GB_BA2:U00015	42325	U00015	Mycobacterium leprae cosmid B1620.	Mycobacterium leprae	38,041	01-MAR-1994
		GB_HTG2:HS225E12	126464	AL031772	Homo sapiens chromosome 6 clone RP1-225E12 map q24, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,756	03-DEC-1999
		GB_HTG2:HS225E12	126464	AL031772	Homo sapiens chromosome 6 clone RP1-225E12 map q24, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,756	03-DEC-1999
rxa00533	1155	GB_BA1:CGLYS	2803	X57226	C. glutamicum lysC-alpha, lysC-beta and asd genes for aspartokinase-alpha and -beta subunits, and aspartate beta semialdehyde dehydrogenase, respectively (EC 2.7.2.4; EC 1.2.1.11).	Corynebacterium glutamicum	99,913	17-Feb-97

Table 4 (continued)

		GB_BA1:CGCYSCASD	1591	X82928	C.glutamicum aspartate-semialdehyde dehydrogenase gene.	Corynebacterium glutamicum	99,221	17-Feb-97
		GB_PAT:A07546	2112	A07546	Recombinant DNA fragment (PstI-XhoI).	synthetic construct	99,391	30-Jul-93
rxa00534	1386	GB_BA1:CGLYS	2803	X57226	C. glutamicum lysC-alpha, lysC-beta and asd genes for aspartokinase-alpha and -beta subunits, and aspartate beta semialdehyde dehydrogenase, respectively (EC 2.7.2.4; EC 1.2.1.11).	Corynebacterium glutamicum	99,856	17-Feb-97
		GB_BA1:CORASKD	2957	L16848	Corynebacterium flavum aspartokinase (ask), and aspartate-semialdehyde dehydrogenase (asd) genes, complete cds.	Corynebacterium flavescens	98,701	11-Jun-93
		GB_PAT:E14514	1643	E14514	DNA encoding Brevibacterium aspartokinase.	Corynebacterium glutamicum	98,773	28-Jul-99
rxa00536	1494	GB_BA1:CGLEUA	3492	X70959	C.glutamicum gene leuA for isopropylmalate synthase.	Corynebacterium glutamicum	100,000	10-Feb-99
		GB_BA1:MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.	Mycobacterium tuberculosis	68,003	24-Jun-99
		GB_BA1:MTU88526	2412	U88526	Mycobacterium tuberculosis putative alpha-isopropyl malate synthase (leuA) gene, complete cds.	Mycobacterium tuberculosis	68,185	26-Feb-97
rxa00537	2409	GB_BA2:SCD25	41622	AL118514	Streptomyces coelicolor cosmid D25.	Streptomyces coelicolor A3(2)	63,187	21-Sep-99
		GB_BA1:MTCY7H7A	10451	Z95618	Mycobacterium tuberculosis H37Rv complete genome; segment 39/162.	Mycobacterium tuberculosis	62,401	17-Jun-98
		GB_BA1:MTU34956	2462	U34956	Mycobacterium tuberculosis phosphoribosylformylglycinamidine synthase (purL) gene, complete cds.	Mycobacterium tuberculosis	62,205	28-Jan-97
rxa00541	792	GB_PAT:I92052	2115	I92052	Sequence 19 from patent US 5726299.	Unknown.	98,359	01-DEC-1998
		GB_BA1:MLCB5	38109	Z95151	Mycobacterium leprae cosmid B5.	Mycobacterium leprae	62,468	24-Jun-97
		GB_BA1:MTCY369	36850	Z80226	Mycobacterium tuberculosis H37Rv complete genome; segment 36/162.	Mycobacterium tuberculosis	60,814	17-Jun-98
rxa00558	1470	GB_BA1:BAPURF	1885	X91252	B.ammoniagenes purF gene.	Corynebacterium ammoniagenes	66,095	5-Jun-97
		GB_BA1:MLU15182	40123	U15182	Mycobacterium leprae cosmid B2266.	Mycobacterium leprae	64,315	09-MAR-1995
		GB_BA1:MTCY7H7A	10451	Z95618	Mycobacterium tuberculosis H37Rv complete genome; segment 39/162.	Mycobacterium tuberculosis	64,863	17-Jun-98
rxa00579	1983	GB_PAT:AR016483	2104	AR016483	Sequence 1 from patent US 5776740.	Unknown.	98,810	05-DEC-1998
		EM_PAT:E11273	2104	E11273	DNA encoding serine hydroxymethyl transferase.	Corynebacterium glutamicum	98,810	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:E12594	2104	E12594	DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum.	Corynebacterium glutamicum	98,810	24-Jun-98
rxa00580	1425	GB_PAT:E12594	2104	E12594	DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum.	Corynebacterium glutamicum	99,368	24-Jun-98

Table 4 (continued)

		GB_PAT:AR016483	2104	AR016483	Sequence 1 from patent US 5776740.	Unknown.	99,368	05-DEC-1998
		EM_PAT:E11273	2104	E11273	DNA encoding serine hydroxymethyl transferase.	Corynebacterium glutamicum	99,368	08-OCT-1997 (Rel. 52, Created)
rxa00581	1092	GB_PAT:E12594	2104	E12594	DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum.	Corynebacterium glutamicum	37,071	24-Jun-98
		EM_PAT:E11273	2104	E11273	DNA encoding serine hydroxymethyl transferase.	Corynebacterium glutamicum	37,071	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:AR016483	2104	AR016483	Sequence 1 from patent US 5776740.	Unknown.	37,071	05-DEC-1998
rxa00584	1248	GB_BA1:CORAHPS	2570	L07603	Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene, complete cds.	Corynebacterium glutamicum	98,236	26-Apr-93
		GB_BA1:AOPCZA361	37941	AJ223998	Amycolatopsis orientalis cosmid PCZA361.	Amycolatopsis orientalis	54,553	29-MAR-1999
		GB_BA1:D90714	14358	D90714	Escherichia coli genomic DNA. (16.8 - 17.1 min).	Escherichia coli	53,312	7-Feb-99
rxa00618	1230	GB_EST19:AA802737	280	AA802737	GM06236.5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM06236 5prime, mRNA sequence.	Drosophila melanogaster	39,928	25-Nov-98
		GB_EST28:AI534381	581	AI534381	SD07186.5prime SD Drosophila melanogaster Schneider L2 cell culture pOT2 Drosophila melanogaster cDNA clone SD07186 5prime similar to X89858: Ani FBgn0011558 PID:g927407 SPTREMBL:Q24240, mRNA sequence.	Drosophila melanogaster	41,136	18-MAR-1999
		GB_IN1:DMANILLIN	4029	X89858	D.melanogaster mRNA for anillin protein.	Drosophila melanogaster	34,398	8-Nov-95
rxa00619	1551	GB_BA1:MTCY369	36850	Z80226	Mycobacterium tuberculosis H37Rv complete genome; segment 36/162.	Mycobacterium tuberculosis	62,776	17-Jun-98
		GB_BA1:MLCB5	38109	Z95151	Mycobacterium leprae cosmid B5.	Mycobacterium leprae	61,831	24-Jun-97
		GB_PAT:A60305	1845	A60305	Sequence 5 from Patent WO9708323.	unidentified	61,785	06-MAR-1998
rxa00620	1014	GB_PL2:AF063247	1450	AF063247	Pneumocystis carinii f. sp. ratti enolase mRNA, complete cds.	Pneumocystis carinii f. sp. ratti	41,060	5-Jan-99
		GB_BA1:STMAPP	2069	M91546	Streptomyces lividans aminopeptidase P (PepP) gene, complete cds.	Streptomyces lividans	37,126	12-Jun-93
		GB_HTG3:AC008763	214575	AC008763	Homo sapiens chromosome 19 clone CITB-E1_3214H19, *** SEQUENCING IN PROGRESS ***, 21 unordered pieces.	Homo sapiens	40,020	3-Aug-99
rxa00624	810	GB_IN1:CEY41E3	150641	Z95559	Caenorhabditis elegans cosmid Y41E3, complete sequence.	Caenorhabditis elegans	36,986	2-Sep-99
		GB_EST13:AA362167	372	AA362167	EST71561 Macrophage I Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	38,378	21-Apr-97
		GB_IN1:CEY41E3	150641	Z95559	Caenorhabditis elegans cosmid Y41E3, complete sequence.	Caenorhabditis elegans	37,694	2-Sep-99
rxa00626	1386	GB_BA1:MTCY369	36850	Z80226	Mycobacterium tuberculosis H37Rv complete genome; segment 36/162.	Mycobacterium tuberculosis	57,971	17-Jun-98
		GB_BA1:MLCB5	38109	Z95151	Mycobacterium leprae cosmid B5.	Mycobacterium leprae	58,806	24-Jun-97
		GB_BA1:MLU15187	36138	U15187	Mycobacterium leprae cosmid L296.	Mycobacterium leprae	38,007	09-MAR-1995

Table 4 (continued)

rxa00632	795	GB_BA1:BRLBIOAD	2272	D14083	Brevibacterium flavum genes for 7,8-diaminopelargonic acid aminotransferase and dethiobiotin synthetase, complete cds.	Corynebacterium glutamicum	97,358	3-Feb-99
		GB_PAT:E04041	675	E04041	DNA sequence coding for desthiobiotinsynthetase.	Corynebacterium glutamicum	98,074	29-Sep-97
		GB_PAT:E04040	1272	E04040	DNA sequence coding for diamino pelargonic acid aminotransferase.	Corynebacterium glutamicum	93,814	29-Sep-97
rxa00633	1392	GB_BA1:BRLBIOAD	2272	D14083	Brevibacterium flavum genes for 7,8-diaminopelargonic acid aminotransferase and dethiobiotin synthetase, complete cds.	Corynebacterium glutamicum	95,690	3-Feb-99
		GB_PAT:E04040	1272	E04040	DNA sequence coding for diamino pelargonic acid aminotransferase.	Corynebacterium glutamicum	95,755	29-Sep-97
		GB_BA2:EHU38519	1290	U38519	Erwinia herbicola adenosylmethionine-8-amino-7-oxononanoate transaminase (bioA) gene, complete cds.	Erwinia herbicola	55,564	4-Nov-96
rxa00688	666	GB_BA1:MTV041	28826	AL021958	Mycobacterium tuberculosis H37Rv complete genome; segment 35/162.	Mycobacterium tuberculosis	60,030	17-Jun-98
		GB_BA1:BRLSECY	1516	D14162	Brevibacterium flavum gene for SecY protein (complete cds) and gene or adenylate kinase (partial cds).	Corynebacterium glutamicum	99,563	3-Feb-99
		GB_BA2:MBU77912	7163	U77912	Mycobacterium bovis MBE50a gene, partial cds; and MBE50b, MBE50c, preprotein translocase SecY subunit (secY), adenylate kinase (adk), methionine aminopeptidase (map), RNA polymerase ECF sigma factor (sigE50), MBE50d, and MBE50e genes, complete cds.	Mycobacterium bovis	60,030	27-Jan-99
rxa00708	930	GB_BA2:AF157493	25454	AF157493	Zymomonas mobilis ZM4 fosmid clone 42D7, complete sequence.	Zymomonas mobilis	39,116	5-Jul-99
		GB_PAT:I00836	1853	I00836	Sequence 1 from Patent US 4758514.	Unknown.	47,419	21-MAY-1993
		GB_PAT:E00311	1853	E00311	DNA coding of 2,5-diketogluconic acid reductase.	unidentified	47,419	29-Sep-97
rxa00717	1083	GB_PAT:I78753	1187	I78753	Sequence 9 from patent US 5693781.	Unknown.	37,814	3-Apr-98
		GB_PAT:I92042	1187	I92042	Sequence 9 from patent US 5726299.	Unknown.	37,814	01-DEC-1998
		GB_BA1:MTCI125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	50,647	17-Jun-98
rxa00718	831	GB_BA1:MTCI125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	55,228	17-Jun-98
		GB_BA1:MTCI125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	40,300	17-Jun-98
		GB_GSS12:AQ420755	671	AQ420755	RPCI-11-168G18.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-168G18, genomic survey sequence.	Homo sapiens	35,750	23-MAR-1999
rxa00727	1035	GB_HTG3:AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPCI-98 48.D.10 map 34A-34A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 78 unordered pieces.	Drosophila melanogaster	40,634	6-Aug-99
		GB_HTG3:AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPCI-98 48.D.10 map 34A-34A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 78 unordered pieces.	Drosophila melanogaster	40,634	6-Aug-99

Table 4 (continued)

		GB_HTG3:AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPCI-98 48.D.10 map 34A-34A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 78 unordered pieces.	Drosophila melanogaster	33,888	6-Aug-99
rxa00766	966	GB_HTG2:AC006789	83823	AC006789	Caenorhabditis elegans clone Y49F6, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.	Caenorhabditis elegans	36,737	25-Feb-99
		GB_HTG2:AC006789	83823	AC006789	Caenorhabditis elegans clone Y49F6, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.	Caenorhabditis elegans	36,737	25-Feb-99
		GB_BA1:D90810	20476	D90810	E.coli genomic DNA, Kohara clone #319(37.4-37.8 min.).	Escherichia coli	36,526	29-MAY-1997
rxa00770	1293	GB_BA1:MTV043	68848	AL022004	Mycobacterium tuberculosis H37Rv complete genome; segment 40/162.	Mycobacterium tuberculosis	66,193	24-Jun-99
		GB_BA1:MLU15182	40123	U15182	Mycobacterium leprae cosmid B2266.	Mycobacterium leprae	61,443	09-MAR-1995
		GB_BA2:SCD25	41622	AL118514	Streptomyces coelicolor cosmid D25.	Streptomyces coelicolor A3(2)	59,938	21-Sep-99
rxa00779	1056	GB_HTG1:CER08A5	51920	Z82281	Caenorhabditis elegans chromosome V clone R08A5, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	64,896	14-OCT-1998
		GB_HTG1:CER08A5	51920	Z82281	Caenorhabditis elegans chromosome V clone R08A5, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	64,896	14-OCT-1998
		GB_PL2:AF078693	1492	AF078693	Chlamydomonas reinhardtii putative O-acetylserine(thiol)lyase precursor (Crcys-1A) mRNA, nuclear gene encoding organellar protein, complete cds.	Chlamydomonas reinhardtii	57,970	3-Nov-99
rxa00780	669	GB_BA1:MTCY98	31225	Z83860	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162.	Mycobacterium tuberculosis	54,410	17-Jun-98
		GB_BA1:AVINIFREG	7099	M60090	Azotobacter chroococcum nifU, nifS, nifV, nifP, nifW, nifZ and nifM genes, complete cds.	Azotobacter chroococcum	51,729	26-Apr-93
		GB_BA2:AF001780	6701	AF001780	Cyanothece PCC 8801 NifP (nifP), nitrogenase (nifB), FdxN (fdxN), NifS (nifS) and NifU (nifU) genes, complete cds, and NifH (nifH) gene, partial cds.	Cyanothece PCC8801	36,309	08-MAR-1999
rxa00838	1023	GB_EST1:Z30506	329	Z30506	ATTS2430 AC16H Arabidopsis thaliana cDNA clone TAI306 3', mRNA sequence.	Arabidopsis thaliana	44,308	11-MAR-1994
		GB_PL2:AC006258	110469	AC006258	Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5 cM, complete sequence.	Arabidopsis thaliana	35,571	28-DEC-1998
		GB_EST37:AI998439	455	AI998439	701545695 A. thaliana, Columbia Col-0, rosette-2 Arabidopsis thaliana cDNA clone 701545695, mRNA sequence.	Arabidopsis thaliana	36,044	8-Sep-99
xa00863	867	GB_BA1:BLDAPAB	3572	Z21502	B.lactofermentum dapA and dapB genes for dihydrodipicolinate synthase and dihydrodipicolinate reductase.	Corynebacterium glutamicum	99,539	16-Aug-93
		GB_PAT:E16749	2001	E16749	gDNA encoding dihydrodipicolinate synthase (DDPS).	Corynebacterium glutamicum	99,539	28-Jul-99
		GB_PAT:E14520	2001	E14520	DNA encoding Brevibacterium dihydrodipicolinic acid synthase.	Corynebacterium glutamicum	99,539	28-Jul-99
xa00864	873	GB_BA1:BLDAPAB	3572	Z21502	B.lactofermentum dapA and dapB genes for dihydrodipicolinate synthase and dihydrodipicolinate reductase.	Corynebacterium glutamicum	99,885	16-Aug-93
		GB_BA1:CGDAPB	1902	X67737	C.glutamicum dapB gene for dihydrodipicolinate reductase.	Corynebacterium glutamicum	100,000	1-Apr-93

Table 4 (continued)

		GB_PAT:E14520	2001	E14520	DNA encoding Brevibacterium dihydrodipicolinic acid synthase.	Corynebacterium glutamicum	100,000	28-Jul-99
rxa00865	1026	GB_BA1:BLDAPAB	3572	Z21502	B.lactofermentum dapA and dapB genes for dihydrodipicolinate synthase and dihydrodipicolinate reductase.	Corynebacterium glutamicum	100,000	16-Aug-93
		GB_PAT:E16752	1411	E16752	gDNA encoding dihydrodipicolinate reductase (DDPR).	Corynebacterium glutamicum	99,805	28-Jul-99
		GB_PAT:AR038113	1411	AR038113	Sequence 18 from patent US 5804414.	Unknown.	99,805	29-Sep-99
rxa00867	650	GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	39,179	17-Jun-98
		GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	39,482	22-Aug-97
		GB_BA1:SAU19858	2838	U19858	Streptomyces antibioticus guanosine pentaphosphate synthetase (gpsl) gene, complete cds.	Streptomyces antibioticus	69,706	25-OCT-1996
rxa00873	779	GB_BA1:SCO001206	9184	AJ001206	Streptomyces coelicolor A3(2), glycogen metabolism cluster II.	Streptomyces coelicolor	63,415	29-MAR-1999
		GB_BA1:SCO001205	9589	AJ001205	Streptomyces coelicolor A3(2) glycogen metabolism clusterI.	Streptomyces coelicolor	61,617	29-MAR-1999
		GB_BA1:D78198	2304	D78198	Pimelobacter sp. DNA for trehalose synthase, complete cds.	Pimelobacter sp.	60,594	5-Feb-99
rxa00884	1263	GB_BA1:MTCY253	41230	Z81368	Mycobacterium tuberculosis H37Rv complete genome; segment 106/162.	Mycobacterium tuberculosis	37,785	17-Jun-98
		GB_BA1:MSGY222	41156	AD000010	Mycobacterium tuberculosis sequence from clone y222.	Mycobacterium tuberculosis	38,006	03-DEC-1996
		GB_GSS15:AQ654600	468	AQ654600	Sheared DNA-1O14.TF Sheared DNA Trypanosoma brucei genomic clone Sheared DNA-1O14, genomic survey sequence.	Trypanosoma brucei	33,974	22-Jun-99
rxa00891	1102	GB_BA1:MTCI418B	11700	Z96071	Mycobacterium tuberculosis H37Rv complete genome; segment 7/162.	Mycobacterium tuberculosis	63,297	18-Jun-98
		GB_BA1:SCO001206	9184	AJ001206	Streptomyces coelicolor A3(2), glycogen metabolism cluster II.	Streptomyces coelicolor	61,965	29-MAR-1999
		GB_BA1:SCO001205	9589	AJ001205	Streptomyces coelicolor A3(2) glycogen metabolism clusterI.	Streptomyces coelicolor	61,727	29-MAR-1999
rxa00952	963	EM_PAT:E10963	3118	E10963	gDNA encoding tryptophan synthase.	Corynebacterium glutamicum	99,688	08-OCT-1997 (Rel. 52, Created)
		GB_BA1:BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	98,847	10-Feb-99
		GB_PAT:E01688	7725	E01688	Genomic DNA of trp operon of prepibacterium latophelmentamn.	unidentified	98,428	29-Sep-97
rxa00954	644	GB_PAT:E01375	7726	E01375	DNA sequence of tryptophan operon.	Corynebacterium glutamicum	98,758	29-Sep-97
		GB_PAT:E01688	7725	E01688	Genomic DNA of trp operon of prepibacterium latophelmentamn.	unidentified	98,758	29-Sep-97
		GB_BA1:BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	98,758	10-Feb-99
rxa00955	1545	GB_PAT:E01375	7726	E01375	DNA sequence of tryptophan operon.	Corynebacterium glutamicum	98,372	29-Sep-97

Table 4 (continued)

		GB_BA1:BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	98,372	10-Feb-99
		GB_PAT:E01688	7725	E01688	Genomic DNA of trp operon of prepibacterium latophelmentamn.	unidentified	98,242	29-Sep-97
rxa00956	1237	EM_PAT:E10963	3118	E10963	gDNA encoding tryptophan synthase.	Corynebacterium glutamicum	98,949	08-OCT-1997 (Rel. 52, Created)
		GB_BA1:BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	99,107	10-Feb-99
		GB_PAT:E01375	7726	E01375	DNA sequence of tryptophan operon.	Corynebacterium glutamicum	98,945	29-Sep-97
rxa00957	1677	GB_BA1:BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	99,165	10-Feb-99
		GB_PAT:E01375	7726	E01375	DNA sequence of tryptophan operon.	Corynebacterium glutamicum	98,927	29-Sep-97
		GB_PAT:E01688	7725	E01688	Genomic DNA of trp operon of prepibacterium latophelmentamn.	unidentified	98,867	29-Sep-97
rxa00958	747	GB_BA1:BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	98,792	10-Feb-99
		GB_PAT:E01375	7726	E01375	DNA sequence of tryptophan operon.	Corynebacterium glutamicum	98,792	29-Sep-97
		GB_PAT:E01688	7725	E01688	Genomic DNA of trp operon of prepibacterium latophelmentamn.	unidentified	98,658	29-Sep-97
rxa00970	1050	GB_BA1:CGHOMTHR	3685	Y00546	Corynebacterium glutamicum hom-thrB genes for homoserine dehydrogenase and homoserine kinase.	Corynebacterium glutamicum	99,905	12-Sep-93
		GB_PAT:I09077	3685	I09077	Sequence 1 from Patent WO 8809819.	Unknown.	99,810	02-DEC-1994
		GB_PAT:E01358	2615	E01358	DNA encoding for homoserine dehydrogenase(HDH)and homoserine kinase(HK).	Corynebacterium glutamicum	97,524	29-Sep-97
rxa00972	1458	GB_PAT:E16755	3579	E16755	gDNA encoding diaminopimelate decarboxylase (DDC) and arginyl-tRNA synthase.	Corynebacterium glutamicum	99,931	28-Jul-99
		GB_PAT:AR038110	3579	AR038110	Sequence 15 from patent US 5804414.	Unknown.	99,931	29-Sep-99
		GB_PAT:E14508	3579	E14508	DNA encoding Brevibacterium diaminopimelic acid decarboxylase and arginyl-tRNA synthase.	Corynebacterium glutamicum	99,931	28-Jul-99
rxa00981	753	GB_OV:GGA245664	512	AJ245664	Gallus gallus partial mRNA for ATP-citrate lyase (ACL gene).	Gallus gallus	37,538	28-Sep-99
		GB_PL2:AC007887	159434	AC007887	Genomic sequence for Arabidopsis thaliana BAC F15O4 from chromosome I, complete sequence.	Arabidopsis thaliana	37,600	04-OCT-1999
		GB_GSS1:CNS00RNW	542	AL087338	Arabidopsis thaliana genome survey sequence T7 end of BAC F14D7 of IGF library from strain Columbia of Arabidopsis thaliana, genomic survey sequence.	Arabidopsis thaliana	41,264	28-Jun-99
rxa00989	1644	GB_BA1:MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	Mycobacterium tuberculosis	40,773	17-Jun-98
		GB_BA1:SCVALSFP	3619	Y13070	S.coelicolor valS, fpgs, ndk genes.	Streptomyces coelicolor	58,119	03-MAR-1998
		GB_BA1:MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	Mycobacterium tuberculosis	38,167	17-Jun-98

Table 4 (continued)

rxa00997	705	GB_BA2:CGU31225	1817	U31225	Corynebacterium glutamicum L-proline:NADP+ 5-oxidoreductase (proC) gene, complete cds.	Corynebacterium glutamicum	40,841	2-Aug-96
		GB_HTG1:CEY39C12	282838	AL009026	Caenorhabditis elegans chromosome IV clone Y39C12, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	36,416	26-OCT-1999
		GB_IN1:CEB0001	39416	Z69634	Caenorhabditis elegans cosmid B0001, complete sequence.	Caenorhabditis elegans	36,416	2-Sep-99
rxa01019	1110	GB_HTG2:AC005052	144734	AC005052	Homo sapiens clone RG038K21, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	39,172	12-Jun-98
		GB_HTG2:AC005052	144734	AC005052	Homo sapiens clone RG038K21, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	39,172	12-Jun-98
		GB_GSS9:AQ171808	512	AQ171808	HS_3179_A1_G03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3179 Col=5 Row=M, genomic survey sequence.	Homo sapiens	34,661	17-OCT-1998
rxa01026	1782	GB_BA1:SC1C2	42210	AL031124	Streptomyces coelicolor cosmid 1C2.	Streptomyces coelicolor	68,275	15-Jan-99
		GB_BA1:ATLEUCD	2982	X84647	A.teichomyceticus leuC and leuD genes.	Actinoplanes teichomyceticus	65,935	04-OCT-1995
		GB_BA1:MTV012	70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome; segment 132/162.	Mycobacterium tuberculosis	40,454	23-Jun-99
rxa01027	1131	GB_BA1:MLCB637	44882	Z99263	Mycobacterium leprae cosmid B637.	Mycobacterium leprae	38,636	17-Sep-97
		GB_BA1:MTCY349	43523	Z83018	Mycobacterium tuberculosis H37Rv complete genome; segment 131/162.	Mycobacterium tuberculosis	51,989	17-Jun-98
		GB_BA1:SPUNGMUTX	1172	Z21702	S.pneumoniae ung gene and mutX genes encoding uracil-DNA glycosylase and 8-oxodGTP nucleoside triphosphatase.	Streptococcus pneumoniae	38,088	15-Jun-94
rxa01073	954	GB_BA1:BACOUTB	1004	M15811	Bacillus subtilis outB gene encoding a sporulation protein, complete cds.	Bacillus subtilis	53,723	26-Apr-93
		GB_PR4:AC007938	167237	AC007938	Homo sapiens clone UWGC:djs201 from 7q31, complete sequence.	Homo sapiens	34,322	1-Jul-99
		GB_PL2:ATAC006282	92577	AC006282	Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete sequence.	Arabidopsis thaliana	36,181	13-MAR-1999
rxa01079	2226	GB_BA2:AF112535	4363	AF112535	Corynebacterium glutamicum putative glutaredoxin NrdH (nrdH), NrdI (nrdI), and ribonucleotide reductase alpha-chain (nrdE) genes, complete cds.	Corynebacterium glutamicum	99,820	5-Aug-99
		GB_BA1:CANRDFGEN	6054	Y09572	Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes.	Corynebacterium ammoniagenes	75,966	18-Apr-98
		GB_BA1:MTV012	70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome; segment 132/162.	Mycobacterium tuberculosis	38,296	23-Jun-99
rxa01080	567	GB_BA2:AF112535	4363	AF112535	Corynebacterium glutamicum putative glutaredoxin NrdH (nrdH), NrdI (nrdI), and ribonucleotide reductase alpha-chain (nrdE) genes, complete cds.	Corynebacterium glutamicum	100,000	5-Aug-99
		GB_BA1:CANRDFGEN	6054	Y09572	Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes.	Corynebacterium ammoniagenes	65,511	18-Apr-98
		GB_BA1:STNRD	4894	X73226	S.typhimurium nrdEF operon.	Salmonella typhimurium	52,477	03-MAR-1997
rxa01087	999	GB_IN2:AF063412	1093	AF063412	Limnadia lenticularis elongation factor 1-alpha mRNA, partial cds.	Limnadia lenticularis	43,750	29-MAR-1999
		GB_PR3:HS24M15	134539	Z94055	Human DNA sequence from PAC 24M15 on chromosome 1. Contains tenascin-R (restrictin), EST.	Homo sapiens	37,475	23-Nov-99
		GB_IN2:ARU85702	1240	U85702	Anathix ralla elongation factor-1 alpha (EF-1a) gene, partial cds.	Anathix ralla	37,319	16-Jul-97

Table 4 (continued)

rxa01095	857	GB_BA1:MTCY01B2	35938	Z95554	Mycobacterium tuberculosis H37Rv complete genome; segment 72/162.	Mycobacterium tuberculosis	43,243	17-Jun-98
		GB_HTG5:AC011632	175917	AC011632	Homo sapiens clone RP11-3N13, WORKING DRAFT SEQUENCE, 9 unordered pieces.	Homo sapiens	36,471	19-Nov-99
		GB_HTG5:AC011632	175917	AC011632	Homo sapiens clone RP11-3N13, WORKING DRAFT SEQUENCE, 9 unordered pieces.	Homo sapiens	36,836	19-Nov-99
rxa01097	477	GB_BA2:AF030405	774	AF030405	Corynebacterium glutamicum cyclase (hisF) gene, complete cds.	Corynebacterium glutamicum	100,000	13-Nov-97
		GB_BA2:AF030405	774	AF030405	Corynebacterium glutamicum cyclase (hisF) gene, complete cds.	Corynebacterium glutamicum	41,206	13-Nov-97
rxa01098	897	GB_BA2:AF030405	774	AF030405	Corynebacterium glutamicum cyclase (hisF) gene, complete cds.	Corynebacterium glutamicum	97,933	13-Nov-97
		GB_BA1:MSGY223	42061	AD000019	Mycobacterium tuberculosis sequence from clone y223.	Mycobacterium tuberculosis	40,972	10-DEC-1996
		GB_BA1:MLCB1610	40055	AL049913	Mycobacterium leprae cosmid B1610.	Mycobacterium leprae	61,366	27-Aug-99
rxa01100	861	GB_BA2:AF051846	738	AF051846	Corynebacterium glutamicum phosphoribosylformimino-5-amino-1-phosphoribosyl-4- imidazolecarboxamide isomerase (hisA) gene, complete cds.	Corynebacterium glutamicum	97,154	12-MAR-1998
		GB_BA2:AF060558	636	AF060558	Corynebacterium glutamicum glutamine amidotransferase (hisH) gene, complete cds.	Corynebacterium glutamicum	95,455	29-Apr-98
		GB_HTG1:HSDJ140A9	221755	AL109917	Homo sapiens chromosome 1 clone RP1-140A9, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	30,523	23-Nov-99
rxa01101	756	GB_BA2:AF060558	636	AF060558	Corynebacterium glutamicum glutamine amidotransferase (hisH) gene, complete cds.	Corynebacterium glutamicum	94,462	29-Apr-98
		GB_BA1:SC4G6	36917	AL096884	Streptomyces coelicolor cosmid 4G6.	Streptomyces coelicolor A3(2)	38,378	23-Jul-99
		GB_BA1:STMHISOPA	3981	M31628	S.coelicolor histidine biosynthesis operon encoding hisD, partial cds., and hisC, hisB, hisH, and hisA genes, complete cds.	Streptomyces coelicolor	60,053	26-Apr-93
rxa01104	729	GB_BA1:STMHISOPA	3981	M31628	S.coelicolor histidine biosynthesis operon encoding hisD, partial cds., and hisC, hisB, hisH, and hisA genes, complete cds.	Streptomyces coelicolor	58,333	26-Apr-93
		GB_BA1:SC4G6	36917	AL096884	Streptomyces coelicolor cosmid 4G6.	Streptomyces coelicolor A3(2)	39,045	23-Jul-99
		GB_BA1:MTCY336	32437	Z95586	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.	Mycobacterium tuberculosis	60,364	24-Jun-99
rxa01105	1221	GB_BA1:MTCY336	32437	Z95586	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.	Mycobacterium tuberculosis	60,931	24-Jun-99
		GB_BA1:MSGY223	42061	AD000019	Mycobacterium tuberculosis sequence from clone y223.	Mycobacterium tuberculosis	36,851	10-DEC-1996
		GB_BA1:MLCB1610	40055	AL049913	Mycobacterium leprae cosmid B1610.	Mycobacterium leprae	60,902	27-Aug-99
rxa01106	1449	GB_BA1:MSGY223	42061	AD000019	Mycobacterium tuberculosis sequence from clone y223.	Mycobacterium tuberculosis	37,233	10-DEC-1996

Table 4 (continued)

		GB_BA1:MSHISCD	2298	X65542	M.smegmatis genes hisD and hisC for histidinol dehydrogenase and histidinol-phosphate aminotransferase, respectively.	Mycobacterium smegmatis	60,111	30-Jun-93
		GB_BA1:MTCY336	32437	Z95586	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.	Mycobacterium tuberculosis	58,420	24-Jun-99
rxa01145	1137	GB_BA1:CORAIA	4705	L09232	Corynebacterium glutamicum acetohydroxy acid synthase (ilvB) and (ilvN) genes, and acetohydroxy acid isomeroreductase (ilvC) gene, complete cds.	Corynebacterium glutamicum	100,000	23-Feb-95
		GB_BA1:BRLILVCA	1364	D14551	Brevibacterium flavum ilvC gene for acetohydroxy acid isomeroreductase, complete cds.	Corynebacterium glutamicum	99,560	3-Feb-99
		GB_PAT:E08232	1017	E08232	DNA encoding acetohydroxy-acid isomeroreductase.	Corynebacterium glutamicum	99,803	29-Sep-97
rxa01162	1449	GB_PAT:A60299	2869	A60299	Sequence 18 from Patent WO9706261.	Aspergillus niger	38,675	06-MAR-1998
		GB_PR3:HS24E5	35506	Z82185	Human DNA sequence from Fosmid 24E5 on chromosome 22q11.2-qter contains parvalbumin, ESTs, STS.	Homo sapiens	36,204	23-Nov-99
		GB_PR3:AC005265	43900	AC005265	Homo sapiens chromosome 19, cosmid F19750, complete sequence.	Homo sapiens	38,363	6-Jul-98
rxa01208	846	GB_HTG2:AC004965	323792	AC004965	Homo sapiens clone DJ1106H14, *** SEQUENCING IN PROGRESS ***, 42 unordered pieces.	Homo sapiens	36,058	12-Jun-98
		GB_HTG2:AC004965	323792	AC004965	Homo sapiens clone DJ1106H14, *** SEQUENCING IN PROGRESS ***, 42 unordered pieces.	Homo sapiens	36,058	12-Jun-98
		GB_PL2:TAU55859	2397	U55859	Triticum aestivum heat shock protein 80 mRNA, complete cds..	Triticum aestivum	37,269	1-Feb-99
rxa01209	1528	GB_HTG3:AC011469	113436	AC011469	Homo sapiens chromosome 19 clone CIT-HSPC_475D23, *** SEQUENCING IN PROGRESS ***, 31 unordered pieces.	Homo sapiens	40,000	07-OCT-1999
		GB_HTG3:AC011469	113436	AC011469	Homo sapiens chromosome 19 clone CIT-HSPC_475D23, *** SEQUENCING IN PROGRESS ***, 31 unordered pieces.	Homo sapiens	40,000	07-OCT-1999
		GB_PL1:AB010077	77380	AB010077	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH19, complete sequence.	Arabidopsis thaliana	36,803	20-Nov-99
rxa01215	1098	GB_BA1:MTCY10G2	38970	Z92539	Mycobacterium tuberculosis H37Rv complete genome; segment 47/162.	Mycobacterium tuberculosis	37,047	17-Jun-98
		GB_IN1:LEIPRPP	1887	M76553	Leishmania donovani phosphoribosylpyrophosphate synthetase gene, complete cds.	Leishmania donovani	50,738	7-Jun-93
		GB_HTG2:HSJ799D16	130149	AL050344	Homo sapiens chromosome 1 clone RP4-799D16 map p34.3-36.1, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	38,135	29-Nov-99
rxa01239	2556	GB_BA1:MTCY48	35377	Z74020	Mycobacterium tuberculosis H37Rv complete genome; segment 69/162.	Mycobacterium tuberculosis	38,139	17-Jun-98
		GB_PR2:AB029032	6377	AB029032	Homo sapiens mRNA for KIAA1109 protein, partial cds.	Homo sapiens	39,394	4-Aug-99
		GB_GSS9:AQ107201	355	AQ107201	HS_3098_A1_C03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3098 Col=5 Row=E, genomic survey sequence.	Homo sapiens	41,408	28-Aug-98
rxa01253	873	GB_PL2:F5O8	99923	AC005990	Arabidopsis thaliana chromosome 1 BAC F5O8 sequence, complete sequence.	Arabidopsis thaliana	36,118	23-DEC-1998
		GB_PL2:F5O8	99923	AC005990	Arabidopsis thaliana chromosome 1 BAC F5O8 sequence, complete sequence.	Arabidopsis thaliana	35,574	23-DEC-1998
		GB_IN1:CELC06G1	31205	U41014	Caenorhabditis elegans cosmid C06G1.	Caenorhabditis elegans	38,560	30-Nov-95

Table 4 (continued)

rxa01321	1044	GB_GSS14:AQ518843	441	AQ518843	HS_5106_A1_D10_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=682 Col=19 Row=G, genomic survey sequence.	Homo sapiens	41,121	05-MAY-1999
		GB_HTG2:AC007473	194859	AC007473	Drosophila melanogaster chromosome 2 clone BACR38D12 (D590) RPCI-98 38.D.12 map 48A-48B strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 60 unordered pieces.	Drosophila melanogaster	40,634	2-Aug-99
		GB_HTG4:AC011696	115847	AC011696	Drosophila melanogaster chromosome 2 clone BACR35F01 (D1156) RPCI-98 35.F.1 map 48A-48C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 108 unordered pieces.	Drosophila melanogaster	38,290	26-OCT-1999
rxa01352	706	GB_PL2:ATAC005167	83260	AC005167	Arabidopsis thaliana chromosome II BAC F12A24 genomic sequence, complete sequence.	Arabidopsis thaliana	34,311	15-OCT-1998
		GB_PL2:ATAC005825	97380	AC005825	Arabidopsis thaliana chromosome II BAC T24I21 genomic sequence, complete sequence.	Arabidopsis thaliana	34,311	12-Apr-99
		GB_HTG3:AC011150	127222	AC011150	Homo sapiens clone 4_K_17, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	37,722	01-OCT-1999
rxa01360	259	GB_EST32:AI725583	728	AI725583	BNLGHi12371 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (U86081) root hair defective 3 [Arabidopsis thaliana], mRNA sequence.	Gossypium hirsutum	38,492	11-Jun-99
		GB_PR2:HS227P17	82951	Z81007	Human DNA sequence from PAC 227P17, between markers DXS6791 andDXS8038 on chromosome X contains CpG island, EST.	Homo sapiens	39,738	23-Nov-99
		GB_EST34:AV171099	173	AV171099	AV171099 Mus musculus head C57BL/6J 14, 17 day embryo Mus musculus cDNA clone 3200002M11, mRNA sequence.	Mus musculus	46,237	6-Jul-99
rxa01361	629	GB_RO:AB008915S1	530	AB008915	Mus musculus mGpi1 gene, exon 1.	Mus musculus	45,574	28-Sep-99
		GB_EST22:AI050532	293	AI050532	uc83d10.y1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:1432243 5' similar to TR:O35120 O35120 MGPI1P. ;, mRNA sequence.	Mus musculus	44,097	9-Jul-98
		GB_RO:AB008895	3062	AB008895	Mus musculus mRNA for mGpi1p, complete cds.	Mus musculus	41,316	23-Nov-97
rxa01381	944	GB_PL1:AB005237	87835	AB005237	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3,complete sequence.	Arabidopsis thaliana	36,606	20-Nov-99
		GB_GSS5:AQ766840	491	AQ766840	HS_2026_A2_C09_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=18 Row=E, genomic survey sequence.	Homo sapiens	37,916	28-Jul-99
		GB_BA1:MTV043	68848	AL022004	Mycobacterium tuberculosis H37Rv complete genome; segment 40/162.	Mycobacterium tuberculosis	37,419	24-Jun-99
rxa01393	993	GB_BA1:CGLYSEG	2374	X96471	C.glutamicum lysE and lysG genes.	Corynebacterium glutamicum	34,831	24-Feb-97
		GB_BA1:SC5A7	40337	AL031107	Streptomyces coelicolor cosmid 5A7.	Streptomyces coelicolor	35,138	27-Jul-98
		GB_PR3:AC004054	112184	AC004054	Homo sapiens chromosome 4 clone B220G8 map 4q21, complete sequence.	Homo sapiens	37,277	9-Jul-98
rxa01394	822	GB_BA1:CGLYSEG	2374	X96471	C.glutamicum lysE and lysG genes.	Corynebacterium glutamicum	100,000	24-Feb-97
		GB_GSS5:AQ769223	500	AQ769223	HS_3155_B2_G10_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3155 Col=20 Row=N, genomic survey sequence.	Homo sapiens	38,400	28-Jul-99

Table 4 (continued)

		GB_BA1:CGLYSEG	2374	X96471	C.glutamicum lysE and lysG genes.	Corynebacterium glutamicum	33,665	24-Feb-97
rxa01416	630	GB_BA1:SC3C3	31382	AL031231	Streptomyces coelicolor cosmid 3C3.	Streptomyces coelicolor	62,726	10-Aug-98
		GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	39,159	22-Aug-97
		GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	37,340	17-Jun-98
rxa01442	1347	GB_BA1:D90827	18886	D90827	E.coli genomic DNA, Kohara clone #336(41.2-41.6 min.).	Escherichia coli	58,517	21-MAR-1997
		GB_BA1:D90828	14590	D90828	E.coli genomic DNA, Kohara clone #336gap(41.6-41.9 min.).	Escherichia coli	56,151	21-MAR-1997
		GB_BA2:AE000279	10855	AE000279	Escherichia coli K-12 MG1655 section 169 of 400 of the complete genome.	Escherichia coli	56,021	12-Nov-98
rxa01446	1413	GB_BA1:SCH10	39524	AL049754	Streptomyces coelicolor cosmid H10.	Streptomyces coelicolor	39,037	04-MAY-1999
		GB_BA1:MTY13E10	35019	Z95324	Mycobacterium tuberculosis H37Rv complete genome; segment 18/162.	Mycobacterium tuberculosis	40,130	17-Jun-98
		GB_BA1:MLCB4	36310	AL023514	Mycobacterium leprae cosmid B4.	Mycobacterium leprae	37,752	27-Aug-99
rxa01463	1395	GB_BA1:MTCY98	31225	Z83860	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162.	Mycobacterium tuberculosis	39,057	17-Jun-98
		GB_BA1:MSGB1229CS	30670	L78812	Mycobacterium leprae cosmid B1229 DNA sequence.	Mycobacterium leprae	54,382	15-Jun-96
		GB_BA2:AF027507	5168	AF027507	Mycobacterium smegmatis dGTPase (dgt), and primase (dnaG) genes, complete cds; tRNA-Asn gene, complete sequence.	Mycobacterium smegmatis	52,941	16-Jan-98
rxa01486	757	GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	40,941	17-Jun-98
		GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	38,451	22-Aug-97
		GB_BA1:SC3C3	31382	AL031231	Streptomyces coelicolor cosmid 3C3.	Streptomyces coelicolor	61,194	10-Aug-98
rxa01489	1146	GB_BA1:CORFADS	1547	D37967	Corynebacterium ammoniagenes gene for FAD synthetase, complete cds.	Corynebacterium ammoniagenes	58,021	8-Feb-99
		GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	38,414	22-Aug-97
		GB_BA1:SC10A7	39739	AL078618	Streptomyces coelicolor cosmid 10A7.	Streptomyces coelicolor	36,930	9-Jun-99
rxa01491	774	GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	37,062	17-Jun-98
		GB_EST13:AA356956	255	AA356956	EST65614 Jurkat T-cells III Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	37,647	21-Apr-97
		GB_OV:OMDNAPROI	7327	X92380	O.mossambicus prolactin I gene.	Tilapia mossambica	38,289	19-OCT-1995
rxa01508	1662	GB_IN1:CEF28C12	14653	Z93380	Caenorhabditis elegans cosmid F28C12, complete sequence.	Caenorhabditis elegans	37,984	23-Nov-98
		GB_IN1:CEF28C12	14653	Z93380	Caenorhabditis elegans cosmid F28C12, complete sequence.	Caenorhabditis elegans	38,469	23-Nov-98
rxa01512	723	GB_BA1:SCE9	37730	AL049841	Streptomyces coelicolor cosmid E9.	Streptomyces coelicolor	39,021	19-MAY-1999
		GB_BA1:MAU88875	840	U88875	Mycobacterium avium hypoxanthine-guanine phosphoribosyl transferase gene, complete cds.	Mycobacterium avium	57,521	05-MAR-1997

Table 4 (continued)

		GB_BA1:MTY15C10	33050	Z95436	Mycobacterium tuberculosis H37Rv complete genome; segment 154/162.	Mycobacterium tuberculosis	40,086	17-Jun-98
rxa01514	711	GB_BA1:MTCY7H7B	24244	Z95557	Mycobacterium tuberculosis H37Rv complete genome; segment 153/162.	Mycobacterium tuberculosis	43,343	18-Jun-98
		GB_BA1:MLCB2548	38916	AL023093	Mycobacterium leprae cosmid B2548.	Mycobacterium leprae	38,177	27-Aug-99
		GB_PL1:EGGTPCHI	242	Z49757	E.gracilis mRNA for GTP cyclohydrolase I (core region).	Euglena gracilis	64,876	20-OCT-1995
rxa01515	975	GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	38,943	17-Apr-96
		GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	37,500	17-Apr-96
		GB_BA1:MTCY49	39430	Z73966	Mycobacterium tuberculosis H37Rv complete genome; segment 93/162.	Mycobacterium tuberculosis	38,010	24-Jun-99
rxa01516	513	GB_IN1:DME238847	5419	AJ238847	Drosophila melanogaster mRNA for drosophila dodeca-satellite protein 1 (DDP-1).	Drosophila melanogaster	36,346	13-Aug-99
		GB_HTG3:AC009210	103814	AC009210	Drosophila melanogaster chromosome 2 clone BACR01I06 (D1054) RPCI-98 01.I.6 map 55D-55D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 86 unordered pieces.	Drosophila melanogaster	37,897	20-Aug-99
		GB_IN2:AF132179	4842	AF132179	Drosophila melanogaster clone LD21677 unknown mRNA.	Drosophila melanogaster	36,149	3-Jun-99
rxa01517	600	GB_PL2:F6H8	82596	AF178045	Arabidopsis thaliana BAC F6H8.	Arabidopsis thaliana	35,846	19-Aug-99
		GB_PL2:AF038831	647	AF038831	Sorosporium saponariae internal transcribed spacer 1, 5.8S ribosomal RNA gene; and internal transcribed spacer 2, complete sequence.	Sorosporium saponariae	40,566	13-Apr-99
		GB_PL2:ATAC005957	108355	AC005957	Arabidopsis thaliana chromosome II BAC T15J14 genomic sequence, complete sequence.	Arabidopsis thaliana	38,095	7-Jan-99
rxa01521	921	GB_BA1:ANANIFBH	5936	J05111	Anabaena sp. (clone AnH20.1) nitrogen fixation operon nifB, fdxN, nifS, nifU, and nifH genes, complete cds.	Anabaena sp.	38,206	26-Apr-93
		GB_PR2:AC002461	197273	AC002461	Human BAC clone RG204I16 from 7q31, complete sequence.	Homo sapiens	36,623	20-Aug-97
		GB_PR2:AC002461	197273	AC002461	Human BAC clone RG204I16 from 7q31, complete sequence.	Homo sapiens	34,719	20-Aug-97
rxa01528	651	GB_RO:MM437P9	165901	AL049866	Mus musculus chromosome X, clone 437P9.	Mus musculus	37,500	29-Jun-99
		GB_PR3:AC005740	186780	AC005740	Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.	Homo sapiens	37,031	01-OCT-1998
		GB_PR3:AC005740	186780	AC005740	Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.	Homo sapiens	38,035	01-OCT-1998
rxa01551	1998	GB_BA1:MTCY22G10	35420	Z84724	Mycobacterium tuberculosis H37Rv complete genome; segment 21/162.	Mycobacterium tuberculosis	38,371	17-Jun-98
		GB_BA2:ECOUW89	176195	U00006	E. coli chromosomal region from 89.2 to 92.8 minutes.	Escherichia coli	38,084	17-DEC-1993
		GB_BA1:SCQ11	15441	AL096823	Streptomyces coelicolor cosmid Q11.	Streptomyces coelicolor	60,775	8-Jul-99
rxa01561	1053	GB_IN1:CEY62H9A	47396	AL032630	Caenorhabditis elegans cosmid Y62H9A, complete sequence.	Caenorhabditis elegans	38,514	2-Sep-99
		GB_PR4:HSU51003	3202	U51003	Homo sapiens DLX-2 (DLX-2) gene, complete cds.	Homo sapiens	37,730	07-DEC-1999
		GB_OM:PIGDAO1	395	M18444	Pig D-amino acid oxidase (DAO) gene, exon 1.	Sus scrofa	39,340	27-Apr-93
rxa01599	1785	GB_BA1:MTCI125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	63,300	17-Jun-98
		GB_BA1:U00021	39193	U00021	Mycobacterium leprae cosmid L247.	Mycobacterium leprae	36,756	29-Sep-94

Table 4 (continued)

		GB_BA1:MLCB1351	38936	Z95117	Mycobacterium leprae cosmid B1351.	Mycobacterium leprae	36,756	24-Jun-97
rxa01617	795	GB_PR2:HSMTM0	217657	AL034384	Human chromosome Xq28, cosmid clones 7H3, 14D7, C1230, 11E7, F1096, A12197, 12G8, A09100; complete sequence bases 1. .217657.	Homo sapiens	40,811	5-Jul-99
		GB_PR2:HS13D10	153147	AL021407	Homo sapiens DNA sequence from PAC 13D10 on chromosome 6p22.3-23. Contains CpG island.	Homo sapiens	38,768	23-Nov-99
		GB_PR2:HSMTM0	217657	AL034384	Human chromosome Xq28, cosmid clones 7H3, 14D7, C1230, 11E7, F1096, A12197, 12G8, A09100; complete sequence bases 1. .217657.	Homo sapiens	39,018	5-Jul-99
rxa01657	723	GB_BA1:MTCY1A10	25949	Z95387	Mycobacterium tuberculosis H37Rv complete genome; segment 117/162.	Mycobacterium tuberculosis	40,656	17-Jun-98
		GB_EST6:D79278	392	D79278	HUM213D06B Human aorta polyA+ (TFujiwara) Homo sapiens cDNA clone GEN-213D06 5', mRNA sequence.	Homo sapiens	44,262	9-Feb-96
		GB_BA2:AF129925	10243	AF129925	Thiobacillus ferrooxidans carboxysome operon, complete cds.	Thiobacillus ferrooxidans	40,709	17-MAY-1999
rxa01660	675	GB_BA1:MTV013	11364	AL021309	Mycobacterium tuberculosis H37Rv complete genome; segment 134/162.	Mycobacterium tuberculosis	40,986	17-Jun-98
		GB_RO:MMFV1	6480	X97719	M.musculus retrovirus restriction gene Fv1.	Mus musculus	35,364	29-Aug-96
		GB_PAT:A67508	6480	A67508	Sequence 1 from Patent WO9743410.	Mus musculus	35,364	05-MAY-1999
rxa01678	651	GB_VI:TVU95309	600	U95309	Tula virus O64 nucleocapsid protein gene, partial cds.	Tula virus	41,894	28-OCT-1997
		GB_VI:TVU95303	600	U95303	Tula virus O52 nucleocapsid protein gene, partial cds.	Tula virus	41,712	28-OCT-1997
		GB_VI:TVU95302	600	U95302	Tula virus O24 nucleocapsid protein gene, partial cds.	Tula virus	39,576	28-OCT-1997
rxa01679	1359	GB_EST5:H91843	362	H91843	ys81e01.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:221208 3' similar to gb:X63749_rna1 GUANINE NUCLEOTIDE-BINDING PROTEIN G(T), ALPHA-1 (HUMAN);, mRNA sequence.	Homo sapiens	39,157	29-Nov-95
		GB_STS:G26925	362	G26925	human STS SHGC-30023, sequence tagged site.	Homo sapiens	39,157	14-Jun-96
		GB_PL2:AF139451	1202	AF139451	Gossypium robinsonii CelA2 pseudogene, partial sequence.	Gossypium robinsonii	38,910	1-Jun-99
rxa01690	1224	GB_BA1:SC1C2	42210	AL031124	Streptomyces coelicolor cosmid 1C2.	Streptomyces coelicolor	60,644	15-Jan-99
		GB_EST22:AI064232	493	AI064232	GH04563.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH04563 5prime, mRNA sequence.	Drosophila melanogaster	38,037	24-Nov-98
		GB_IN2:AF117896	1020	AF117896	Drosophila melanogaster neuropeptide F (npf) gene, complete cds.	Drosophila melanogaster	36,122	2-Jul-99
rxa01692	873	GB_BA2:AF067123	1034	AF067123	Lactobacillus reuteri cobalamin biosynthesis protein J (cbiJ) gene, partial cds; and uroporphyrin-III C-methyltransferase (sumT) gene, complete cds.	Lactobacillus reuteri	48,079	3-Jun-98
		GB_RO:RATNFHPEP	3085	M37227	Rat heavy neurofilament (NF-H) polypeptide, partial cds.	Rattus norvegicus	37,093	27-Apr-93
		GB_RO:RSNFH	3085	X13804	Rat mRNA for heavy neurofilament polypeptide NF-H C-terminus.	Rattus sp.	37,093	14-Jul-95
rxa01698	1353	GB_BA2:AF124600	4115	AF124600	Corynebacterium glutamicum chorismate synthase (aroC), shikimate kinase (aroK), and 3-dehydroquinate synthase (aroB) genes, complete cds; and putative cytoplasmic peptidase (pepQ) gene, partial cds.	Corynebacterium glutamicum	100,000	04-MAY-1999
		GB_BA1:MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome; segment 111/162.	Mycobacterium tuberculosis	36,323	17-Jun-98

Table 4 (continued)

		GB_BA1:MSGB937CS	38914	L78820	Mycobacterium leprae cosmid B937 DNA sequence.	Mycobacterium leprae	62,780	15-Jun-96
rxa01699	693	GB_BA2:AF124600	4115	AF124600	Corynebacterium glutamicum chorismate synthase (aroC), shikimate kinase (aroK), and 3-dehydroquinate synthase (aroB) genes, complete cds; and putative cytoplasmic peptidase (pepQ) gene, partial cds.	Corynebacterium glutamicum	100,000	04-MAY-1999
		GB_BA2:AF016585	41097	AF016585	Streptomyces caelestis cytochrome P-450 hydroxylase homolog (nidi) gene, partial cds; polyketide synthase modules 1 through 7 (nidA) genes, complete cds; and N-methyltransferase homolog gene, partial cds.	Streptomyces caelestis	40,260	07-DEC-1997
		GB_EST9:C19712	399	C19712	C19712 Rice panicle at ripening stage Oryza sativa cDNA clone E10821_1A, mRNA sequence.	Oryza sativa	45,425	24-OCT-1996
rxa01712	805	GB_EST21:AA952466	278	AA952466	TENS1404 T. cruzi epimastigote normalized cDNA Library Trypanosoma cruzi cDNA clone 1404 5', mRNA sequence.	Trypanosoma cruzi	40,876	29-OCT-1998
		GB_EST21:AA952466	278	AA952466	TENS1404 T. cruzi epimastigote normalized cDNA Library Trypanosoma cruzi cDNA clone 1404 5', mRNA sequence.	Trypanosoma cruzi	41,367	29-OCT-1998
rxa01719	684	GB_HTG1:HSDJ534K7	154416	AL109925	Homo sapiens chromosome 1 clone RP4-534K7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	35,651	23-Nov-99
		GB_HTG1:HSDJ534K7	154416	AL109925	Homo sapiens chromosome 1 clone RP4-534K7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	35,651	23-Nov-99
		GB_EST27:AI447108	431	AI447108	mq91e08.x1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:586118 3', mRNA sequence.	Mus musculus	39,671	09-MAR-1999
rxa01720	1332	GB_PR4:AC006322	179640	AC006322	Homo sapiens PAC clone DJ1060B11 from 7q11.23-q21.1, complete sequence.	Homo sapiens	35,817	18-MAR-1999
		GB_PL2:TM018A10	106184	AF013294	Arabidopsis thaliana BAC TM018A10.	Arabidopsis thaliana	35,698	12-Jul-97
		GB_PR4:AC006322	179640	AC006322	Homo sapiens PAC clone DJ1060B11 from 7q11.23-q21.1, complete sequence.	Homo sapiens	37,243	18-MAR-1999
rxa01746	876	GB_EST3:R46227	443	R46227	yg52a03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:36000 3', mRNA sequence.	Homo sapiens	42,812	22-MAY-1995
		GB_EST3:R46227	443	R46227	yg52a03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:36000 3', mRNA sequence.	Homo sapiens	42,655	22-MAY-1995
rxa01747	1167	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	59,294	17-Jun-98
		GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	57,584	22-Aug-97
		GB_BA1:SC5F7	40024	AL096872	Streptomyces coelicolor cosmid 5F7.	Streptomyces coelicolor A3(2)	61,810	22-Jul-99
rxa01757	924	GB_EST21:AA918454	416	AA918454	om38c02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1543298 3' similar to WP:F28F8.3 CE09757 SMALL NUCLEAR RIBONUCLEOPROTEIN E ;, mRNA sequence.	Homo sapiens	39,655	23-Jun-98
		GB_EST4:H34042	345	H34042	EST110563 Rat PC-12 cells, NGF-treated (9 days) Rattus sp. cDNA clone RPNBI81 5' end, mRNA sequence.	Rattus sp.	35,942	2-Apr-98
		GB_EST20:AA899038	450	AA899038	NCP6G8T7 Perithecial Neurospora crassa cDNA clone NP6G8 3' end, mRNA sequence.	Neurospora crassa	40,000	12-Apr-98

Table 4 (continued)

rxa01807	915	GB_BA1:AP000063	185300	AP000063	Aeropyrum pernix genomic DNA, section 6/7.	Aeropyrum pernix	40,067	22-Jun-99
		GB_HTG4:AC010694	115857	AC010694	Drosophila melanogaster clone RPCI98-6H2, *** SEQUENCING IN PROGRESS ***, 75 unordered pieces.	Drosophila melanogaster	35,450	16-OCT-1999
		GB_HTG4:AC010694	115857	AC010694	Drosophila melanogaster clone RPCI98-6H2, *** SEQUENCING IN PROGRESS ***, 75 unordered pieces.	Drosophila melanogaster	35,450	16-OCT-1999
rxa01821	401	GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	Corynebacterium glutamicum	100,000	7-Jan-99
		GB_RO:RATALGL	7601	M24108	Rattus norvegicus (clone A2U42) alpha2u globulin gene, exons 1-7.	Rattus norvegicus	38,692	15-DEC-1994
		GB_OV:APIGY2	1381	X78272	Anas platyrhynchos (Super M) IgY upsilon heavy chain gene, exon 2.	Anas platyrhynchos	36,962	15-Feb-99
rxa01835	654	GB_EST30:AI629479	353	AI629479	486101D10.x1 486 - leaf primordia cDNA library from Hake lab Zea mays cDNA, mRNA sequence.	Zea mays	38,109	26-Apr-99
		GB_STS:G48245	515	G48245	SHGC-62915 Human Homo sapiens STS genomic, sequence tagged site.	Homo sapiens	37,021	26-MAR-1999
		GB_GSS3:B49052	515	B49052	RPCI11-4I12.TV RPCI-11 Homo sapiens genomic clone RPCI-11-4I12, genomic survey sequence.	Homo sapiens	37,021	8-Apr-99
rxa01850	1470	GB_BA2:ECOUW67_0	110000	U18997	Escherichia coli K-12 chromosomal region from 67.4 to 76.0 minutes.	Escherichia coli	37,196	U18997
		GB_BA2:AE000392	10345	AE000392	Escherichia coli K-12 MG1655 section 282 of 400 of the complete genome.	Escherichia coli	38,021	12-Nov-98
		GB_BA2:U32715	13136	U32715	Haemophilus influenzae Rd section 30 of 163 of the complete genome.	Haemophilus influenzae Rd	39,860	29-MAY-1998
rxa01878	1002	GB_HTG1:CEY64F11	177748	Z99776	Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	37,564	14-OCT-1998
		GB_HTG1:CEY64F11	177748	Z99776	Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	37,564	14-OCT-1998
		GB_HTG1:CEY64F11	177748	Z99776	Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	37,576	14-OCT-1998
rxa01892	852	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	35,910	19-Jun-98
		GB_BA1:MLCB250	40603	Z97369	Mycobacterium leprae cosmid B250.	Mycobacterium leprae	64,260	27-Aug-99
		GB_BA1:MSGB1529CS	36985	L78824	Mycobacterium leprae cosmid B1529 DNA sequence.	Mycobacterium leprae	64,260	15-Jun-96
rxa01894	978	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	37,229	19-Jun-98
		GB_IN1:CELF46H5	38886	U41543	Caenorhabditis elegans cosmid F46H5.	Caenorhabditis elegans	38,525	29-Nov-96
		GB_HTG3:AC009204	115633	AC009204	Drosophila melanogaster chromosome 2 clone BACR03E19 (D1033) RPCI-98 03.E.19 map 36E-37C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 94 unordered pieces.	Drosophila melanogaster	31,579	18-Aug-99
rxa01920	1125	GB_BA2:AF112536	1798	AF112536	Corynebacterium glutamicum ribonucleotide reductase beta-chain (nrdF) gene, complete cds.	Corynebacterium glutamicum	99,733	5-Aug-99
		GB_BA1:CANRDFGEN	6054	Y09572	Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes.	Corynebacterium ammoniagenes	70,321	18-Apr-98

Table 4 (continued)

		GB_BA2:AF050168	1228	AF050168	Corynebacterium ammoniagenes ribonucleoside diphosphate reductase small subunit (nrdF) gene, complete cds.	Corynebacterium ammoniagenes	72,082	23-Apr-98
rxa01928	960	GB_BA1:CGPAN	2164	X96580	C.glutamicum panB, panC & xylB genes.	Corynebacterium glutamicum	100,000	11-MAY-1999
		GB_PL1:AP000423	154478	AP000423	Arabidopsis thaliana chloroplast genomic DNA, complete sequence, strain:Columbia.	Chloroplast Arabidopsis thaliana	35,917	15-Sep-99
		GB_PL1:AP000423	154478	AP000423	Arabidopsis thaliana chloroplast genomic DNA, complete sequence, strain:Columbia.	Chloroplast Arabidopsis thaliana	33,925	15-Sep-99
rxa01929	936	GB_BA1:CGPAN	2164	X96580	C.glutamicum panB, panC & xylB genes.	Corynebacterium glutamicum	100,000	11-MAY-1999
		GB_BA1:XCU33548	8429	U33548	Xanthomonas campestris hrpB pathogenicity locus proteins HrpB1, HrpB2, HrpB3, HrpB4, HrpB5, HrpB6, HrpB7, HrpB8, HrpA1, and ORF62 genes, complete cds.	Xanthomonas campestris pv. vesicatoria	38,749	19-Sep-96
		GB_BA1:XANHRPB6A	1329	M99174	Xanthomonas campestris hrpB6 gene, complete cds.	Xanthomonas campestris	39,305	14-Sep-93
rxa01940	1059	GB_IN2:CFU43371	1060	U43371	Crithidia fasciculata inosine-uridine preferring nucleoside hydrolase (IUNH) gene, complete cds.	Crithidia fasciculata	61,417	18-Jun-96
		GB_BA2:AE001467	11601	AE001467	Helicobacter pylori, strain J99 section 28 of 132 of the complete genome.	Helicobacter pylori J99	38,560	20-Jan-99
		GB_RO:AF175967	3492	AF175967	Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.	Mus musculus	40,275	26-Sep-99
rxa02022	1230	GB_BA1:CGDAPE	1966	X81379	C.glutamicum dapE gene and orf2.	Corynebacterium glutamicum	100,000	8-Aug-95
		GB_BA1:CGDNAAROP	2612	X85965	C.glutamicum ORF3 and aroP gene.	Corynebacterium glutamicum	38,889	30-Nov-97
		GB_BA1:APU47055	6469	U47055	Anabaena PCC7120 nitrogen fixation proteins (nifE, nifN, nifX, nifW) genes, complete cds, and nitrogenase (nifK) and hesA genes, partial cds.	Anabaena PCC7120	36,647	17-Feb-96
rxa02024	859	GB_BA1:MTCI364	29540	Z93777	Mycobacterium tuberculosis H37Rv complete genome; segment 52/162.	Mycobacterium tuberculosis	59,415	17-Jun-98
		GB_BA1:MSGB1912CS	38503	L01536	M. leprae genomic dna sequence, cosmid b1912.	Mycobacterium leprae	57,093	14-Jun-96
		GB_BA1:MLU15180	38675	U15180	Mycobacterium leprae cosmid B1756.	Mycobacterium leprae	57,210	09-MAR-1995
rxa02027								
rxa02031								
rxa02072	1464	GB_BA1:CGGDHA	2037	X72855	C.glutamicum GDHA gene.	Corynebacterium glutamicum	99,317	24-MAY-1993
		GB_BA1:CGGDH	2037	X59404	Corynebacterium glutamicum, gdh gen for glutamate dehydrogenase.	Corynebacterium glutamicum	94,387	30-Jul-99
		GB_BA1:PAE18494	1628	Y18494	Pseudomonas aeruginosa gdhA gene, strain PAC1.	Pseudomonas aeruginosa	62,247	6-Feb-99

Table 4 (continued)

rxa02085	2358	GB_BA1:MTCY22G8	22550	Z95585	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162.	Mycobacterium tuberculosis	38,442	17-Jun-98
		GB_BA1:MLCB33	42224	Z94723	Mycobacterium leprae cosmid B33.	Mycobacterium leprae	56,486	24-Jun-97
		GB_BA1:ECOUW85	91414	M87049	E. coli genomic sequence of the region from 84.5 to 86.5 minutes.	Escherichia coli	52,127	29-MAY-1995
rxa02093	927	GB_EST14:AA448146	452	AA448146	zw82h01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782737 5', mRNA sequence.	Homo sapiens	34,163	4-Jun-97
		GB_EST17:AA641937	444	AA641937	ns18b10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1183963 5', mRNA sequence.	Homo sapiens	35,586	27-OCT-1997
		GB_PR3:AC003074	143029	AC003074	Human PAC clone DJ0596O09 from 7p15, complete sequence.	Homo sapiens	31,917	6-Nov-97
rxa02106	1179	GB_BA1:SC1A6	37620	AL023496	Streptomyces coelicolor cosmid 1A6.	Streptomyces coelicolor	35,818	13-Jan-99
		GB_PR4:AC005553	179651	AC005553	Homo sapiens chromosome 17, clone hRPK.112_J_9, complete sequence.	Homo sapiens	34,274	31-DEC-1998
		GB_EST3:R49746	397	R49746	yg71g10.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:38768 5' similar to gb:V00567 BETA-2-MICROGLOBULIN PRECURSOR (HUMAN);, mRNA sequence.	Homo sapiens	41,162	18-MAY-1995
rxa02111	1407	GB_BA1:SC6G10	36734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	50,791	24-MAR-1999
		GB_BA1:U00010	41171	U00010	Mycobacterium leprae cosmid B1170.	Mycobacterium leprae	37,563	01-MAR-1994
		GB_BA1:MTCY336	32437	Z95586	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.	Mycobacterium tuberculosis	39,504	24-Jun-99
rxa02112	960	GB_HTG3:AC010579	157658	AC010579	Drosophila melanogaster chromosome 3 clone BACR09D08 (D1101) RPCI-98 09.D.8 map 96F-96F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 121 unordered pieces.	Drosophila melanogaster	37,909	24-Sep-99
		GB_GSS3:B09839	1191	B09839	T12A12-Sp6 TAMU Arabidopsis thaliana genomic clone T12A12, genomic survey sequence.	Arabidopsis thaliana	37,843	14-MAY-1997
		GB_HTG3:AC010579	157658	AC010579	Drosophila melanogaster chromosome 3 clone BACR09D08 (D1101) RPCI-98 09.D.8 map 96F-96F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 121 unordered pieces.	Drosophila melanogaster	37,909	24-Sep-99
rxa02134	1044	GB_BA1:SCSECYDNA	6154	X83011	S.coelicolor secY locus DNA.	Streptomyces coelicolor	36,533	02-MAR-1998
		GB_EST32:AI731596	568	AI731596	BNLGHi10185 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AC004005) putative ribosomal protein L7 [Arabidopsis thaliana], mRNA sequence.	Gossypium hirsutum	33,451	11-Jun-99
		GB_BA1:SCSECYDNA	6154	X83011	S.coelicolor secY locus DNA.	Streptomyces coelicolor	36,756	02-MAR-1998
rxa02135	1197	GB_PR3:HS525L6	168111	AL023807	Human DNA sequence from clone RP3-525L6 on chromosome 6p22.3-23 Contains CA repeat, STSs, GSSs and a CpG island, complete sequence.	Homo sapiens	34,365	23-Nov-99
		GB_PL2:ATF21P8	85785	AL022347	Arabidopsis thaliana DNA chromosome 4, BAC clone F21P8 (ESSA project).	Arabidopsis thaliana	34,325	9-Jun-99
		GB_PL2:U89959	106973	U89959	Arabidopsis thaliana BAC T7I23, complete sequence.	Arabidopsis thaliana	33,874	26-Jun-98

Table 4 (continued)

rxa02136	645	GB_PL2:ATAC005819	57752	AC005819	Arabidopsis thaliana chromosome II BAC T3A4 genomic sequence, complete sequence.	Arabidopsis thaliana	34,123	3-Nov-98
		GB_PL2:F15K9	71097	AC005278	Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence.	Arabidopsis thaliana	31,260	7-Nov-98
		GB_PL2:U89959	106973	U89959	Arabidopsis thaliana BAC T7I23, complete sequence.	Arabidopsis thaliana	34,281	26-Jun-98
rxa02139	1962	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	62,904	17-Jun-98
		GB_BA1:MSGB1554CS	36548	L78814	Mycobacterium leprae cosmid B1554 DNA sequence.	Mycobacterium leprae	36,648	15-Jun-96
		GB_BA1:MSGB1551CS	36548	L78813	Mycobacterium leprae cosmid B1551 DNA sequence.	Mycobacterium leprae	36,648	15-Jun-96
rxa02153	903	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,104	1-Jul-98
		GB_BA1:AF005242	1044	AF005242	Corynebacterium glutamicum N-acetylglutamate-5-semialdehyde dehydrogenase (argC) gene, complete cds.	Corynebacterium glutamicum	99,224	2-Jul-97
		GB_BA1:CGARGCJBD	4355	X86157	C.glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	25-Jul-96
rxa02154	414	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	98,551	1-Jul-98
		GB_BA1:AF005242	1044	AF005242	Corynebacterium glutamicum N-acetylglutamate-5-semialdehyde dehydrogenase (argC) gene, complete cds.	Corynebacterium glutamicum	98,477	2-Jul-97
		GB_BA1:CGARGCJBD	4355	X86157	C.glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	25-Jul-96
rxa02155	1287	GB_BA1:CGARGCJBD	4355	X86157	C.glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	99,767	25-Jul-96
		GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,378	1-Jul-98
		GB_BA1:MSGB1133CS	42106	L78811	Mycobacterium leprae cosmid B1133 DNA sequence.	Mycobacterium leprae	55,504	15-Jun-96
rxa02156	1074	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	100,000	1-Jul-98

Table 4 (continued)

		GB_BA1:CGARGCJBD	4355	X86157	C.glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	25-Jul-96
		GB_BA2:AE001816	10007	AE001816	Thermotoga maritima section 128 of 136 of the complete genome.	Thermotoga maritima	50,238	2-Jun-99
rxa02157	1296	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,612	1-Jul-98
		GB_BA1:CGARGCJBD	4355	X86157	C.glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	99,612	25-Jul-96
		GB_BA1:MTCY06H11	38000	Z85982	Mycobacterium tuberculosis H37Rv complete genome; segment 73/162.	Mycobacterium tuberculosis	57,278	17-Jun-98
rxa02158	1080	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	100,000	1-Jul-98
		GB_BA2:AF031518	2045	AF031518	Corynebacterium glutamicum ornithine carbamolytransferase (argF) gene, complete cds.	Corynebacterium glutamicum	99,898	5-Jan-99
		GB_BA1:CGARGCJBD	4355	X86157	C.glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	25-Jul-96
rxa02159	636	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,843	1-Jul-98
		GB_BA2:AF031518	2045	AF031518	Corynebacterium glutamicum ornithine carbamolytransferase (argF) gene, complete cds.	Corynebacterium glutamicum	88,679	5-Jan-99
		GB_BA2:AF041436	516	AF041436	Corynebacterium glutamicum arginine repressor (argR) gene, complete cds.	Corynebacterium glutamicum	100,000	5-Jan-99
rxa02160	1326	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,774	1-Jul-98
		GB_BA2:AF030520	1206	AF030520	Corynebacterium glutamicum argininosuccinate synthetase (argG) gene, complete cds.	Corynebacterium glutamicum	99,834	19-Nov-97
		GB_BA1:SCARGGH	1909	Z49111	S.clavuligerus argG gene and argH gene (partial).	Streptomyces clavuligerus	65,913	22-Apr-96
rxa02162	1554	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	88,524	1-Jul-98

Table 4 (continued)

		GB_BA2:AF048764	1437	AF048764	Corynebacterium glutamicum argininosuccinate lyase (argH) gene,complete cds.	Corynebacterium glutamicum	87,561	1-Jul-98
		GB_BA1:MTCY06H11	38000	Z85982	Mycobacterium tuberculosis H37Rv complete genome; segment 73/162.	Mycobacterium tuberculosis	64,732	17-Jun-98
rxa02176	1251	GB_BA1:MTCY31	37630	Z73101	Mycobacterium tuberculosis H37Rv complete genome; segment 41/162.	Mycobacterium tuberculosis	36,998	17-Jun-98
		GB_BA1:CGGLTG	3013	X66112	C.glutamicum glt gene for citrate synthase and ORF.	Corynebacterium glutamicum	39,910	17-Feb-95
		GB_PL2:PGU65399	2700	U65399	Basidiomycete CECT 20197 phenoloxidase (pox1) gene, complete cds.	basidiomycete CECT 20197	38,474	19-Jul-97
rxa02189	861	GB_PR3:AC002468	115888	AC002468	Human Chromosome 15q26.1 PAC clone pDJ417d7, complete sequence.	Homo sapiens	35,941	16-Sep-98
		GB_BA1:MSGB1970CS	39399	L78815	Mycobacterium leprae cosmid B1970 DNA sequence.	Mycobacterium leprae	40,286	15-Jun-96
		GB_PR3:AC002468	115888	AC002468	Human Chromosome 15q26.1 PAC clone pDJ417d7, complete sequence.	Homo sapiens	33,689	16-Sep-98
rxa02193	1701	GB_BA1:BRLASPA	1987	D25316	Brevibacterium flavum aspA gene for aspartase, complete cds.	Corynebacterium glutamicum	99,353	6-Feb-99
		GB_PAT:E04307	1581	E04307	DNA encoding Brevibacterium flavum aspartase.	Corynebacterium glutamicum	99,367	29-Sep-97
		GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	37,651	17-Apr-96
rxa02194	966	GB_BA2:AF050166	840	AF050166	Corynebacterium glutamicum ATP phosphoribosyltransferase (hisG) gene, complete cds.	Corynebacterium glutamicum	98,214	5-Jan-99
		GB_BA1:BRLASPA	1987	D25316	Brevibacterium flavum aspA gene for aspartase, complete cds.	Corynebacterium glutamicum	93,805	6-Feb-99
		GB_PAT:E08649	188	E08649	DNA encoding part of aspartase from coryneform bacteria.	Corynebacterium glutamicum	100,000	29-Sep-97
rxa02195	393	GB_BA2:AF086704	264	AF086704	Corynebacterium glutamicum phosphoribosyl-ATP-pyrophosphohydrolase (hisE) gene, complete cds.	Corynebacterium glutamicum	100,000	8-Feb-99
		GB_BA1:EAY17145	6019	Y17145	Eubacterium acidaminophilum grdR, grdI, grdH genes and partial ldc, grdT genes.	Eubacterium acidaminophilum	39,075	5-Aug-98
		GB_STS:G01195	332	G01195	fruit fly STS Dm1930 clone DS06959 T7.	Drosophila melanogaster	35,542	28-Feb-95
rxa02197	551	GB_BA1:MTCY261	27322	Z97559	Mycobacterium tuberculosis H37Rv complete genome; segment 95/162.	Mycobacterium tuberculosis	33,938	17-Jun-98
		GB_BA1:MLCB2533	40245	AL035310	Mycobacterium leprae cosmid B2533.	Mycobacterium leprae	65,517	27-Aug-99
		GB_BA1:U00017	42157	U00017	Mycobacterium leprae cosmid B2126.	Mycobacterium leprae	36,770	01-MAR-1994
rxa02198	2599	GB_BA1:U00017	42157	U00017	Mycobacterium leprae cosmid B2126.	Mycobacterium leprae	38,674	01-MAR-1994
		GB_BA1:MLCB2533	40245	AL035310	Mycobacterium leprae cosmid B2533.	Mycobacterium leprae	65,465	27-Aug-99
		GB_BA1:MTCY261	27322	Z97559	Mycobacterium tuberculosis H37Rv complete genome; segment 95/162.	Mycobacterium tuberculosis	37,577	17-Jun-98
rxa02208	1025	GB_BA1:U00017	42157	U00017	Mycobacterium leprae cosmid B2126.	Mycobacterium leprae	59,823	01-MAR-1994
		GB_BA1:AP000063	185300	AP000063	Aeropyrum pernix genomic DNA, section 6/7.	Aeropyrum pernix	39,442	22-Jun-99

Table 4 (continued)

		GB_PR4:AC006236	127593	AC006236	Homo sapiens chromosome 17, clone hCIT.162_E_12, complete sequence.	Homo sapiens	37,191	29-DEC-1998
rxa02229	948	GB_BA1:MSGY154	40221	AD000002	Mycobacterium tuberculosis sequence from clone y154.	Mycobacterium tuberculosis	53,541	03-DEC-1996
		GB_BA1:MTCY154	13935	Z98209	Mycobacterium tuberculosis H37Rv complete genome; segment 121/162.	Mycobacterium tuberculosis	40,407	17-Jun-98
		GB_BA1:U00019	36033	U00019	Mycobacterium leprae cosmid B2235.	Mycobacterium leprae	40,541	01-MAR-1994
rxa02234	3462	GB_BA1:MSGB937CS	38914	L78820	Mycobacterium leprae cosmid B937 DNA sequence.	Mycobacterium leprae	66,027	15-Jun-96
		GB_BA1:MTCY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	71,723	18-Jun-98
		GB_BA2:U01072	4393	U01072	Mycobacterium bovis BCG orotidine-5'-monophosphate decarboxylase (uraA) gene.	Mycobacterium bovis	67,101	22-DEC-1993
rxa02235	727	GB_BA1:MSU91572	960	U91572	Mycobacterium smegmatis carbamoyl phosphate synthetase (pyrAB) gene, partial cds and orotidine 5'-monophosphate decarboxylase (pyrF) gene, complete cds.	Mycobacterium smegmatis	60,870	22-MAR-1997
		GB_HTG3:AC009364	192791	AC009364	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 57 unordered pieces.	Homo sapiens	37,994	1-Sep-99
		GB_HTG3:AC009364	192791	AC009364	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 57 unordered pieces.	Homo sapiens	37,994	1-Sep-99
rxa02237	693	GB_BA1:MTCY21B4	39150	Z80108	Mycobacterium tuberculosis H37Rv complete genome; segment 62/162.	Mycobacterium tuberculosis	55,844	23-Jun-98
		GB_BA2:AF077324	5228	AF077324	Rhodococcus equi strain 103 plasmid RE-VP1 fragment f.	Rhodococcus equi	41,185	5-Nov-98
		GB_EST22:AU017763	586	AU017763	AU017763 Mouse two-cell stage embryo cDNA Mus musculus cDNA clone J0744A04 3', mRNA sequence.	Mus musculus	38,616	19-OCT-1998
rxa02239	1389	GB_BA1:MTCY21B4	39150	Z80108	Mycobacterium tuberculosis H37Rv complete genome; segment 62/162.	Mycobacterium tuberculosis	56,282	23-Jun-98
		GB_HTG3:AC010745	193862	AC010745	Homo sapiens clone NH0549D18, *** SEQUENCING IN PROGRESS ***, 30 unordered pieces.	Homo sapiens	36,772	21-Sep-99
		GB_HTG3:AC010745	193862	AC010745	Homo sapiens clone NH0549D18, *** SEQUENCING IN PROGRESS ***, 30 unordered pieces.	Homo sapiens	36,772	21-Sep-99
rxa02240	1344	EM_PAT:E09855	1239	E09855	gDNA encoding S-adenosylmethionine synthetase.	Corynebacterium glutamicum	99,515	07-OCT-1997 (Rel. 52, Created)
		GB_PAT:A37831	5392	A37831	Sequence 1 from Patent WO9408014.	Streptomyces pristinaespiralis	63,568	05-MAR-1997
		GB_BA2:AF117274	2303	AF117274	Streptomyces spectabilis flavoprotein homolog Dfp (dfp) gene, partial cds; and S-adenosylmethionine synthetase (metK) gene, complete cds.	Streptomyces spectabilis	65,000	31-MAR-1999
rxa02246	1107	EM_BA1:AB003693	5589	AB003693	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	52,909	03-OCT-1997 (Rel. 52, Created)

Table 4 (continued)

		GB_PAT:E07957	5589	E07957	gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase.	Corynebacterium ammoniagenes	52,909	29-Sep-97
		GB_PAT:I32742	5589	I32742	Sequence 1 from patent US 5589355.	Unknown.	52,909	6-Feb-97
rxa02247	756	GB_PAT:I32743	2689	I32743	Sequence 2 from patent US 5589355.	Unknown.	57,937	6-Feb-97
		EM_BA1:AB003693	5589	AB003693	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	57,937	03-OCT-1997 (Rel. 52, Created)
		GB_PAT:I32742	5589	I32742	Sequence 1 from patent US 5589355.	Unknown.	57,937	6-Feb-97
rxa02248	1389	GB_PAT:I32742	5589	I32742	Sequence 1 from patent US 5589355.	Unknown.	61,843	6-Feb-97
		EM_BA1:AB003693	5589	AB003693	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	61,843	03-OCT-1997 (Rel. 52, Created)
		GB_PAT:E07957	5589	E07957	gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase.	Corynebacterium ammoniagenes	61,843	29-Sep-97
rxa02249	600	GB_PAT:E07957	5589	E07957	gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase.	Corynebacterium ammoniagenes	64,346	29-Sep-97
		GB_PAT:I32742	5589	I32742	Sequence 1 from patent US 5589355.	Unknown.	64,346	6-Feb-97
		GB_PAT:I32743	2689	I32743	Sequence 2 from patent US 5589355.	Unknown.	64,346	6-Feb-97
rxa02250	643	GB_PAT:E07957	5589	E07957	gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase.	Corynebacterium ammoniagenes	56,318	29-Sep-97
		GB_PAT:I32742	5589	I32742	Sequence 1 from patent US 5589355.	Unknown.	56,318	6-Feb-97
		EM_BA1:AB003693	5589	AB003693	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	56,318	03-OCT-1997 (Rel. 52, Created)
rxa02262	1269	GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	Corynebacterium glutamicum	100,000	7-Jan-99
		GB_BA1:CGAMTGENE	2028	X93513	C.glutamicum amt gene.	Corynebacterium glutamicum	100,000	29-MAY-1996
		GB_VI:HEHCMVCG	229354	X17403	Human cytomegalovirus strain AD169 complete genome.	human herpesvirus 5	38,651	10-Feb-99
rxa02263	488	GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	Corynebacterium glutamicum	100,000	7-Jan-99
		GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	Corynebacterium glutamicum	37,526	7-Jan-99
rxa02272	1368	EM_PAT:E09373	1591	E09373	Creatinine deiminase gene.	Bacillus sp.	96,928	08-OCT-1997 (Rel. 52, Created)
		GB_BA1:D38505	1591	D38505	Bacillus sp. gene for creatinine deaminase, complete cds.	Bacillus sp.	96,781	7-Aug-98
		GB_HTG2:AC006595	146070	AC006595	Homo sapiens, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	Homo sapiens	36,264	20-Feb-99
rxa02281	1545	GB_GSS12:AQ411010	551	AQ411010	HS_2257_B1_H02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2257 Col=3 Row=P, genomic survey sequence.	Homo sapiens	36,197	17-MAR-1999

Table 4 (continued)

		GB_EST23:AI128623	363	AI128623	qa62c01.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1691328 3', mRNA sequence.	Homo sapiens	37,017	05-OCT-1998
		GB_PL2:ATAC007019	102335	AC007019	Arabidopsis thaliana chromosome II BAC F7D8 genomic sequence, complete sequence.	Arabidopsis thaliana	33,988	16-MAR-1999
rxa02299	531	GB_BA2:AF116184	540	AF116184	Corynebacterium glutamicum L-aspartate-alpha-decarboxylase precursor (panD) gene, complete cds.	Corynebacterium glutamicum	100,000	02-MAY-1999
		GB_GSS9:AQ164310	507	AQ164310	HS_2171_A2_E01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=2 Row=I, genomic survey sequence.	Homo sapiens	37,278	16-OCT-1998
		GB_VI:MH68TKH	4557	X93468	Murine herpesvirus type 68 thymidine kinase and glycoprotein H genes.	murine herpesvirus 68	40,288	3-Sep-96
rxa02311	813	GB_HTG4:AC006091	176878	AC006091	Drosophila melanogaster chromosome 3 clone BACR48G05 (D475) RPCI-98 48.G.5 map 91F1-91F13 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	Drosophila melanogaster	36,454	27-OCT-1999
		GB_HTG4:AC006091	176878	AC006091	Drosophila melanogaster chromosome 3 clone BACR48G05 (D475) RPCI-98 48.G.5 map 91F1-91F13 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	Drosophila melanogaster	36,454	27-OCT-1999
		GB_BA2:RRU65510	16259	U65510	Rhodospirillum rubrum CO-induced hydrogenase operon (cooM, cooK, cooL, cooX, cooU, cooH) genes, iron sulfur protein (cooF) gene, carbon monoxide dehydrogenase (cooS) gene, carbon monoxide dehydrogenase accessory proteins (cooC, cooT, cooJ) genes, putative transcriptional activator (cooA) gene, nicotinate-nucleotide pyrophosphorylase (nadC) gene, complete cds, L-aspartate oxidase (nadB) gene, and alkyl hydroperoxide reductase (ahpC) gene, partial cds.	Rhodospirillum rubrum	37,828	9-Apr-97
rxa02315	1752	GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	49,418	03-DEC-1996
		GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	49,360	17-Jun-98
		GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	38,150	03-DEC-1996
rxa02318	402	GB_HTG3:AC011348	111083	AC011348	Homo sapiens chromosome 5 clone CIT-HSPC_303E13, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces.	Homo sapiens	35,821	06-OCT-1999
		GB_HTG3:AC011348	111083	AC011348	Homo sapiens chromosome 5 clone CIT-HSPC_303E13, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces.	Homo sapiens	35,821	06-OCT-1999
		GB_HTG3:AC011412	89234	AC011412	Homo sapiens chromosome 5 clone CIT978SKB_81K21, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces.	Homo sapiens	36,181	06-OCT-1999
rxa02319	1080	GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	37,792	03-DEC-1996
		GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	37,792	17-Jun-98
		GB_EST23:AI117213	476	AI117213	ub83h02.r1 Soares 2NbMT Mus musculus cDNA clone IMAGE:1395123 5',mRNA sequence.	Mus musculus	35,084	2-Sep-98

Table 4 (continued)

rxa02345	1320	GB_BA1:BAPURKE	2582	X91189	B.ammoniagenes purK and purE genes.	Corynebacterium ammoniagenes	61,731	14-Jan-97
		GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	Mycobacterium tuberculosis	39,624	10-Feb-99
		GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	Mycobacterium tuberculosis	39,847	10-Feb-99
rxa02350	618	GB_BA1:BAPURKE	2582	X91189	B.ammoniagenes purK and purE genes.	Corynebacterium ammoniagenes	64,286	14-Jan-97
		GB_PL1:SC130KBXV	129528	X94335	S.cerevisiae 130kb DNA fragment from chromosome XV.	Saccharomyces cerevisiae	36,617	15-Jul-97
		GB_PL1:SCXVORFS	50984	X90518	S.cerevisiae DNA of 51 Kb from chromosome XV right arm.	Saccharomyces cerevisiae	36,617	1-Nov-95
rxa02373	1038	GB_PAT:E00311	1853	E00311	DNA coding of 2,5-diketogluconic acid reductase.	unidentified	56,123	29-Sep-97
		GB_PAT:I06030	1853	I06030	Sequence 4 from Patent EP 0305608.	Unknown.	56,220	02-DEC-1994
		GB_PAT:I00836	1853	I00836	Sequence 1 from Patent US 4758514.	Unknown.	56,220	21-MAY-1993
rxa02375	1350	GB_BA2:CGU31230	3005	U31230	Corynebacterium glutamicum Obg protein homolog gene, partial cds, gamma glutamyl kinase (proB) gene, complete cds, and (unkdh) gene, complete cds.	Corynebacterium glutamicum	99,332	2-Aug-96
		GB_HTG3:AC009946	169072	AC009946	Homo sapiens clone NH0012C17, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces.	Homo sapiens	36,115	8-Sep-99
		GB_HTG3:AC009946	169072	AC009946	Homo sapiens clone NH0012C17, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces.	Homo sapiens	36,115	8-Sep-99
rxa02380	777	GB_BA1:MTCY253	41230	Z81368	Mycobacterium tuberculosis H37Rv complete genome; segment 106/162.	Mycobacterium tuberculosis	38,088	17-Jun-98
		GB_HTG4:AC010658	120754	AC010658	Drosophila melanogaster chromosome 3L/75C1 clone RPCI98-3B20, *** SEQUENCING IN PROGRESS ***, 78 unordered pieces.	Drosophila melanogaster	35,817	16-OCT-1999
		GB_HTG4:AC010658	120754	AC010658	Drosophila melanogaster chromosome 3L/75C1 clone RPCI98-3B20, *** SEQUENCING IN PROGRESS ***, 78 unordered pieces.	Drosophila melanogaster	35,817	16-OCT-1999
rxa02382	1419	GB_BA1:CGPROAGEN	1783	X82929	C.glutamicum proA gene.	Corynebacterium glutamicum	98,802	23-Jan-97
		GB_BA1:MTCY428	26914	Z81451	Mycobacterium tuberculosis H37Rv complete genome; segment 107/162.	Mycobacterium tuberculosis	38,054	17-Jun-98
		GB_BA2:CGU31230	3005	U31230	Corynebacterium glutamicum Obg protein homolog gene, partial cds, gamma glutamyl kinase (proB) gene, complete cds, and (unkdh) gene, complete cds.	Corynebacterium glutamicum	98,529	2-Aug-96
rxa02400	693	GB_BA1:CGACEA	2427	X75504	C.glutamicum aceA gene and thiX genes (partial).	Corynebacterium glutamicum	100,000	9-Sep-94
		GB_PAT:I86191	2135	I86191	Sequence 3 from patent US 5700661.	Unknown.	100,000	10-Jun-98
		GB_PAT:I13693	2135	I13693	Sequence 3 from patent US 5439822.	Unknown.	100,000	26-Sep-95
rxa02432	1098	GB_GSS15:AQ606842	574	AQ606842	HS_5404_B2_E07_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=980 Col=14 Row=J, genomic survey sequence.	Homo sapiens	39,716	10-Jun-99

Table 4 (continued)

		GB_EST1:T05804	406	T05804	EST03693 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBDG63 similar to EST containing Alu repeat, mRNA sequence.	Homo sapiens	37,915	30-Jun-93
		GB_PL1:AB006699	77363	AB006699	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22, complete sequence.	Arabidopsis thaliana	35,526	20-Nov-99
rxa02458	1413	GB_BA2:AF114233	1852	AF114233	Corynebacterium glutamicum 5-enolpyruvylshikimate 3-phosphate synthase (aroA) gene, complete cds.	Corynebacterium glutamicum	100,000	7-Feb-99
		GB_EST37:AW013061	578	AW013061	ODT-0033 Winter flounder ovary Pleuronectes americanus cDNA clone ODT-0033 5' similar to FRUCTOSE-BISPHOSPHATE ALDOLASE B (LIVER), mRNA sequence.	Pleuronectes americanus	39,175	10-Sep-99
		GB_GSS15:AQ650027	728	AQ650027	Sheared DNA-5L2.TF Sheared DNA Trypanosoma brucei genomic clone Sheared DNA-5L2, genomic survey sequence.	Trypanosoma brucei	39,281	22-Jun-99
rxa02469	1554	GB_BA1:MTCY359	36021	Z83859	Mycobacterium tuberculosis H37Rv complete genome; segment 84/162.	Mycobacterium tuberculosis	39,634	17-Jun-98
		GB_BA1:MLCB1788	39228	AL008609	Mycobacterium leprae cosmid B1788.	Mycobacterium leprae	59,343	27-Aug-99
		GB_BA1:SCAJ10601	4692	AJ010601	Streptomyces coelicolor A3(2) DNA for whiD and whiK loci.	Streptomyces coelicolor	48,899	17-Sep-98
rxa02497	1050	GB_BA2:CGU31224	422	U31224	Corynebacterium glutamicum (ppx) gene, partial cds.	Corynebacterium glutamicum	96,445	2-Aug-96
		GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Mycobacterium tuberculosis	59,429	17-Jun-98
		GB_BA1:SCE7	16911	AL049819	Streptomyces coelicolor cosmid E7.	Streptomyces coelicolor	39,510	10-MAY-1999
rxa02499	933	GB_BA2:CGU31225	1817	U31225	Corynebacterium glutamicum L-proline:NADP+ 5-oxidoreductase (proC) gene, complete cds.	Corynebacterium glutamicum	97,749	2-Aug-96
		GB_BA1:NG17PILA	1920	X13965	Neisseria gonorrhoeae pilA gene.	Neisseria gonorrhoeae	43,249	30-Sep-93
		GB_HTG2:AC007984	129715	AC007984	Drosophila melanogaster chromosome 3 clone BACR05C10 (D781) RPCI-98 05.C.10 map 97D-97E strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 87 unordered pieces.	Drosophila melanogaster	33,406	2-Aug-99
rxa02501	1188	GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Mycobacterium tuberculosis	39,357	17-Jun-98
		GB_BA1:U00018	42991	U00018	Mycobacterium leprae cosmid B2168.	Mycobacterium leprae	51,768	01-MAR-1994
		GB_VI:HE1CG	152261	X14112	Herpes simplex virus (HSV) type 1 complete genome.	human herpesvirus 1	39,378	17-Apr-97
rxa02503	522	GB_PR3:AC005328	35414	AC005328	Homo sapiens chromosome 19, cosmid R26660, complete sequence.	Homo sapiens	39,922	28-Jul-98
		GB_PR3:AC005545	43514	AC005545	Homo sapiens chromosome 19, cosmid R26634, complete sequence.	Homo sapiens	39,922	3-Sep-98
		GB_PR3:AC005328	35414	AC005328	Homo sapiens chromosome 19, cosmid R26660, complete sequence.	Homo sapiens	34,911	28-Jul-98
rxa02504	681	GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Mycobacterium tuberculosis	54,940	17-Jun-98
		GB_PR3:AC005328	35414	AC005328	Homo sapiens chromosome 19, cosmid R26660, complete sequence.	Homo sapiens	41,265	28-Jul-98
		GB_PR3:AC005545	43514	AC005545	Homo sapiens chromosome 19, cosmid R26634, complete sequence.	Homo sapiens	41,265	3-Sep-98
rxa02516	1386	GB_BA1:MLCL536	36224	Z99125	Mycobacterium leprae cosmid L536.	Mycobacterium leprae	37,723	04-DEC-1998
		GB_BA1:U00013	35881	U00013	Mycobacterium leprae cosmid B1496.	Mycobacterium leprae	37,723	01-MAR-1994

Table 4 (continued)

		GB_BA1:MTV007	32806	AL021184	Mycobacterium tuberculosis H37Rv complete genome; segment 64/162.	Mycobacterium tuberculosis	61,335	17-Jun-98
rxa02517	570	GB_BA1:MLCL536	36224	Z99125	Mycobacterium leprae cosmid L536.	Mycobacterium leprae	37,018	04-DEC-1998
		GB_BA1:U00013	35881	U00013	Mycobacterium leprae cosmid B1496.	Mycobacterium leprae	37,018	01-MAR-1994
		GB_BA1:SCC22	22115	AL096839	Streptomyces coelicolor cosmid C22.	Streptomyces coelicolor	37,071	12-Jul-99
rxa02532	1170	GB_OV:AF137219	831	AF137219	Amia calva mixed lineage leukemia-like protein (Mll) gene, partial cds.	Amia calva	36,853	7-Sep-99
		GB_EST30:AI645057	301	AI645057	vs52a10.y1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:1149882 5', mRNA sequence.	Mus musculus	41,860	29-Apr-99
		GB_EST20:AA822595	429	AA822595	vs52a10.r1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:1149882 5', mRNA sequence.	Mus musculus	42,353	17-Feb-98
rxa02536	879	GB_HTG2:AF130866	118874	AF130866	Homo sapiens chromosome 8 clone PAC 172N13 map 8q24, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	40,754	21-MAR-1999
		GB_HTG2:AF130866	118874	AF130866	Homo sapiens chromosome 8 clone PAC 172N13 map 8q24, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	40,754	21-MAR-1999
		GB_PL1:ATT12J5	84499	AL035522	Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5 (ESSAII project).	Arabidopsis thaliana	35,063	24-Feb-99
rxa02550	1434	GB_BA1:MTCY279	9150	Z97991	Mycobacterium tuberculosis H37Rv complete genome; segment 17/162.	Mycobacterium tuberculosis	37,773	17-Jun-98
		GB_BA1:MSGB1970CS	39399	L78815	Mycobacterium leprae cosmid B1970 DNA sequence.	Mycobacterium leprae	39,024	15-Jun-96
		GB_BA2:SC2H4	25970	AL031514	Streptomyces coelicolor cosmid 2H4.	Streptomyces coelicolor A3(2)	37,906	19-OCT-1999
rxa02559	1026	GB_BA1:MTV004	69350	AL009198	Mycobacterium tuberculosis H37Rv complete genome; segment 144/162.	Mycobacterium tuberculosis	47,358	18-Jun-98
		GB_PAT:I28684	5100	I28684	Sequence 1 from patent US 5573915.	Unknown.	39,138	6-Feb-97
		GB_BA1:MTU27357	5100	U27357	Mycobacterium tuberculosis cyclopropane mycolic acid synthase (cma1) gene, complete cds.	Mycobacterium tuberculosis	39,138	26-Sep-95
rxa02622	1683	GB_BA2:AE001780	11997	AE001780	Thermotoga maritima section 92 of 136 of the complete genome.	Thermotoga maritima	44,914	2-Jun-99
		GB_OV:AF064564	49254	AF064564	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds.	Fugu rubripes	39,732	17-Aug-99
		GB_OV:AF064564	49254	AF064564	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds.	Fugu rubripes	36,703	17-Aug-99
rxa02623	714	GB_GSS5:AQ818728	444	AQ818728	HS_5268_A1_G09_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=844 Col=17 Row=M, genomic survey sequence.	Homo sapiens	38,801	26-Aug-99
		GB_HTG5:AC011083	198586	AC011083	Homo sapiens chromosome 9 clone RP11-111M7 map 9, WORKING DRAFT SEQUENCE, 51 unordered pieces.	Homo sapiens	35,714	19-Nov-99
		GB_GSS6:AQ826948	544	AQ826948	HS_5014_A2_C12_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=590 Col=24 Row=E, genomic survey sequence.	Homo sapiens	39,146	27-Aug-99

Table 4 (continued)

rxa02629	708	GB_VI:BRSMGP	462	M86652	Bovine respiratory syncytial virus membrane glycoprotein mRNA, complete cds.	Bovine respiratory syncytial virus	37,013	28-Apr-93
		GB_VI:BRSMGP	462	M86652	Bovine respiratory syncytial virus membrane glycoprotein mRNA, complete cds.	Bovine respiratory syncytial virus	37,013	28-Apr-93
rxa02645	1953	GB_PAT:A45577	1925	A45577	Sequence 1 from Patent WO9519442.	Corynebacterium glutamicum	39,130	07-MAR-1997
		GB_PAT:A45581	1925	A45581	Sequence 5 from Patent WO9519442.	Corynebacterium glutamicum	39,130	07-MAR-1997
		GB_BA1:CORILVA	1925	L01508	Corynebacterium glutamicum threonine dehydratase (ilvA) gene, complete cds.	Corynebacterium glutamicum	39,130	26-Apr-93
rxa02646	1392	GB_BA1:CORILVA	1925	L01508	Corynebacterium glutamicum threonine dehydratase (ilvA) gene, complete cds.	Corynebacterium glutamicum	99,138	26-Apr-93
		GB_PAT:A45585	1925	A45585	Sequence 9 from Patent WO9519442.	Corynebacterium glutamicum	99,066	07-MAR-1997
		GB_PAT:A45583	1925	A45583	Sequence 7 from Patent WO9519442.	Corynebacterium glutamicum	99,066	07-MAR-1997
rxa02648	1326	GB_OV:ICTCNC	2049	M83111	Ictalurus punctatus cyclic nucleotide-gated channel RNA sequence.	Ictalurus punctatus	38,402	24-MAY-1993
		GB_EST11:AA265464	345	AA265464	mx91c06.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:693706 5', mRNA sequence.	Mus musculus	38,655	20-MAR-1997
		GB_GSS8:AQ006950	480	AQ006950	CIT-HSP-2294E14.TR CIT-HSP Homo sapiens genomic clone 2294E14, genomic survey sequence.	Homo sapiens	36,074	27-Jun-98
rxa02653								
rxa02687	1068	GB_BA1:CORPHEA	1088	M13774	C.glutamicum pheA gene encoding prephenate dehydratase, complete cds.	Corynebacterium glutamicum	99,715	26-Apr-93
		GB_PAT:E04483	948	E04483	DNA encoding prephenate dehydratase.	Corynebacterium glutamicum	98,523	29-Sep-97
		GB_PAT:E06110	948	E06110	DNA encoding prephenate dehydratase.	Corynebacterium glutamicum	98,523	29-Sep-97
rxa02717	1005	GB_PL1:HVCH4H	59748	Y14573	Hordeum vulgare DNA for chromosome 4H.	Hordeum vulgare	36,593	25-MAR-1999
		GB_PR2:HS310H5	29718	Z69705	Human DNA sequence from cosmid 310H5 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains EST and CpG island.	Homo sapiens	36,089	22-Nov-99
		GB_PR3:AC004754	39188	AC004754	Homo sapiens chromosome 16, cosmid clone RT286 (LANL), complete sequence.	Homo sapiens	36,089	28-MAY-1998
rxa02754	1461	GB_HTG2:AC008223	130212	AC008223	Drosophila melanogaster chromosome 3 clone BACR16I18 (D815) RPCI-98 16.I.18 map 95A-95A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 101 unordered pieces.	Drosophila melanogaster	32,757	2-Aug-99

Table 4 (continued)

		GB_HTG2:AC008223	130212	AC008223	Drosophila melanogaster chromosome 3 clone BACR16I18 (D815) RPCI-98 16.I.18 map 95A-95A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 101 unordered pieces.	Drosophila melanogaster	32,757	2-Aug-99
		GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	Mycobacterium tuberculosis	37,838	10-Feb-99
rxa02758	1422	GB_HTG5:AC011678	171967	AC011678	Homo sapiens clone 14_B_7, *** SEQUENCING IN PROGRESS ***, 20 unordered pieces.	Homo sapiens	35,331	5-Nov-99
		GB_HTG5:AC011678	171967	AC011678	Homo sapiens clone 14_B_7, *** SEQUENCING IN PROGRESS ***, 20 unordered pieces.	Homo sapiens	33,807	5-Nov-99
		GB_BA2:AF064070	23183	AF064070	Burkholderia pseudomallei putative dihydroorotase (pyrC) gene, partial cds; putative 1-acyl-sn-glycerol-3-phosphate acyltransferase (plsC), putative diadenosine tetraphosphatase (apaH), complete cds; type II O-antigen biosynthesis gene cluster, complete sequence; putative undecaprenyl phosphate N-acetylglucosaminyltransferase, and putative UDP-glucose 4-epimerase genes, complete cds; and putative galactosyl transferase gene, partial cds.	Burkholderia pseudomallei	36,929	20-Jan-99
rxa02771	678	GB_BA2:AF038651	4077	AF038651	Corynebacterium glutamicum dipeptide-binding protein (dciAE) gene, partial cds; adenine phosphoribosyltransferase (apt) and GTP pyrophosphokinase (rel) genes, complete cds; and unknown gene.	Corynebacterium glutamicum	99,852	14-Sep-98
		GB_IN1:CELT19B4	37121	U80438	Caenorhabditis elegans cosmid T19B4.	Caenorhabditis elegans	43,836	04-DEC-1996
		GB_EST36:AV193572	360	AV193572	AV193572 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk618h8 5', mRNA sequence.	Caenorhabditis elegans	48,588	22-Jul-99
rxa02772	1158	GB_BA2:AF038651	4077	AF038651	Corynebacterium glutamicum dipeptide-binding protein (dciAE) gene, partial cds; adenine phosphoribosyltransferase (apt) and GTP pyrophosphokinase (rel) genes, complete cds; and unknown gene.	Corynebacterium glutamicum	99,914	14-Sep-98
		GB_BA1:MTCY227	35946	Z77724	Mycobacterium tuberculosis H37Rv complete genome; segment 114/162.	Mycobacterium tuberculosis	38,339	17-Jun-98
		GB_BA1:U00011	40429	U00011	Mycobacterium leprae cosmid B1177.	Mycobacterium leprae	38,996	01-MAR-1994
rxa02790	1266	GB_BA1:MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome; segment 111/162.	Mycobacterium tuberculosis	37,640	17-Jun-98
		GB_PR4:AC006581	172931	AC006581	Homo sapiens 12p21 BAC RPCI11-259O18 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	37,906	3-Jun-99
		GB_PR4:AC006581	172931	AC006581	Homo sapiens 12p21 BAC RPCI11-259O18 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	35,280	3-Jun-99
rxa02791	951	GB_BA1:MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome; segment 111/162.	Mycobacterium tuberculosis	39,765	17-Jun-98
		GB_OV:CHKCEK2	3694	M35195	Chicken tyrosine kinase (cek2) mRNA, complete cds.	Gallus gallus	38,937	28-Apr-93
		GB_BA1:MSASDASK	5037	Z17372	M.smegmatis asd, ask-alpha, and ask-beta genes.	Mycobacterium smegmatis	38,495	9-Aug-94
rxa02802	1194	GB_EST24:AI223401	169	AI223401	qg48g01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838448 3' similar to WP:C25D7.8 CE08394 ;, mRNA sequence.	Homo sapiens	40,828	27-OCT-1998

Table 4 (continued)

		GB_EST24:AI223401	169	AI223401	qg48g01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838448 3' similar to WP:C25D7.8 CE08394 ;, mRNA sequence.	Homo sapiens	40,828	27-OCT-1998
rxa02814	494	GB_BA1:MTCY7D11	22070	Z95120	Mycobacterium tuberculosis H37Rv complete genome; segment 138/162.	Mycobacterium tuberculosis	58,418	17-Jun-98
		GB_BA1:MTCY7D11	22070	Z95120	Mycobacterium tuberculosis H37Rv complete genome; segment 138/162.	Mycobacterium tuberculosis	40,496	17-Jun-98
		GB_PR1:HSAJ2962	778	AJ002962	Homo sapiens mRNA for hB-FABP.	Homo sapiens	39,826	8-Jan-98
rxa02843	608	GB_BA1:CGAJ4934	1160	AJ004934	Corynebacterium glutamicum dapD gene, complete CDS.	Corynebacterium glutamicum	100,000	17-Jun-98
		GB_BA1:MTCI364	29540	Z93777	Mycobacterium tuberculosis H37Rv complete genome; segment 52/162.	Mycobacterium tuberculosis	37,710	17-Jun-98
		GB_BA1:MLU15180	38675	U15180	Mycobacterium leprae cosmid B1756.	Mycobacterium leprae	39,626	09-MAR-1995
rxs03205	963	GB_BA1:BLSIGBGN	2906	Z49824	B.lactofermentum orf1 gene and sigB gene.	Corynebacterium glutamicum	98,854	25-Apr-96
		GB_EST21:AA980237	377	AA980237	ua32a12.r1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:1348414 5' similar to TR:Q61025 Q61025 HYPOTHETICAL 15.2 KD PROTEIN. ;, mRNA sequence.	Mus musculus	41,489	27-MAY-1998
		GB_EST23:AI158316	371	AI158316	ud27c05.r1 Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:1447112 5', mRNA sequence.	Mus musculus	38,005	30-Sep-98
rxs03223	1237	GB_IN1:LMFL2743	38368	AL031910	Leishmania major Friedlin chromosome 4 cosmid L2743.	Leishmania major	39,869	15-DEC-1999
		GB_PR3:HSDJ61B2	119666	AL096710	Human DNA sequence from clone RP1-61B2 on chromosome 6p11.2-12.3 Contains isoforms 1 and 3 of BPAG1 (bullous pemphigoid antigen 1 (230/240kD), an exon of a gene similar to murine MACF cytoskeletal protein, STSs and GSSs, complete sequence.	Homo sapiens	34,930	17-DEC-1999
		GB_PR3:HSDJ61B2	119666	AL096710	Human DNA sequence from clone RP1-61B2 on chromosome 6p11.2-12.3 Contains isoforms 1 and 3 of BPAG1 (bullous pemphigoid antigen 1 (230/240kD), an exon of a gene similar to murine MACF cytoskeletal protein, STSs and GSSs, complete sequence.	Homo sapiens	34,634	17-DEC-1999

Exemplification

Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC 13032

A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose, 2.46 g/l $MgSO_4 \times 7H_2O$, 10 ml/l KH_2PO_4 solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l $(NH_4)_2SO_4$, 1 g/l NaCl, 2 g/l $MgSO_4 \times 7H_2O$, 0.2 g/l $CaCl_2$, 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l $FeSO_4 \times H_2O$, 10 mg/l $ZnSO_4 \times 7 H_2O$, 3 mg/l $MnCl_2 \times 4 H_2O$, 30 mg/l H_3BO_3 20 mg/l $CoCl_2 \times 6 H_2O$, 1 mg/l $NiCl_2 \times 6 H_2O$, 3 mg/l $Na_2MoO_4 \times 2 H_2O$, 500 mg/l complexing agent (EDTA or critic acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-panthothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca.18 h at 37°C. The DNA was purified by extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20 µg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30

min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.

Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (*see e.g.,* Sambrook, J. *et al.* (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.)

Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA,* 75:3737-3741); pACYC177 (Change & Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCos1 (Stratagene, LaJolla, USA) or Lorist6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene libraries specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Example 3: DNA Sequencing and Computational Functional Analysis

Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using ABI377 sequencing machines (see *e.g.*, Fleischman, R.D. *et al.* (1995) "Whole-genome Random Sequencing and Assembly of Haemophilus Influenzae Rd., Science, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-GGAAACAGTATGACCATG-3' or 5'-GTAAAACGACGGCCAGT-3'.

Example 4: *In vivo* Mutagenesis

In vivo mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (*e.g. Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain

the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (*e.g.*, mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D. (1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to those of ordinary skill in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) <u>*Strategies*</u> 7: 32-34.

Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum*

Several *Corynebacterium* and *Brevibacterium* species contain endogenous plasmids (as *e.g.*, pHM1519 or pBL1) which replicate autonomously (for review see, *e.g.*, Martin, J.F. *et al.* (1987) *Biotechnology*, 5:137-146). Shuttle vectors for *Escherichia coli* and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for *E. coli* (Sambrook, J. *et al.* (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons) to which a origin or replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are genes for kanamycin resistance (such as those derived from the Tn5 or Tn903 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the literature of the construction of a wide variety of shuttle vectors which replicate in both *E. coli and C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see *e.g.*, Yoshihama, M. *et al.* (1985) *J. Bacteriol.* 162:591-597, Martin J.F. *et al.* (1987) *Biotechnology*, 5:137-146 and Eikmanns, B.J. *et al.* (1991) *Gene*, 102:93-98).

Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vectors into strains of *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by protoplast transformation (Kastsumata, R. *et al.* (1984) *J. Bacteriol.* 159306-311), electroporation (Liebl, E. *et al.* (1989) *FEMS Microbiol. Letters*, 53:399-303) and in cases where special vectors are used, also by conjugation (as described *e.g.* in Schäfer, A *et al.*

(1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an Mcr-deficient *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

Genes may be overexpressed in *C. glutamicum* strains using plasmids which comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980) *Proc. Natl. Acad. Sci. USA* 77(12): 7176-7180). In addition, genes may be overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other Corynebacterium or Brevibacterium species may be accomplished by well-known methods, such as homologous recombination with genomic region(s), restriction endonuclease mediated integration (REMI) (see, *e.g.*, DE Patent 19823834), or through the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (*e.g.*, a promoter, a repressor, and/or an enhancer) by sequence modification, insertion, or deletion using site-directed methods (such as homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional terminators may also be inserted 3' to the coding region of one or more genes of the invention; such terminators are well-known in the art and are described, for example, in Winnacker, E.L. (1987) From Genes to Clones – Introduction to Gene Technology. VCH: Weinheim.

Example 6: Assessment of the Expression of the Mutant Protein

Observations of the activity of a mutated protein in a transformed host cell rely on the fact that the mutant protein is expressed in a similar fashion and in a similar quantity to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.*

(1988) Current Protocols in Molecular Biology, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.* (1992) *Mol. Microbiol.* 6: 317-326.

To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York). In this process, total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

Example 7: Growth of Genetically Modified Corynebacterium glutamicum — Media and Culture Conditions

Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for Corynebacteria are both well-known and readily available (Lieb *et al.* (1989) *Appl. Microbiol. Biotechnol.*, 32:205-210; von der Osten *et al.* (1998) Biotechnology Letters, 11:11-16; Patent DE 4,120,867; Liebl (1992) "The Genus *Corynebacterium*, in: The Procaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex compounds such as molasses or other by-products from sugar refinement. It can also be

advantageous to supply mixtures of different carbon sources. Other possible carbon sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials which contain these compounds. Exemplary nitrogen sources include ammonia gas or ammonia salts, such as NH_4Cl or $(NH_4)_2SO_4$, NH_4OH, nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt, molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuate, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook "Applied Microbiol. Physiology, A Practical Approach (*eds.* P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0 19 963577 3). It is also possible to select growth media from commercial suppliers, like standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and 121°C) or by sterile filtration. The components can either be sterilized together or, if necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can be altered during the experiment. The pH of the medium should be in the range of 5 to 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media. An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It

is also possible to maintain a constant culture pH through the addition of NaOH or NH_4OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex compounds have high buffer capacities. If a fermentor is utilized for culturing the micro-organisms, the pH can also be controlled using gaseous ammonia.

The incubation time is usually in a range from several hours to several days. This time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes. For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD_{600} of 0.5 – 1.5 using cells grown on agar plates, such as CM plates (10 g/l glucose, 2,5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

Example 8 – *In vitro* Analysis of the Function of Mutant Proteins

The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications and examples for the determination of many enzyme activities may be

found, for example, in the following references: Dixon, M., and Webb, E.C., (1979) Enzymes. Longmans: London; Fersht, (1985) Enzyme Structure and Mechanism. Freeman: New York; Walsh, (1979) Enzymatic Reaction Mechanisms. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) Fundamentals of Enzymology. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) The Enzymes, 3rd ed. Academic Press: New York; Bisswanger, H., (1994) Enzymkinetik, 2nd ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) Methods of Enzymatic Analysis, 3rd ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 352-363.

The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as beta-galactosidase, green fluorescent protein, and several others.

The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in Biomembranes, Molecular Structure and Function, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired Product

The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified microorganism under suitable conditions (such as those described above) and analyzing the medium and/or the cellular component for increased production of the desired product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining methods of various kinds, enzymatic and microbiological methods, and analytical chromatography such as high performance liquid chromatography (see, for example,

Ullman, Encyclopedia of Industrial Chemistry, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. *et al.*, (1987) "Applications of HPLC in Biochemistry" in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm *et al.* (1993) Biotechnology, vol. 3, Chapter III: "Product recovery and purification", page 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J.A. and Henry, J.D. (1988) Biochemical separations, in: Ulmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications.)

In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the production of the desired compound, such as intermediates and side-products, to determine the overall efficiency of production of the compound. Analysis methods include measurements of nutrient levels in the medium (*e.g.*, sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and measurement of gasses produced during fermentation. Standard methods for these measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

Example 10: Purification of the Desired Product from *C. glutamicum* Culture

Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art. If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such as mechanical force or sonication. The cellular debris is removed by centrifugation, and the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum*

cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate chromatography resins and in their most efficacious application for a particular molecule to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. Biochemical Engineering Fundamentals, McGraw-Hill: New York (1986).

The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994) *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotekhnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. Ulmann's Encyclopedia of Industrial Chemistry, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley and Sons; Fallon, A. *et al.* (1987) Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17.

Example 11: Analysis of the Gene Sequences of the Invention

The comparison of sequences and determination of percent homology between two sequences are art-known techniques, and can be accomplished using a mathematical algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci.* USA 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci.* USA

90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to MP nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to MP protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, one of ordinary skill in the art will know how to optimize the parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art, and include ADVANCE and ADAM. described in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

The percent homology between two amino acid sequences can also be accomplished using the GAP program in the GCG software package (available at http://www.gcg.com), using either a Blosum 62 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using standard parameters, such as a gap weight of 50 and a length weight of 3.

A comparative analysis of the gene sequences of the invention with those present in Genbank has been performed using techniques known in the art (see, *e.g.*, Bexevanis and Ouellette, eds. (1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins. John Wiley and Sons: New York). The gene sequences of the invention

were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (*e.g.*, a local alignment analysis) was performed for each of the sequences of the invention against the nucleotide sequences present in Genbank, and the top 500 hits were retained for further analysis. A subsequent FASTA search (*e.g.*, a combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was subsequently globally aligned to each of the top three FASTA hits, using the GAP program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the length of the query sequences by methods well-known in the art. The results of this analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP (global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment homology percentages set forth in Table 4 under the heading "% homology (GAP)" are listed in the European numerical format, wherein a ',' represents a decimal point. For example, a value of "40,345" in this column represents "40.345%".

Example 12: Construction and Operation of DNA Microarrays

The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are well known in the art, and are described, for example, in Schena, M. *et al.* (1995) *Science* 270: 467-470; Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367; DeSaizieu, A. *et al.* (1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.* (1997) *Science* 278: 680-686).

DNA microarrays are solid or flexible supports consisting of nitrocellulose, nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label

may be used to monitor and measure the individual signal intensities of the hybridized molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic acid sample or mixture. DNA microarrays, therefore, permit an analysis of the expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, *e.g.*, Schena, M. (1996) *BioEssays* 18(5): 427-431).

The sequences of the invention may be used to design oligonucleotide primers which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice and design of the 5' or 3' oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium described above (and also described, for example, Schena, M. *et al.* (1995) *Science* 270: 467-470).

Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide synthesis as described by Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be labeled according to standard methods. In brief, nucleic acid molecules (*e.g.*, mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or fluorescently labeled nucleotides, *e.g.*, during reverse transcription or DNA synthesis. Hybridization of labeled nucleic acids to microarrays is described (*e.g.*, in Schena, M. *et al.* (1995) *supra*; Wodicka, L. *et al.* (1997), *supra*; and DeSaizieu A. *et al.* (1998), *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as

described in Schena, M. *et al.* (1995) *supra*) and fluorescent labels may be detected, for example, by the method of Shalon *et al.* (1996) *Genome Research* 6: 639-645).

The application of the sequences of the invention to DNA microarray technology, as described above, permits comparative analyses of different strains of *C. glutamicum* or other Corynebacteria. For example, studies of inter-strain variations based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

Example 13: Analysis of the Dynamics of Cellular Protein Populations (Proteomics)

The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (*e.g.*, in comparison with the protein populations of other organisms), those proteins which are active under specific environmental or metabolic conditions (*e.g.*, during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18:

1451-1463). Other separation techniques may also be utilized for protein separation, such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein precursors (*e.g.*, ^{35}S-methionine, ^{35}S-cysteine, ^{14}C-labelled amino acids, ^{15}N-amino acids, $^{15}NO_3$ or $^{15}NH_4^+$ or ^{13}C-labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly, fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined quantitatively using, for example, optical methods and can be compared to the amount of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

To determine the identity of any given protein, direct sequencing or other standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (see, *e.g.*, Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192)). The protein sequences provided herein can be used for the identification of *C. glutamicum* proteins by these techniques.

The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (*e.g.*, different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments alone, or in combination with other techniques, can be used for various applications, such as to compare the behavior of various organisms in a given (*e.g.*, metabolic) situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

Equivalents

Those of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

What is claimed:

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding a metabolic pathway protein, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

2. The isolated nucleic acid molecule of claim 1, wherein said metabolic pathway protein is selected from the group consisting of proteins involved in the metabolism of an amino acid, a vitamin, a cofactor, a nutraceutical, a nucleotide, a nucleoside, or trehalose.

3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing , or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide selected from the group of amino acid sequences consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, or

a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of a nucleic acid comprising a nucleotide sequence selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.

9. An isolated nucleic acid molecule comprising the nucleic acid molecule of any one of claims 1-8 or a portion thereof and a nucleotide sequence encoding a heterologous polypeptide.

10. A vector comprising the nucleic acid molecule of any one of claims 1-9.

11. The vector of claim 10, which is an expression vector.

12. A host cell transfected with the expression vector of claim 11.

13. The host cell of claim 12, wherein said cell is a microorganism.

14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.

15. The host cell of claim 12, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.

16. The host cell of claim 15, wherein said fine chemical is selected from the group consisting of: organic acids, nonproteinogenic amino acids, purine and pyrimidine

bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

17. A method of producing a polypeptide comprising culturing the host cell of claim 12 in an appropriate culture medium to, thereby, produce the polypeptide.

18. An isolated metabolic pathway polypeptide from *Corynebacterium glutamicum*, or a portion thereof.

19. The protein of claim 18, wherein said polypeptide is selected from the group of metabolic pathway proteins which participate in the metabolism of an amino acid, a vitamin, a cofactor, a nutraceutical, a nucleotide, a nucleoside, or trehalose.

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

21. An isolated polypeptide comprising a naturally occurring allelic variant of a polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

22. The isolated polypeptide of any of claims 18-21, further comprising heterologous amino acid sequences.

23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.

24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.

26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.

27. The method of claim 25, wherein said method further comprises the step of transfecting said cell with the vector of claim 11 to result in a cell containing said vector.

28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium.*

29. The method of claim 25, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum, Corynebacterium herculis, Corynebacterium, lilium, Corynebacterium acetoacidophilum, Corynebacterium acetoglutamicum, Corynebacterium acetophilum, Corynebacterium ammoniagenes, Corynebacterium fujiokense, Corynebacterium nitrilophilus, Brevibacterium ammoniagenes, Brevibacterium butanicum, Brevibacterium divaricatum, Brevibacterium flavum, Brevibacterium healii, Brevibacterium ketoglutamicum, Brevibacterium ketosoreductum, Brevibacterium lactofermentum, Brevibacterium linens, Brevibacterium paraffinolyticum,* and those strains set forth in Table 3.

30. The method of claim 25, wherein expression of the nucleic acid molecule from said vector results in modulation of production of said fine chemical.

31. The method of claim 25, wherein said fine chemical is selected from the group consisting of: organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

32. The method of claim 25, wherein said fine chemical is an amino acid.

33. The method of claim 32, wherein said amino acid is drawn from the group consisting of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine, tyrosine, phenylalanine, and tryptophan.

34. A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-9.

35. A method for diagnosing the presence or activity of *Corynebacterium diphtheriae* in a subject, comprising detecting the presence of one or more of SEQ ID NOs 1 through 1156 of the Sequence Listing in the subject, provided that the sequences are not or are not encoded by any of the F-designated sequences set forth in Table 1, thereby diagnosing the presence or activity of *Corynebacterium diphtheriae* in the subject.

36. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the Sequence Listing , wherein the nucleic acid molecule is disrupted.

37. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs in the Sequence Listing , wherein the nucleic acid molecule comprises one or more nucleic acid

modifications from the sequence set forth as odd-numbered SEQ ID NOs of the Sequence Listing s.

38. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the Sequence Listing , wherein the regulatory region of the nucleic acid molecule is modified relative to the wild-type regulatory region of the molecule.

SEQUENCE LISTING

<110> BASF Aktiengesellschaft
<120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
METABOLIC PATHWAY PROTEINS
<130> BGI-121CPPC
<140>
<141>
<160> 1156

<210> 1
<211> 948
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(925)
<223> RXA02229

<400> 1
gctggttcaa cagagaccac cgcgtgtcct gggtcgacgc ctctggcgat cccaccgcac 60

aagccttgga gattttgggt ctacaatagc gagggtgaat ttg acc atc ccc ttt 115
Leu Thr Ile Pro Phe
1 5

gcc aaa ggc cac gcc acc gaa aac gac ttc atc atc atc ccc gat gag 163
Ala Lys Gly His Ala Thr Glu Asn Asp Phe Ile Ile Ile Pro Asp Glu
10 15 20

gat gcg cgc cta gat tta act cca gaa atg gtg gtc acg ctg tgt gac 211
Asp Ala Arg Leu Asp Leu Thr Pro Glu Met Val Val Thr Leu Cys Asp
25 30 35

cgc cgc gcc ggg atc ggt gct gat ggt atc ctc cgc gtg gtt aaa gct 259
Arg Arg Ala Gly Ile Gly Ala Asp Gly Ile Leu Arg Val Val Lys Ala
40 45 50

gca gac gta gaa ggc tcc acg gtc gac cca tcg ctg tgg ttc atg gat 307
Ala Asp Val Glu Gly Ser Thr Val Asp Pro Ser Leu Trp Phe Met Asp
55 60 65

tac cgc aac gcc gat gga tct ttg gct gaa atg tgc ggc aat ggt gtg 355
Tyr Arg Asn Ala Asp Gly Ser Leu Ala Glu Met Cys Gly Asn Gly Val
70 75 80 85

cgc ctg ttc gcg cac tgg ctg tac tcc cgc ggt ctt gtt gat aat acg 403
Arg Leu Phe Ala His Trp Leu Tyr Ser Arg Gly Leu Val Asp Asn Thr
90 95 100

agc ttt gat atc ggt acc cgc gcc ggt gtc cgc cac gtt gat att ttg 451
Ser Phe Asp Ile Gly Thr Arg Ala Gly Val Arg His Val Asp Ile Leu
105 110 115

cag gca gat caa cat tct gcg cag gtc cgc gtt gat atg ggc atc cct 499
Gln Ala Asp Gln His Ser Ala Gln Val Arg Val Asp Met Gly Ile Pro
120 125 130

gac gtc acg gga tta tcc acc tgc gac atc aac ggc caa gta ttc gct 547
Asp Val Thr Gly Leu Ser Thr Cys Asp Ile Asn Gly Gln Val Phe Ala

135 140 145

ggc ctt ggc gtt gat atg ggt aac cca cac cta gcg tgc gtt gtg ccg 595
Gly Leu Gly Val Asp Met Gly Asn Pro His Leu Ala Cys Val Val Pro
150 155 160 165

ggc tta agt gcg tcg gct ctt gcc gat atg gaa ctg cgc gca cct acg 643
Gly Leu Ser Ala Ser Ala Leu Ala Asp Met Glu Leu Arg Ala Pro Thr
170 175 180

ttt gat cag gaa ttc ttc ccc cac ggt gtg aac gta gaa atc gtc aca 691
Phe Asp Gln Glu Phe Phe Pro His Gly Val Asn Val Glu Ile Val Thr
185 190 195

gaa tta gaa gat gac gca gta tcg atg cgc gtg tgg gaa cgc gga gtg 739
Glu Leu Glu Asp Asp Ala Val Ser Met Arg Val Trp Glu Arg Gly Val
200 205 210

ggc gaa acc cgc tcc tgt ggc acg gga acc gtt gct gca gcg tgt gct 787
Gly Glu Thr Arg Ser Cys Gly Thr Gly Thr Val Ala Ala Ala Cys Ala
215 220 225

gct tta gct gat gct gga ttg gga gaa ggc aca gct aaa gtg tgc gtt 835
Ala Leu Ala Asp Ala Gly Leu Gly Glu Gly Thr Ala Lys Val Cys Val
230 235 240 245

cca cgt ggg gaa gta gaa gtc cag atc ttt gac gac ggc tcc aca ctc 883
Pro Arg Gly Glu Val Glu Val Gln Ile Phe Asp Asp Gly Ser Thr Leu
250 255 260

acc ggc cca agc gcc atc atc gca ctc ggt gag gtg cag atc 925
Thr Gly Pro Ser Ala Ile Ile Ala Leu Gly Glu Val Gln Ile
265 270 275

taagattcgc gattgtagtt cgg 948

<210> 2
<211> 275
<212> PRT
<213> Corynebacterium glutamicum

<400> 2
Leu Thr Ile Pro Phe Ala Lys Gly His Ala Thr Glu Asn Asp Phe Ile
1 5 10 15

Ile Ile Pro Asp Glu Asp Ala Arg Leu Asp Leu Thr Pro Glu Met Val
20 25 30

Val Thr Leu Cys Asp Arg Arg Ala Gly Ile Gly Ala Asp Gly Ile Leu
35 40 45

Arg Val Val Lys Ala Ala Asp Val Glu Gly Ser Thr Val Asp Pro Ser
50 55 60

Leu Trp Phe Met Asp Tyr Arg Asn Ala Asp Gly Ser Leu Ala Glu Met
65 70 75 80

Cys Gly Asn Gly Val Arg Leu Phe Ala His Trp Leu Tyr Ser Arg Gly
85 90 95

Leu Val Asp Asn Thr Ser Phe Asp Ile Gly Thr Arg Ala Gly Val Arg
100 105 110

His Val Asp Ile Leu Gln Ala Asp Gln His Ser Ala Gln Val Arg Val
115 120 125

Asp Met Gly Ile Pro Asp Val Thr Gly Leu Ser Thr Cys Asp Ile Asn
130 135 140

Gly Gln Val Phe Ala Gly Leu Gly Val Asp Met Gly Asn Pro His Leu
145 150 155 160

Ala Cys Val Val Pro Gly Leu Ser Ala Ser Ala Leu Ala Asp Met Glu
165 170 175

Leu Arg Ala Pro Thr Phe Asp Gln Glu Phe Phe Pro His Gly Val Asn
180 185 190

Val Glu Ile Val Thr Glu Leu Glu Asp Asp Ala Val Ser Met Arg Val
195 200 205

Trp Glu Arg Gly Val Gly Glu Thr Arg Ser Cys Gly Thr Gly Thr Val
210 215 220

Ala Ala Ala Cys Ala Ala Leu Ala Asp Ala Gly Leu Gly Glu Gly Thr
225 230 235 240

Ala Lys Val Cys Val Pro Arg Gly Glu Val Glu Val Gln Ile Phe Asp
245 250 255

Asp Gly Ser Thr Leu Thr Gly Pro Ser Ala Ile Ile Ala Leu Gly Glu
260 265 270

Val Gln Ile
275

<210> 3
<211> 1491
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1468)
<223> RXS02970

<400> 3
aaccgacaaa acagccgttc acgtgctaaa gcagctcggc ttgatctagg gtgaggtgag 60

ttatttaaag acttcataat attttgggga gtgaactggt ttg gca ttg aag ggt 115
Leu Ala Leu Lys Gly
1 5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
10 15 20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
25 30 35

```
cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct   259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
         40                  45                  50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac   307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
     55                  60                  65

atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga   355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
 70                  75                  80                  85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac   403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
                 90                  95                 100

ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg   451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
            105                 110                 115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc   499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
        120                 125                 130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga   547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
    135                 140                 145

cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga   595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
150                 155                 160                 165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc   643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
                170                 175                 180

acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc   691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser
            185                 190                 195

tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag   739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys
        200                 205                 210

cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg   787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala
    215                 220                 225

atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca   835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro
230                 235                 240                 245

gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc   883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile
                250                 255                 260

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa   931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys
            265                 270                 275
```

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile
280 285 290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc
1027
Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile
295 300 305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc
1075
Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser
310 315 320 325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag
1123
Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys
330 335 340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct
1171
Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala
345 350 355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa
1219
Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu
360 365 370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca
1267
Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
375 380 385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa
1315
Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
390 395 400 405

ttc aag gaa cgc ggc gtg tgg ccg atg atc tcc ggc aac cga ttc cac
1363
Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His
410 415 420

atc gcg ccg ccg ctg acc acc act gat gac gaa ttg gta gca ctg ctg
1411
Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu
425 430 435

gac gcg gtg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg
1459
Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly
440 445 450

gcg ttg ttc taagttttct agataacaag gcc
1491
Ala Leu Phe
455

<210> 4

<211> 456
<212> PRT
<213> Corynebacterium glutamicum

<400> 4
Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe
1 5 10 15

Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp
20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
115 120 125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
130 135 140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
145 150 155 160

His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
165 170 175

Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
180 185 190

Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
195 200 205

Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
210 215 220

Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
225 230 235 240

Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
245 250 255

Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
260 265 270

Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
275 280 285

Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
290 295 300

Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
305 310 315 320

Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
325 330 335

Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
340 345 350

Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
355 360 365

Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
370 375 380

Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
385 390 395 400

Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser
405 410 415

Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu
420 425 430

Leu Val Ala Leu Leu Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu
435 440 445

Leu Thr Phe Ala Gly Ala Leu Phe
450 455

<210> 5
<211> 1330
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1330)
<223> FRXA01009

<400> 5
aaccgacaaa acagccgttc acgtgctaaa gcagctcggc ttgatctagg gtgaggtgag 60

ttatttaaag acttcataat attttgggga gtgaactggt ttg gca ttg aag ggt 115
Leu Ala Leu Lys Gly
1 5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
10 15 20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
25 30 35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
40 45 50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
55 60 65

atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
70 75 80 85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
90 95 100

ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
105 110 115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
120 125 130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
135 140 145

cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
150 155 160 165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
170 175 180

acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser
185 190 195

tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag 739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys
200 205 210

cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg 787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala
215 220 225

atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca 835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro
230 235 240 245

gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc 883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile
250 255 260

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys
265 270 275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile
280 285 290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc
1027
Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile
295 300 305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc
1075
Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser
310 315 320 325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag
1123
Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys
330 335 340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct
1171
Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala
345 350 355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa
1219
Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu
360 365 370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca
1267
Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
375 380 385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa
1315
Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
390 395 400 405

ttc aag gaa cgc ggc
1330
Phe Lys Glu Arg Gly
410

<210> 6
<211> 410
<212> PRT
<213> Corynebacterium glutamicum

<400> 6
Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe
1 5 10 15

Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp
20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
115 120 125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
130 135 140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
145 150 155 160

His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
165 170 175

Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
180 185 190

Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
195 200 205

Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
210 215 220

Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
225 230 235 240

Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
245 250 255

Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
260 265 270

Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
275 280 285

Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
290 295 300

Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
305 310 315 320

Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
325 330 335

Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
340 345 350

Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
355 360 365

Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
370 375 380

Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
385 390 395 400

```
Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly
                405                 410


<210> 7
<211> 792
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(769)
<223> RXC02390

<400> 7
gctggtggtg ctgacccata cgctggaact ccaactgctg ttgataccgc caagatgttt    60

ggccgcgagg atctcgtagc tcgcttcgag tcataggccg gtg gag tgg acc gct     115
                                            Val Glu Trp Thr Ala
                                            1               5

ttt ggc acc ctg att ctg ctc aat ttg gtg ggc agt tta tcc ccg ggg     163
Phe Gly Thr Leu Ile Leu Leu Asn Leu Val Gly Ser Leu Ser Pro Gly
                10                  15                  20

cct gat acc ttt ttc ctc ctc cgc tta gcc acc cgc tcc aga gcg cac     211
Pro Asp Thr Phe Phe Leu Leu Arg Leu Ala Thr Arg Ser Arg Ala His
            25                  30                  35

gcg atc gct ggc gtc gcc ggc atc gtc acc gga ctc acg gtg tgg gtg     259
Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly Leu Thr Val Trp Val
        40                  45                  50

acg ctg acg gtc gtg gga gca gcg gcg ctg ctc acc act tat ccg tcg     307
Thr Leu Thr Val Val Gly Ala Ala Ala Leu Leu Thr Thr Tyr Pro Ser
    55                  60                  65

att ctc gga atc atc cag ctc gtc ggc ggc acg tac cta agc ttc att     355
Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr Tyr Leu Ser Phe Ile
70                  75                  80                  85

ggg tac aag ttg ctg cgc tcg gcg tcg aga gag ctt atc gac gcc cgc     403
Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Glu Leu Ile Asp Ala Arg
                90                  95                  100

cag ttc cgt ttc aac gcc gat gcc cga cct atc ccg gat gcg gta gaa     451
Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile Pro Asp Ala Val Glu
            105                 110                 115

gca ctg gga acc cgc act cag gta tat cga caa ggt ttg gcc acc aac     499
Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln Gly Leu Ala Thr Asn
        120                 125                 130

ctg tca aac cct aaa gtt gtc atg tac ttc gcg gca att ctg gct ccg     547
Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala Ala Ile Leu Ala Pro
    135                 140                 145

ttg atg cca gcg cac cca tca ccg gtg ctg gcg ttc tct atc atc gtg     595
Leu Met Pro Ala His Pro Ser Pro Val Leu Ala Phe Ser Ile Ile Val
150                 155                 160                 165
```

gcg att tta gtg cag acc ttt gtt acc ttc tct gct gtg tgc ctc att 643
Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser Ala Val Cys Leu Ile
170 175 180

gtc tct acg gag cgt gtg cgc aaa gca atg ctg cgt gca ggt ccc tgg 691
Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu Arg Ala Gly Pro Trp
185 190 195

ttt gac ctg ctt gct ggc gtt gtc ttc ctc gtt gtg ggt gtg act ctg 739
Phe Asp Leu Leu Ala Gly Val Val Phe Leu Val Val Gly Val Thr Leu
200 205 210

ctg tat gaa ggc ctg acc ggt tta ctc ggg taaaggcata aaaaatggct 789
Leu Tyr Glu Gly Leu Thr Gly Leu Leu Gly
215 220

tcc 792

<210> 8
<211> 223
<212> PRT
<213> Corynebacterium glutamicum

<400> 8
Val Glu Trp Thr Ala Phe Gly Thr Leu Ile Leu Leu Asn Leu Val Gly
1 5 10 15

Ser Leu Ser Pro Gly Pro Asp Thr Phe Phe Leu Leu Arg Leu Ala Thr
20 25 30

Arg Ser Arg Ala His Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly
35 40 45

Leu Thr Val Trp Val Thr Leu Thr Val Val Gly Ala Ala Ala Leu Leu
50 55 60

Thr Thr Tyr Pro Ser Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr
65 70 75 80

Tyr Leu Ser Phe Ile Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Glu
85 90 95

Leu Ile Asp Ala Arg Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile
100 105 110

Pro Asp Ala Val Glu Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln
115 120 125

Gly Leu Ala Thr Asn Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala
130 135 140

Ala Ile Leu Ala Pro Leu Met Pro Ala His Pro Ser Pro Val Leu Ala
145 150 155 160

Phe Ser Ile Ile Val Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser
165 170 175

Ala Val Cys Leu Ile Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu
180 185 190

Arg Ala Gly Pro Trp Phe Asp Leu Leu Ala Gly Val Val Phe Leu Val
195 200 205

Val Gly Val Thr Leu Leu Tyr Glu Gly Leu Thr Gly Leu Leu Gly
210 215 220

<210> 9
<211> 897
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(874)
<223> RXC01796

<400> 9
atgtaactcg atcaggtgga aatgcccgca aaagtggcgg cggtggccga gggatggccg 60

ttggtgcggc atcggtggcc tgctactagt cgggctcttc ttg ctc ctt ggc ggt 115
Leu Leu Leu Gly Gly
1 5

aac cct gcc gag atc gac cag gtt tta ggt ggc gat caa acc cag atc 163
Asn Pro Ala Glu Ile Asp Gln Val Leu Gly Gly Asp Gln Thr Gln Ile
10 15 20

gag tct gga gag tcc acc gga gcc ggc gac ttt gat cac tgc caa acc 211
Glu Ser Gly Glu Ser Thr Gly Ala Gly Asp Phe Asp His Cys Gln Thr
25 30 35

ggc gca gat gcc aac gcc agt gat gat tgt cgc ctt tac tac acc tca 259
Gly Ala Asp Ala Asn Ala Ser Asp Asp Cys Arg Leu Tyr Tyr Thr Ser
40 45 50

ttc tcc gtc aat gaa atg tgg cag act ttg ctt cca gct cag gct ggt 307
Phe Ser Val Asn Glu Met Trp Gln Thr Leu Leu Pro Ala Gln Ala Gly
55 60 65

atc gaa tac acc gag ccg aca ttg act ctt ttc aaa aac tcc acc caa 355
Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe Lys Asn Ser Thr Gln
70 75 80 85

acc ggc tgc ggt ttc gct tct gcg tcc act ggg ccg ttt tac tgt ccg 403
Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly Pro Phe Tyr Cys Pro
90 95 100

tca gac caa gat gct tat ttt gac ttg act ttc ttc gat cag atg cgt 451
Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe Phe Asp Gln Met Arg
105 110 115

cag ttc ggt gca gaa aac gcc ccg ctt gcc cag atg tac atc gtg gcg 499
Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln Met Tyr Ile Val Ala
120 125 130

cac gag tac ggc cac cac gtc caa aac ctc gag ggc aca ctc gga ctg 547
His Glu Tyr Gly His His Val Gln Asn Leu Glu Gly Thr Leu Gly Leu
135 140 145

tcc aat tac aac gat ccg ggc gct gat tcc aac gcc gtc aag atc gag 595

```
Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn Ala Val Lys Ile Glu
150                 155                 160                 165

ttg cag gcc gat tgc tac gca ggc att tgg gct aat cac tcc agc gaa    643
Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala Asn His Ser Ser Glu
                170                 175                 180

ggc ccg gat ccg cta ctc caa ccc atc acc gaa tct gag cta gat tcc    691
Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu Ser Glu Leu Asp Ser
            185                 190                 195

gct ctc ctt gct gca agc gcc gtg ggc gac gac aat atc cag caa cga    739
Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp Asn Ile Gln Gln Arg
        200                 205                 210

tcc ggt ggc gat gtc aat cct gaa agc tgg act cac ggc tca tcg cag    787
Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr His Gly Ser Ser Gln
    215                 220                 225

cag cgc aaa gac gcg ttc ctc gcc ggc tac aac acc ggc cag atg agc    835
Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn Thr Gly Gln Met Ser
230                 235                 240                 245

gcc tgc gac ttc ctc ggc cgg ggc gtc tac aac gac gct taaagcattg     884
Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn Asp Ala
                250                 255

cttttcgacg tct                                                     897


<210> 10
<211> 258
<212> PRT
<213> Corynebacterium glutamicum

<400> 10
Leu Leu Leu Gly Gly Asn Pro Ala Glu Ile Asp Gln Val Leu Gly Gly
  1               5                  10                  15

Asp Gln Thr Gln Ile Glu Ser Gly Glu Ser Thr Gly Ala Gly Asp Phe
             20                  25                  30

Asp His Cys Gln Thr Gly Ala Asp Ala Asn Ala Ser Asp Asp Cys Arg
         35                  40                  45

Leu Tyr Tyr Thr Ser Phe Ser Val Asn Glu Met Trp Gln Thr Leu Leu
     50                  55                  60

Pro Ala Gln Ala Gly Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe
 65                  70                  75                  80

Lys Asn Ser Thr Gln Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly
                 85                  90                  95

Pro Phe Tyr Cys Pro Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe
            100                 105                 110

Phe Asp Gln Met Arg Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln
        115                 120                 125

Met Tyr Ile Val Ala His Glu Tyr Gly His His Val Gln Asn Leu Glu
```

130 135 140

Gly Thr Leu Gly Leu Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn
145 150 155 160

Ala Val Lys Ile Glu Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala
165 170 175

Asn His Ser Ser Glu Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu
180 185 190

Ser Glu Leu Asp Ser Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp
195 200 205

Asn Ile Gln Gln Arg Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr
210 215 220

His Gly Ser Ser Gln Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn
225 230 235 240

Thr Gly Gln Met Ser Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn
245 250 255

Asp Ala

<210> 11
<211> 771
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(748)
<223> RXC01207

<400> 11
cttcatgatc tcaccggcag agcgcgtttt gttacagcgc gtaaactgtg actttgaaaa 60

atttttgaac aatccgtaca ccaacttcag gagaaaaaca gtg agc aga atc tat 115
Val Ser Arg Ile Tyr
1 5

gac tgt gcc gac caa gac tcc cgt gca gca ggc cta aag gcg gct gtc 163
Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly Leu Lys Ala Ala Val
10 15 20

gat gca gtc aaa gcc ggt cag ctc gtt gtc ctt ccc acg gat acc ctt 211
Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu Pro Thr Asp Thr Leu
25 30 35

tat gga ctc ggc tgc gac gct ttc aac aac gag gca gta gcc aac ctt 259
Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu Ala Val Ala Asn Leu
40 45 50

ctg gcc acc aaa cac cgt ggc ccc gat atg ccc gtt cca gtg ctc gtc 307
Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro Val Pro Val Leu Val
55 60 65

ggc agc tgg gac acc att caa gga ctt gtg cac tcc tat tct gcg cag 355

```
Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His Ser Tyr Ser Ala Gln
 70                 75                  80                  85

gca aaa gcg ctt gtg gag gcg ttc tgg cct ggt gga ctg tcc atc atc      403
Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly Gly Leu Ser Ile Ile
                 90                  95                 100

gtt ccg cag gca cca agc ctt ccg tgg aac ctt ggc gat acc cgt ggc      451
Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu Gly Asp Thr Arg Gly
            105                 110                 115

acc gta atg ctg cgc atg cca ctg cac cca gtt gcc att gaa ttg ctg      499
Thr Val Met Leu Arg Met Pro Leu His Pro Val Ala Ile Glu Leu Leu
        120                 125                 130

cgc caa acc gga cca atg gct gtc tcc tcc gcc aac atc tcc gga cat      547
Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala Asn Ile Ser Gly His
    135                 140                 145

act cct cca acc acc gtg ctg gag gct cgt cag cag ctc aac caa aat      595
Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln Gln Leu Asn Gln Asn
150                 155                 160                 165

gtc gct gtc tac ctc gat ggt ggc gaa tgc gcg ctg gcc acc cct tca      643
Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala Leu Ala Thr Pro Ser
                170                 175                 180

acc atc gtg gat att tca ggc ccc gca cca aag att ttg cgt gag ggt      691
Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys Ile Leu Arg Glu Gly
            185                 190                 195

gcc atc agc gca gaa cgc gtt ggc gaa gta ctt gga gtg tcg gca gaa      739
Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu Gly Val Ser Ala Glu
        200                 205                 210

agc ctg cgc taaatgggag tcggtttcgc ggg                                771
Ser Leu Arg
    215


<210> 12
<211> 216
<212> PRT
<213> Corynebacterium glutamicum

<400> 12
Val Ser Arg Ile Tyr Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly
  1               5                  10                  15

Leu Lys Ala Ala Val Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu
             20                  25                  30

Pro Thr Asp Thr Leu Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu
         35                  40                  45

Ala Val Ala Asn Leu Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro
     50                  55                  60

Val Pro Val Leu Val Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His
 65                  70                  75                  80
```

Ser Tyr Ser Ala Gln Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly
85 90 95

Gly Leu Ser Ile Ile Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu
100 105 110

Gly Asp Thr Arg Gly Thr Val Met Leu Arg Met Pro Leu His Pro Val
115 120 125

Ala Ile Glu Leu Leu Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala
130 135 140

Asn Ile Ser Gly His Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln
145 150 155 160

Gln Leu Asn Gln Asn Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala
165 170 175

Leu Ala Thr Pro Ser Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys
180 185 190

Ile Leu Arg Glu Gly Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu
195 200 205

Gly Val Ser Ala Glu Ser Leu Arg
210 215

<210> 13
<211> 1026
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1003)
<223> RXC00657

<400> 13
gtgcggatcg ggtatccgcg ctacacttag aggtgttaga gatcatgagt ttccacgaac 60

tgtaacgcag gattcaccaa tcaatgaaag gtcgaccgac atg agc act gaa gac 115
Met Ser Thr Glu Asp
1 5

att gtc gtc gta gca gta gat ggc tcg gac gcc tca aaa caa gct gtt 163
Ile Val Val Val Ala Val Asp Gly Ser Asp Ala Ser Lys Gln Ala Val
10 15 20

cgg tgg gct gca aat acc gcc aac aaa cgt ggc att cca ctt cgc ttg 211
Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly Ile Pro Leu Arg Leu
25 30 35

gct tcc agc tac acc atg cct cag ttc ctc tac gca gag gga atg gtt 259
Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr Ala Glu Gly Met Val
40 45 50

cca cca caa gag ctt ttc gat gac ctc cag gcc gaa gcc ctg gaa aag 307
Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala Glu Ala Leu Glu Lys
55 60 65

```
att aac gaa gcc cgt gac atc gcc cat gag gta gcg cca gaa atc aag    355
Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val Ala Pro Glu Ile Lys
 70                 75                  80                  85

atc ggg cac acc atc gct gaa ggc agt ccc atc gac atg ctg ttg gaa    403
Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile Asp Met Leu Leu Glu
                 90                  95                 100

atg tct ccc gat gcc aca atg atc gtc atg ggt tcc cgc gga ctc ggc    451
Met Ser Pro Asp Ala Thr Met Ile Val Met Gly Ser Arg Gly Leu Gly
            105                 110                 115

gga ctc tcc gga atg gtc atg ggc tcc gtc tcc ggt gca gtg gtc agc    499
Gly Leu Ser Gly Met Val Met Gly Ser Val Ser Gly Ala Val Val Ser
        120                 125                 130

cac gca aag tgt cca gtc gtt gtt gtc cgt gaa gac agc gca gtc aac    547
His Ala Lys Cys Pro Val Val Val Val Arg Glu Asp Ser Ala Val Asn
    135                 140                 145

gaa gac agc aag tac ggc cca gtc gtc gtc ggt gtg gat ggc tcc gaa    595
Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly Val Asp Gly Ser Glu
150                 155                 160                 165

gtc tcc caa cag gca acc gaa tac gca ttt gcg gaa gct gaa gct cgt    643
Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala Glu Ala Glu Ala Arg
                170                 175                 180

ggc gcc gaa ctc gtt gca gtt cac acc tgg atg gac atg cag gta cag    691
Gly Ala Glu Leu Val Ala Val His Thr Trp Met Asp Met Gln Val Gln
            185                 190                 195

gca tca ctt gca ggt ctt gca gct gct caa cag cag tgg gat gaa gtg    739
Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln Gln Trp Asp Glu Val
        200                 205                 210

gaa cgt cag caa acc gac atg ctg atc gaa cgc ctc gca cca ctg gtg    787
Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg Leu Ala Pro Leu Val
    215                 220                 225

gaa aag tac cca agt gta acc gtc aag aag atc atc acc cgt gac cgc    835
Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile Ile Thr Arg Asp Arg
230                 235                 240                 245

cca gtt cgc gca ctt gca gaa gca tct gaa aac gcg cag ctc cta gtc    883
Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn Ala Gln Leu Leu Val
                250                 255                 260

gtt ggt tcc cat ggt cgt ggc gga ttt aag ggc atg ctc ctt ggc tcc    931
Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly Met Leu Leu Gly Ser
            265                 270                 275

acc tcc cgc gca ctg ctg caa tcc gca ccg tgc cca atg atg gtg gtt    979
Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys Pro Met Met Val Val
        280                 285                 290

cgc cca cct gag aag att aag aag tagtttcttt taagtttcga tgc
1026
Arg Pro Pro Glu Lys Ile Lys Lys
    295                 300
```

<210> 14
<211> 301
<212> PRT
<213> Corynebacterium glutamicum

<400> 14
Met Ser Thr Glu Asp Ile Val Val Val Ala Val Asp Gly Ser Asp Ala
1   5   10   15

Ser Lys Gln Ala Val Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly
            20   25   30

Ile Pro Leu Arg Leu Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr
        35   40   45

Ala Glu Gly Met Val Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala
    50   55   60

Glu Ala Leu Glu Lys Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val
65   70   75   80

Ala Pro Glu Ile Lys Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile
                85   90   95

Asp Met Leu Leu Glu Met Ser Pro Asp Ala Thr Met Ile Val Met Gly
            100   105   110

Ser Arg Gly Leu Gly Gly Leu Ser Gly Met Val Met Gly Ser Val Ser
        115   120   125

Gly Ala Val Val Ser His Ala Lys Cys Pro Val Val Val Val Arg Glu
    130   135   140

Asp Ser Ala Val Asn Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly
145   150   155   160

Val Asp Gly Ser Glu Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala
                165   170   175

Glu Ala Glu Ala Arg Gly Ala Glu Leu Val Ala Val His Thr Trp Met
            180   185   190

Asp Met Gln Val Gln Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln
        195   200   205

Gln Trp Asp Glu Val Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg
    210   215   220

Leu Ala Pro Leu Val Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile
225   230   235   240

Ile Thr Arg Asp Arg Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn
                245   250   255

Ala Gln Leu Leu Val Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly
            260   265   270

Met Leu Leu Gly Ser Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys
        275   280   285

Pro Met Met Val Val Arg Pro Pro Glu Lys Ile Lys Lys
290 295 300

<210> 15
<211> 1059
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1036)
<223> RXC00552

<400> 15
ccgccaacaa ggcagcaaag ctcgatccaa ttgacgcctt gcgttatgag taaaagcctc 60

gtttttaagg tagccacaca tcgcactaga ctgaagaact gtg gct acc tca aaa 115
Val Ala Thr Ser Lys
1 5

att ctt ctt tat tac gca ttc acc ccg ctc tct gac cct aaa gcg gtt 163
Ile Leu Leu Tyr Tyr Ala Phe Thr Pro Leu Ser Asp Pro Lys Ala Val
10 15 20

cag ctg tgg cag cgt gag ctc tgc gag tca ctg aat ctt cgt ggc cgc 211
Gln Leu Trp Gln Arg Glu Leu Cys Glu Ser Leu Asn Leu Arg Gly Arg
25 30 35

atc ctg atc tcc act cac ggc atc aat gga acc gtg ggc gga gat att 259
Ile Leu Ile Ser Thr His Gly Ile Asn Gly Thr Val Gly Gly Asp Ile
40 45 50

gat gat tgc aag gcg tac att aaa aag acc cgc gag tac cca ggt ttc 307
Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg Glu Tyr Pro Gly Phe
55 60 65

aac cgc atg cag ttt aag tgg tcc gag ggt ggc gct gag gat ttc cca 355
Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly Ala Glu Asp Phe Pro
70 75 80 85

aag ctc agt gtc aaa gtc cgc gat gag atc gtt gcc ttc ggc gct cca 403
Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val Ala Phe Gly Ala Pro
90 95 100

gat gag ctc aaa gtg gat gaa aac ggc gtc gtc ggt ggc ggc gtt cac 451
Asp Glu Leu Lys Val Asp Glu Asn Gly Val Val Gly Gly Gly Val His
105 110 115

ctg aaa cca cag cag gtc aat gag ctt gtg gaa gcc cgt ggc gat gaa 499
Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu Ala Arg Gly Asp Glu
120 125 130

gtt gtg ttc ttt gac ggc cgc aac gca atg gaa gcc cag atc ggc aag 547
Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu Ala Gln Ile Gly Lys
135 140 145

ttc aag gac gct gtt gtc cct gac gta gaa acc act cat gat ttc atc 595
Phe Lys Asp Ala Val Val Pro Asp Val Glu Thr Thr His Asp Phe Ile
150 155 160 165

gca gaa att gag tct gga aaa tac gac gat ctc aaa gac aag cct gtg 643
Ala Glu Ile Glu Ser Gly Lys Tyr Asp Asp Leu Lys Asp Lys Pro Val
170 175 180

gtc acc tac tgc acc ggc gga att cgt tgt gag atc ctg agt tca ctc 691
Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu Ile Leu Ser Ser Leu
185 190 195

atg atc aac cgt ggt ttc aaa gag gtc tac caa atc gat ggc ggc atc 739
Met Ile Asn Arg Gly Phe Lys Glu Val Tyr Gln Ile Asp Gly Gly Ile
200 205 210

gtt cgc tac ggc gag cag ttt ggc aac aag ggc ctg tgg gaa ggc tcc 787
Val Arg Tyr Gly Glu Gln Phe Gly Asn Lys Gly Leu Trp Glu Gly Ser
215 220 225

ctc tac gtt ttc gat aag cgc atg cat atg gaa ttc ggc gag gat tac 835
Leu Tyr Val Phe Asp Lys Arg Met His Met Glu Phe Gly Glu Asp Tyr
230 235 240 245

aaa gag gtc gga cac tgc atc cat tgc gat act ccc acc aac aaa ttt 883
Lys Glu Val Gly His Cys Ile His Cys Asp Thr Pro Thr Asn Lys Phe
250 255 260

gag cac tgc ctc aac gaa gat gat tgc cgc gag ctc gtg ttg atg tgc 931
Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu Leu Val Leu Met Cys
265 270 275

cct gat tgc ttc gcc aat gtt gag acc cgt cat tgc aag cgc gaa cgc 979
Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His Cys Lys Arg Glu Arg
280 285 290

tgt gca gca att gct gcg gat ttc gct gag caa gga att gat ccg ctc
1027
Cys Ala Ala Ile Ala Ala Asp Phe Ala Glu Gln Gly Ile Asp Pro Leu
295 300 305

gtt act tct taaaagggt atggtggctg ggt
1059
Val Thr Ser
310

<210> 16
<211> 312
<212> PRT
<213> Corynebacterium glutamicum

<400> 16
Val Ala Thr Ser Lys Ile Leu Leu Tyr Tyr Ala Phe Thr Pro Leu Ser
1 5 10 15

Asp Pro Lys Ala Val Gln Leu Trp Gln Arg Glu Leu Cys Glu Ser Leu
20 25 30

Asn Leu Arg Gly Arg Ile Leu Ile Ser Thr His Gly Ile Asn Gly Thr
35 40 45

Val Gly Gly Asp Ile Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg
50 55 60

Glu Tyr Pro Gly Phe Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly
65 70 75 80

Ala Glu Asp Phe Pro Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val
85 90 95

Ala Phe Gly Ala Pro Asp Glu Leu Lys Val Asp Glu Asn Gly Val Val
100 105 110

Gly Gly Gly Val His Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu
115 120 125

Ala Arg Gly Asp Glu Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu
130 135 140

Ala Gln Ile Gly Lys Phe Lys Asp Ala Val Val Pro Asp Val Glu Thr
145 150 155 160

Thr His Asp Phe Ile Ala Glu Ile Glu Ser Gly Lys Tyr Asp Asp Leu
165 170 175

Lys Asp Lys Pro Val Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu
180 185 190

Ile Leu Ser Ser Leu Met Ile Asn Arg Gly Phe Lys Glu Val Tyr Gln
195 200 205

Ile Asp Gly Gly Ile Val Arg Tyr Gly Glu Gln Phe Gly Asn Lys Gly
210 215 220

Leu Trp Glu Gly Ser Leu Tyr Val Phe Asp Lys Arg Met His Met Glu
225 230 235 240

Phe Gly Glu Asp Tyr Lys Glu Val Gly His Cys Ile His Cys Asp Thr
245 250 255

Pro Thr Asn Lys Phe Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu
260 265 270

Leu Val Leu Met Cys Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His
275 280 285

Cys Lys Arg Glu Arg Cys Ala Ala Ile Ala Ala Asp Phe Ala Glu Gln
290 295 300

Gly Ile Asp Pro Leu Val Thr Ser
305 310

<210> 17
<211> 1578
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1555)
<223> RXN00351

<400> 17
gaaggctgct gctaagaaaa cgaccaagaa gaccactaag aaaactacta aaaagaccac 60

```
cgcaaagaag accacaaaga agtcttaagc cggatcttat atg gat gat tcc aat    115
                                            Met Asp Asp Ser Asn
                                             1               5

agc ttt gta gtt gtt gct aac cgt ctg cca gtg gat atg act gtc cac    163
Ser Phe Val Val Val Ala Asn Arg Leu Pro Val Asp Met Thr Val His
                 10                  15                  20

cca gat ggt agc tat agc atc tcc ccc agc ccc ggt ggc ctt gtc acg    211
Pro Asp Gly Ser Tyr Ser Ile Ser Pro Ser Pro Gly Gly Leu Val Thr
             25                  30                  35

ggg ctt tcc ccc gtt ctg gaa caa cat cgt gga tgt tgg gtc gga tgg    259
Gly Leu Ser Pro Val Leu Glu Gln His Arg Gly Cys Trp Val Gly Trp
         40                  45                  50

cct gga act gta gat gtt gca ccc gaa cca ttt cga aca gat acg ggt    307
Pro Gly Thr Val Asp Val Ala Pro Glu Pro Phe Arg Thr Asp Thr Gly
     55                  60                  65

gtt ttg ctg cac cct gtt gtc ctc act gca agt gac tat gaa ggc ttc    355
Val Leu Leu His Pro Val Val Leu Thr Ala Ser Asp Tyr Glu Gly Phe
 70                  75                  80                  85

tac gag ggc ttt tca aac gca acg ctg tgg cct ctt ttc cac gat ctg    403
Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro Leu Phe His Asp Leu
                 90                  95                 100

att gtt act ccg gtg tac aac acc gat tgg tgg cat gcg ttt cgg gag    451
Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp His Ala Phe Arg Glu
            105                 110                 115

gta aac ctc aag ttc gct gaa gcc gtg agc caa gtg gcg gca cac ggt    499
Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln Val Ala Ala His Gly
        120                 125                 130

gcc act gtg tgg gtg cag gac tat cag ctg ttg ctg gtt cct ggc att    547
Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu Leu Val Pro Gly Ile
    135                 140                 145

ttg cgc cag atg cgc cct gat ttg aag atc ggt ttc ttc ctc cac att    595
Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly Phe Phe Leu His Ile
150                 155                 160                 165

ccc ttc cct tcc cct gat ctg ttc cgt cag ctg ccg tgg cgt gaa gag    643
Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu Pro Trp Arg Glu Glu
                170                 175                 180

att gtt cga ggc atg ctg ggc gca gat ttg gtg gga ttc cat ttg gtt    691
Ile Val Arg Gly Met Leu Gly Ala Asp Leu Val Gly Phe His Leu Val
            185                 190                 195

caa aac gca gaa aac ttc ctt gcg tta acc cag cag gtt gcc ggc act    739
Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr Gln Gln Val Ala Gly Thr
        200                 205                 210

gcc ggg tct cat gtg ggt cag ccg gac acc ttg cag gtc agt ggt gaa    787
Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu Gln Val Ser Gly Glu
    215                 220                 225
```

```
gca ttg gtg cgt gag att ggc gct cat gtt gaa acc gct gac gga agg     835
Ala Leu Val Arg Glu Ile Gly Ala His Val Glu Thr Ala Asp Gly Arg
230                 235                 240                 245

cga gtt agc gtc ggg gcg ttc ccg atc tcg att gat gtt gaa atg ttt     883
Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile Asp Val Glu Met Phe
                250                 255                 260

ggg gag gcg tcg aaa agc gcc gtt ctt gat ctt tta aaa acg ctc gac     931
Gly Glu Ala Ser Lys Ser Ala Val Leu Asp Leu Leu Lys Thr Leu Asp
            265                 270                 275

gag ccg gaa acc gta ttc ctg ggc gtt gac cga ctg gac tac acc aag     979
Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg Leu Asp Tyr Thr Lys
        280                 285                 290

ggc att ttg cag cgc ctg ctt gcg ttt gag gaa ctg ctg gaa tcc ggc
1027
Gly Ile Leu Gln Arg Leu Leu Ala Phe Glu Glu Leu Leu Glu Ser Gly
    295                 300                 305

gcg ttg gag gcc gac aaa gct gtg ttg ctg cag gtc gcg acg cct tcg
1075
Ala Leu Glu Ala Asp Lys Ala Val Leu Leu Gln Val Ala Thr Pro Ser
310                 315                 320                 325

cgt gag cgc att gat cac tat cgt gtg tcg cgt tcg cag gtc gag gaa
1123
Arg Glu Arg Ile Asp His Tyr Arg Val Ser Arg Ser Gln Val Glu Glu
                330                 335                 340

gcc gtc ggc cgt atc aat ggt cgt ttc ggt cgc atg ggg cgt ccc gtg
1171
Ala Val Gly Arg Ile Asn Gly Arg Phe Gly Arg Met Gly Arg Pro Val
            345                 350                 355

gtg cat tat cta cac agg tca ttg agc aaa aat gat ctc cag gtg ctg
1219
Val His Tyr Leu His Arg Ser Leu Ser Lys Asn Asp Leu Gln Val Leu
        360                 365                 370

tat acc gca gcc gat gtc atg ctg gtt acg cct ttt aaa gac ggt atg
1267
Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro Phe Lys Asp Gly Met
    375                 380                 385

aac ttg gtg gct aaa gaa ttc gtg gcc aac cac cgc gac ggc act ggt
1315
Asn Leu Val Ala Lys Glu Phe Val Ala Asn His Arg Asp Gly Thr Gly
390                 395                 400                 405

gct ttg gtg ctg tcc gaa ttt gcc ggc gcg gcc act gag ctg acc ggt
1363
Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala Thr Glu Leu Thr Gly
                410                 415                 420

gcg tat tta tgc aac cca ttt gat gtg gaa tcc atc aaa cgg caa atg
1411
Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser Ile Lys Arg Gln Met
            425                 430                 435
```

gtg gca gct gtc cat gat ttg aag cac aat ccg gaa tct gcg gca acg
1459
Val Ala Ala Val His Asp Leu Lys His Asn Pro Glu Ser Ala Ala Thr
440 445 450

cga atg aaa acg aac agc gag cag gtc tat acc cac gac gtc aac gtg
1507
Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr His Asp Val Asn Val
455 460 465

tgg gct aat agt ttc ctg gat tgt ttg gca cag tcg gga gaa aac tca
1555
Trp Ala Asn Ser Phe Leu Asp Cys Leu Ala Gln Ser Gly Glu Asn Ser
470 475 480 485

tgaaccgcgc acgaatcgcg acc
1578

<210> 18
<211> 485
<212> PRT
<213> Corynebacterium glutamicum

<400> 18
Met Asp Asp Ser Asn Ser Phe Val Val Val Ala Asn Arg Leu Pro Val
1 5 10 15

Asp Met Thr Val His Pro Asp Gly Ser Tyr Ser Ile Ser Pro Ser Pro
20 25 30

Gly Gly Leu Val Thr Gly Leu Ser Pro Val Leu Glu Gln His Arg Gly
35 40 45

Cys Trp Val Gly Trp Pro Gly Thr Val Asp Val Ala Pro Glu Pro Phe
50 55 60

Arg Thr Asp Thr Gly Val Leu Leu His Pro Val Val Leu Thr Ala Ser
65 70 75 80

Asp Tyr Glu Gly Phe Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro
85 90 95

Leu Phe His Asp Leu Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp
100 105 110

His Ala Phe Arg Glu Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln
115 120 125

Val Ala Ala His Gly Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu
130 135 140

Leu
Leu Val Pro Gly Ile Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly
145 150 155 160

Phe Phe Leu His Ile Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu
165 170 175

Pro Trp Arg Glu Glu Ile Val Arg Gly Met Leu Gly Ala Asp Leu Val
180 185 190

Gly Phe His Leu Val Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr Gln
        195   200   205

Gln Val Ala Gly Thr Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu
    210   215   220

Gln Val Ser Gly Glu Ala Leu Val Arg Glu Ile Gly Ala His Val Glu
225   230   235   240

Thr Ala Asp Gly Arg Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile
                245   250   255

Asp Val Glu Met Phe Gly Glu Ala Ser Lys Ser Ala Val Leu Asp Leu
            260   265   270

Leu Lys Thr Leu Asp Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg
        275   280   285

Leu Asp Tyr Thr Lys Gly Ile Leu Gln Arg Leu Leu Ala Phe Glu Glu
    290   295   300

Leu Leu Glu Ser Gly Ala Leu Glu Ala Asp Lys Ala Val Leu Leu Gln
305   310   315   320

Val Ala Thr Pro Ser Arg Glu Arg Ile Asp His Tyr Arg Val Ser Arg
                325   330   335

Ser Gln Val Glu Glu Ala Val Gly Arg Ile Asn Gly Arg Phe Gly Arg
            340   345   350

Met Gly Arg Pro Val Val His Tyr Leu His Arg Ser Leu Ser Lys Asn
        355   360   365

Asp Leu Gln Val Leu Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro
    370   375   380

Phe Lys Asp Gly Met Asn Leu Val Ala Lys Glu Phe Val Ala Asn His
385   390   395   400

Arg Asp Gly Thr Gly Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala
                405   410   415

Thr Glu Leu Thr Gly Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser
            420   425   430

Ile Lys Arg Gln Met Val Ala Ala Val His Asp Leu Lys His Asn Pro
        435   440   445

Glu Ser Ala Ala Thr Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr
    450   455   460

His Asp Val Asn Val Trp Ala Asn Ser Phe Leu Asp Cys Leu Ala Gln
465   470   475   480

Ser Gly Glu Asn Ser
                485

<210> 19
<211> 1546
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1546)
<223> FRXA00351

<400> 19
```
gaaggctgct gctaagaaaa cgaccaagaa gaccactaag aaaactacta aaaagaccac 60

cgcaaagaag accacaaaga agtcttaagc cggatcttat atg gat gat tcc aat   115
                                           Met Asp Asp Ser Asn
                                           1               5

agc ttt gta gtt gtt gct aac cgt ctg cca gtg gat atg act gtc cac   163
Ser Phe Val Val Val Ala Asn Arg Leu Pro Val Asp Met Thr Val His
                10                  15                  20

cca gat ggt agc tat agc atc tcc ccc agc ccc ggt ggc ctt gtc acg   211
Pro Asp Gly Ser Tyr Ser Ile Ser Pro Ser Pro Gly Gly Leu Val Thr
            25                  30                  35

ggg ctt tcc ccc gtt ctg gaa caa cat cgt gga tgt tgg gtc gga tgg   259
Gly Leu Ser Pro Val Leu Glu Gln His Arg Gly Cys Trp Val Gly Trp
        40                  45                  50

cct gga act gta gat gtt gca ccc gaa cca ttt cga aca gat acg ggt   307
Pro Gly Thr Val Asp Val Ala Pro Glu Pro Phe Arg Thr Asp Thr Gly
    55                  60                  65

gtt ttg ctg cac cct gtt gtc ctc act gca agt gac tat gaa ggc ttc   355
Val Leu Leu His Pro Val Val Leu Thr Ala Ser Asp Tyr Glu Gly Phe
70                  75                  80                  85

tac gag ggc ttt tca aac gca acg ctg tgg cct ctt ttc cac gat ctg   403
Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro Leu Phe His Asp Leu
                90                  95                  100

att gtt act ccg gtg tac aac acc gat tgg tgg cat gcg ttt cgg gag   451
Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp His Ala Phe Arg Glu
            105                 110                 115

gta aac ctc aag ttc gct gaa gcc gtg agc caa gtg gcg gca cac ggt   499
Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln Val Ala Ala His Gly
        120                 125                 130

gcc act gtg tgg gtg cag gac tat cag ctg ttg ctg gtt cct ggc att   547
Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu Leu Val Pro Gly Ile
    135                 140                 145

ttg cgc cag atg cgc cct gat ttg aag atc ggt ttc ttc ctc cac att   595
Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly Phe Phe Leu His Ile
150                 155                 160                 165

ccc ttc cct tcc cct gat ctg ttc cgt cag ctg ccg tgg cgt gaa gag   643
Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu Pro Trp Arg Glu Glu
                170                 175                 180

att gtt cga ggc atg ctg ggc gca gat ttg gtg gga ttc cat ttg gtt   691
Ile Val Arg Gly Met Leu Gly Ala Asp Leu Val Gly Phe His Leu Val
            185                 190                 195
```

caa aac gca gaa aac ttc ctt gcg tta acc cag cag gtt gcc ggc act 739
Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr Gln Gln Val Ala Gly Thr
200 205 210

gcc ggg tct cat gtg ggt cag ccg gac acc ttg cag gtc agt ggt gaa 787
Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu Gln Val Ser Gly Glu
215 220 225

gca ttg gtg cgt gag att ggc gct cat gtt gaa acc gct gac gga agg 835
Ala Leu Val Arg Glu Ile Gly Ala His Val Glu Thr Ala Asp Gly Arg
230 235 240 245

cga gtt agc gtc ggg gcg ttc ccg atc tcg att gat gtt gaa atg ttt 883
Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile Asp Val Glu Met Phe
250 255 260

ggg gag gcg tcg aaa agc gcc gtt ctt gat ctt tta aaa acg ctc gac 931
Gly Glu Ala Ser Lys Ser Ala Val Leu Asp Leu Leu Lys Thr Leu Asp
265 270 275

gag ccg gaa acc gta ttc ctg ggc gtt gac cga ctg gac tac acc aag 979
Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg Leu Asp Tyr Thr Lys
280 285 290

ggc att ttg cag cgc ctg ctt gcg ttt gag gaa ctg ctg gaa tcc ggc
1027
Gly Ile Leu Gln Arg Leu Leu Ala Phe Glu Glu Leu Leu Glu Ser Gly
295 300 305

gcg ttg gag gcc gac aaa gct gtg ttg ctg cag gtc gcg acg cct tcg
1075
Ala Leu Glu Ala Asp Lys Ala Val Leu Leu Gln Val Ala Thr Pro Ser
310 315 320 325

cgt gag cgc att gat cac tat cgt gtg tcg cgt tcg cag gtc gag gaa
1123
Arg Glu Arg Ile Asp His Tyr Arg Val Ser Arg Ser Gln Val Glu Glu
330 335 340

gcc gtc ggc cgt atc aat ggt cgt ttc ggt cgc atg ggg cgt ccc gtg
1171
Ala Val Gly Arg Ile Asn Gly Arg Phe Gly Arg Met Gly Arg Pro Val
345 350 355

gtg cat tat cta cac agg tca ttg agc aaa aat gat ctc cag gtg ctg
1219
Val His Tyr Leu His Arg Ser Leu Ser Lys Asn Asp Leu Gln Val Leu
360 365 370

tat acc gca gcc gat gtc atg ctg gtt acg cct ttt aaa gac ggt atg
1267
Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro Phe Lys Asp Gly Met
375 380 385

aac ttg gtg gct aaa gaa ttc gtg gcc aac cac cgc gac ggc act ggt
1315
Asn Leu Val Ala Lys Glu Phe Val Ala Asn His Arg Asp Gly Thr Gly
390 395 400 405

```
gct ttg gtg ctg tcc gaa ttt gcc ggc gcg gcc act gag ctg acc ggt
1363
Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala Thr Glu Leu Thr Gly
                410                     415                     420

gcg tat tta tgc aac cca ttt gat gtg gaa tcc atc aaa cgg caa atg
1411
Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser Ile Lys Arg Gln Met
            425                     430                     435

gtg gca gct gtc cat gat ttg aag cac aat ccg gaa tct gcg gca acg
1459
Val Ala Ala Val His Asp Leu Lys His Asn Pro Glu Ser Ala Ala Thr
        440                     445                     450

cga atg aaa acg aac agc gag cag gtc tat acc cac gac gtc aac gtg
1507
Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr His Asp Val Asn Val
    455                     460                     465

tgg gct aat agt ttc ctg gat tgt ttg gca cag tcg gga
1546
Trp Ala Asn Ser Phe Leu Asp Cys Leu Ala Gln Ser Gly
470                     475                     480


&lt;210&gt; 20
&lt;211&gt; 482
&lt;212&gt; PRT
&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 20
Met Asp Asp Ser Asn Ser Phe Val Val Val Ala Asn Arg Leu Pro Val
  1               5                  10                  15

Asp Met Thr Val His Pro Asp Gly Ser Tyr Ser Ile Ser Pro Ser Pro
             20                  25                  30

Gly Gly Leu Val Thr Gly Leu Ser Pro Val Leu Glu Gln His Arg Gly
         35                  40                  45

Cys Trp Val Gly Trp Pro Gly Thr Val Asp Val Ala Pro Glu Pro Phe
     50                  55                  60

Arg Thr Asp Thr Gly Val Leu Leu His Pro Val Val Leu Thr Ala Ser
 65                  70                  75                  80

Asp Tyr Glu Gly Phe Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro
                 85                  90                  95

Leu Phe His Asp Leu Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp
            100                 105                 110

His Ala Phe Arg Glu Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln
        115                 120                 125

Val Ala Ala His Gly Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu
    130                 135                 140

Leu Val Pro Gly Ile Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly
145                 150                 155                 160
```

Phe Phe Leu His Ile Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu
165 170 175

Pro Trp Arg Glu Glu Ile Val Arg Gly Met Leu Gly Ala Asp Leu Val
180 185 190

Gly Phe His Leu Val Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr Gln
195 200 205

Gln Val Ala Gly Thr Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu
210 215 220

Gln Val Ser Gly Glu Ala Leu Val Arg Glu Ile Gly Ala His Val Glu
225 230 235 240

Thr Ala Asp Gly Arg Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile
245 250 255

Asp Val Glu Met Phe Gly Glu Ala Ser Lys Ser Ala Val Leu Asp Leu
260 265 270

Leu Lys Thr Leu Asp Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg
275 280 285

Leu Asp Tyr Thr Lys Gly Ile Leu Gln Arg Leu Leu Ala Phe Glu Glu
290 295 300

Leu Leu Glu Ser Gly Ala Leu Glu Ala Asp Lys Ala Val Leu Leu Gln
305 310 315 320

Val Ala Thr Pro Ser Arg Glu Arg Ile Asp His Tyr Arg Val Ser Arg
325 330 335

Ser Gln Val Glu Glu Ala Val Gly Arg Ile Asn Gly Arg Phe Gly Arg
340 345 350

Met Gly Arg Pro Val Val His Tyr Leu His Arg Ser Leu Ser Lys Asn
355 360 365

Asp Leu Gln Val Leu Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro
370 375 380

Phe Lys Asp Gly Met Asn Leu Val Ala Lys Glu Phe Val Ala Asn His
385 390 395 400

Arg Asp Gly Thr Gly Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala
405 410 415

Thr Glu Leu Thr Gly Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser
420 425 430

Ile Lys Arg Gln Met Val Ala Ala Val His Asp Leu Lys His Asn Pro
435 440 445

Glu Ser Ala Ala Thr Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr
450 455 460

His Asp Val Asn Val Trp Ala Asn Ser Phe Leu Asp Cys Leu Ala Gln
465 470 475 480

Ser Gly

<210> 21
<211> 779
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(756)
<223> RXA00873

<400> 21
act gcc caa tgg ggt att ttc ctg cgt aat cat gat gag ctc acc ctt 48
Thr Ala Gln Trp Gly Ile Phe Leu Arg Asn His Asp Glu Leu Thr Leu
1 5 10 15

gaa atg gtc tcc gat gag gaa cgc agc tac atg tac tcc caa ttc gcc 96
Glu Met Val Ser Asp Glu Glu Arg Ser Tyr Met Tyr Ser Gln Phe Ala
20 25 30

tcc gaa cct cgc atg cgc gcc aac gta gga atc cgc agg cgc ctt tcc 144
Ser Glu Pro Arg Met Arg Ala Asn Val Gly Ile Arg Arg Arg Leu Ser
35 40 45

cca ctg ctt gaa ggc gac cgc aac cag ctg gaa ctc ctt cac ggt ttg 192
Pro Leu Leu Glu Gly Asp Arg Asn Gln Leu Glu Leu Leu His Gly Leu
50 55 60

ttg ctg tct cta cct ggc tca ccc gtg ttg tat tac ggt gat gaa att 240
Leu Leu Ser Leu Pro Gly Ser Pro Val Leu Tyr Tyr Gly Asp Glu Ile
65 70 75 80

ggc atg ggc gac aat atc tgg ctc cac gac cgc gac gga gtg cgc acc 288
Gly Met Gly Asp Asn Ile Trp Leu His Asp Arg Asp Gly Val Arg Thr
85 90 95

ccc atg cag tgg tcc aac gac cgc aac ggt ggt ttc tcc aaa gct gat 336
Pro Met Gln Trp Ser Asn Asp Arg Asn Gly Gly Phe Ser Lys Ala Asp
100 105 110

cct gaa cgc ctg tac ctt cca gcg atc caa aat gat caa tac ggc tac 384
Pro Glu Arg Leu Tyr Leu Pro Ala Ile Gln Asn Asp Gln Tyr Gly Tyr
115 120 125

gcc caa gta aac gtg gaa agc caa ctc aac cgc gaa aac tcc ctg ctg 432
Ala Gln Val Asn Val Glu Ser Gln Leu Asn Arg Glu Asn Ser Leu Leu
130 135 140

cgc tgg ctc cga aac caa atc ctt atc cgc aag cag tac cgc gca ttt 480
Arg Trp Leu Arg Asn Gln Ile Leu Ile Arg Lys Gln Tyr Arg Ala Phe
145 150 155 160

ggt gcc gga acc tac cgt gaa gtg tcc tcc acc aat gag tca gtg ttg 528
Gly Ala Gly Thr Tyr Arg Glu Val Ser Ser Thr Asn Glu Ser Val Leu
165 170 175

aca ttt tta cga gaa cac aag ggc caa acc att ttg tgt gtc aac aac 576
Thr Phe Leu Arg Glu His Lys Gly Gln Thr Ile Leu Cys Val Asn Asn

```
            180                     185                     190

atg agc aaa tat cct cag gca gtc tcg ctt gat ttg cgt gaa ttt gca      624
Met Ser Lys Tyr Pro Gln Ala Val Ser Leu Asp Leu Arg Glu Phe Ala
        195                     200                     205

gga cac acc cct cga gag atg tcg ggc ggg cag ctg ttc cct acc att      672
Gly His Thr Pro Arg Glu Met Ser Gly Gly Gln Leu Phe Pro Thr Ile
    210                     215                     220

gct gaa cgg gag tgg att gtc act tta gcc cct cac gga ttc ttc tgg      720
Ala Glu Arg Glu Trp Ile Val Thr Leu Ala Pro His Gly Phe Phe Trp
225                     230                     235                     240

ttt gat ctc acc gcc gat gaa aag gac gat atg gaa tgagcattgg          766
Phe Asp Leu Thr Ala Asp Glu Lys Asp Asp Met Glu
                245                     250

ccaacacatc atc                                                      779


<210> 22
<211> 252
<212> PRT
<213> Corynebacterium glutamicum

<400> 22
Thr Ala Gln Trp Gly Ile Phe Leu Arg Asn His Asp Glu Leu Thr Leu
 1               5                  10                  15

Glu Met Val Ser Asp Glu Glu Arg Ser Tyr Met Tyr Ser Gln Phe Ala
            20                  25                  30

Ser Glu Pro Arg Met Arg Ala Asn Val Gly Ile Arg Arg Arg Leu Ser
        35                  40                  45

Pro Leu Leu Glu Gly Asp Arg Asn Gln Leu Glu Leu Leu His Gly Leu
    50                  55                  60

Leu Leu Ser Leu Pro Gly Ser Pro Val Leu Tyr Tyr Gly Asp Glu Ile
65                  70                  75                  80

Gly Met Gly Asp Asn Ile Trp Leu His Asp Arg Asp Gly Val Arg Thr
                85                  90                  95

Pro Met Gln Trp Ser Asn Asp Arg Asn Gly Gly Phe Ser Lys Ala Asp
            100                 105                 110

Pro Glu Arg Leu Tyr Leu Pro Ala Ile Gln Asn Asp Gln Tyr Gly Tyr
        115                 120                 125

Ala Gln Val Asn Val Glu Ser Gln Leu Asn Arg Glu Asn Ser Leu Leu
    130                 135                 140

Arg Trp Leu Arg Asn Gln Ile Leu Ile Arg Lys Gln Tyr Arg Ala Phe
145                 150                 155                 160

Gly Ala Gly Thr Tyr Arg Glu Val Ser Ser Thr Asn Glu Ser Val Leu
                165                 170                 175

Thr Phe Leu Arg Glu His Lys Gly Gln Thr Ile Leu Cys Val Asn Asn
```

```
            180                 185                 190

Met Ser Lys Tyr Pro Gln Ala Val Ser Leu Asp Leu Arg Glu Phe Ala
        195                 200                 205

Gly His Thr Pro Arg Glu Met Ser Gly Gly Gln Leu Phe Pro Thr Ile
    210                 215                 220

Ala Glu Arg Glu Trp Ile Val Thr Leu Ala Pro His Gly Phe Phe Trp
225                 230                 235                 240

Phe Asp Leu Thr Ala Asp Glu Lys Asp Asp Met Glu
                245                 250


<210> 23
<211> 1102
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1102)
<223> RXA00891

<400> 23
tcaatattcc gaagaaaacc gcgcagctct ctcactagtc tcaggtgagg cgaaagtggt 60

gaaagacccg ctacgcatgg tgcgcctggc tttttagaat gtg ctg caa acc tcc   115
                                           Val Leu Gln Thr Ser
                                            1               5

tgg cat ttc tct atc ctg gca ggc atg act gat acc tct ccg ttg aat   163
Trp His Phe Ser Ile Leu Ala Gly Met Thr Asp Thr Ser Pro Leu Asn
                10                  15                  20

tct cag ccg agt gca gat cac cac cct gat cac gcg gct cgc cca gtt   211
Ser Gln Pro Ser Ala Asp His His Pro Asp His Ala Ala Arg Pro Val
            25                  30                  35

ctt gat gcc cac ggc ttg atc gtt gag cac gaa tcg gaa gag ttt cca   259
Leu Asp Ala His Gly Leu Ile Val Glu His Glu Ser Glu Glu Phe Pro
        40                  45                  50

gtc ccc gca ccc gct ccc ggt gaa cag ccc tgg gag aag aaa aac cgc   307
Val Pro Ala Pro Ala Pro Gly Glu Gln Pro Trp Glu Lys Lys Asn Arg
    55                  60                  65

gag tgg tac aaa gac gcc gtt ttc tac gaa gtg ctg gtt cgt gcc ttc   355
Glu Trp Tyr Lys Asp Ala Val Phe Tyr Glu Val Leu Val Arg Ala Phe
70                  75                  80                  85

tac gat cca gaa ggc aac gga gtc gga tcg ttg aaa ggc ctg acc gaa   403
Tyr Asp Pro Glu Gly Asn Gly Val Gly Ser Leu Lys Gly Leu Thr Glu
                90                  95                  100

aaa ctg gat tac atc cag tgg ctc ggc gtg gat tgc att tgg atc cca   451
Lys Leu Asp Tyr Ile Gln Trp Leu Gly Val Asp Cys Ile Trp Ile Pro
            105                 110                 115

ccg ttt tat gat tcc cca ctg cgc gac ggc ggt tac gat atc cgc aac   499
```

```
Pro Phe Tyr Asp Ser Pro Leu Arg Asp Gly Gly Tyr Asp Ile Arg Asn
        120                 125                 130

ttc cgt gaa atc ctg ccc gaa ttc ggc acc gtc gat gac ttc gtg gaa      547
Phe Arg Glu Ile Leu Pro Glu Phe Gly Thr Val Asp Asp Phe Val Glu
    135                 140                 145

ctc gtt gac cac gcc cac cgc cgt ggc ctg cgt gtt atc acc gac ttg      595
Leu Val Asp His Ala His Arg Arg Gly Leu Arg Val Ile Thr Asp Leu
150                 155                 160                 165

gtc atg aat cac acc tcc gac cag cac gca tgg ttc caa gaa tcc cgg      643
Val Met Asn His Thr Ser Asp Gln His Ala Trp Phe Gln Glu Ser Arg
                170                 175                 180

cgc gac cca acc ggc ccc tac gga gat ttc tat gtg tgg agc gat gat      691
Arg Asp Pro Thr Gly Pro Tyr Gly Asp Phe Tyr Val Trp Ser Asp Asp
            185                 190                 195

ccc acc ctg tac aac gaa gcc cgc atc atc ttt gta gat aca gaa gaa      739
Pro Thr Leu Tyr Asn Glu Ala Arg Ile Ile Phe Val Asp Thr Glu Glu
        200                 205                 210

tcc aac tgg acc tat gat ccg gtg cgt ggc cag tac ttc tgg cac cgc      787
Ser Asn Trp Thr Tyr Asp Pro Val Arg Gly Gln Tyr Phe Trp His Arg
    215                 220                 225

ttc ttc tcc cac caa cca gac ctc aac tac gac aac ccc gca gtc caa      835
Phe Phe Ser His Gln Pro Asp Leu Asn Tyr Asp Asn Pro Ala Val Gln
230                 235                 240                 245

gag gcc atg cta gat gtc ttg cgt ttc tgg ctg gac ctg gga ctt gat      883
Glu Ala Met Leu Asp Val Leu Arg Phe Trp Leu Asp Leu Gly Leu Asp
                250                 255                 260

ggt ttc cga cta gat gcc gtt cct tat ctt ttt gaa cgc gaa ggc acc      931
Gly Phe Arg Leu Asp Ala Val Pro Tyr Leu Phe Glu Arg Glu Gly Thr
            265                 270                 275

aac ggc gaa aac ctc aaa gaa acc cac gat ttc ctc aaa ctg tgt cgc      979
Asn Gly Glu Asn Leu Lys Glu Thr His Asp Phe Leu Lys Leu Cys Arg
        280                 285                 290

tct gtc att gag aag gaa tac ccc ggc cga atc ctg ctc gca gaa gcc
1027
Ser Val Ile Glu Lys Glu Tyr Pro Gly Arg Ile Leu Leu Ala Glu Ala
    295                 300                 305

aac caa tgg ccc caa gat gtg gtc gaa tac ttc ggt gaa aaa gac aaa
1075
Asn Gln Trp Pro Gln Asp Val Val Glu Tyr Phe Gly Glu Lys Asp Lys
310                 315                 320                 325

ggc gat gaa tgc cac atg gcc ttc cac
1102
Gly Asp Glu Cys His Met Ala Phe His
                330
```

<210> 24
<211> 334

<212> PRT
<213> Corynebacterium glutamicum

<400> 24
Val Leu Gln Thr Ser Trp His Phe Ser Ile Leu Ala Gly Met Thr Asp
1 5 10 15

Thr Ser Pro Leu Asn Ser Gln Pro Ser Ala Asp His His Pro Asp His
20 25 30

Ala Ala Arg Pro Val Leu Asp Ala His Gly Leu Ile Val Glu His Glu
35 40 45

Ser Glu Glu Phe Pro Val Pro Ala Pro Ala Pro Gly Glu Gln Pro Trp
50 55 60

Glu Lys Lys Asn Arg Glu Trp Tyr Lys Asp Ala Val Phe Tyr Glu Val
65 70 75 80

Leu Val Arg Ala Phe Tyr Asp Pro Glu Gly Asn Gly Val Gly Ser Leu
85 90 95

Lys Gly Leu Thr Glu Lys Leu Asp Tyr Ile Gln Trp Leu Gly Val Asp
100 105 110

Cys Ile Trp Ile Pro Pro Phe Tyr Asp Ser Pro Leu Arg Asp Gly Gly
115 120 125

Tyr Asp Ile Arg Asn Phe Arg Glu Ile Leu Pro Glu Phe Gly Thr Val
130 135 140

Asp Asp Phe Val Glu Leu Val Asp His Ala His Arg Arg Gly Leu Arg
145 150 155 160

Val Ile Thr Asp Leu Val Met Asn His Thr Ser Asp Gln His Ala Trp
165 170 175

Phe Gln Glu Ser Arg Arg Asp Pro Thr Gly Pro Tyr Gly Asp Phe Tyr
180 185 190

Val Trp Ser Asp Asp Pro Thr Leu Tyr Asn Glu Ala Arg Ile Ile Phe
195 200 205

Val Asp Thr Glu Glu Ser Asn Trp Thr Tyr Asp Pro Val Arg Gly Gln
210 215 220

Tyr Phe Trp His Arg Phe Phe Ser His Gln Pro Asp Leu Asn Tyr Asp
225 230 235 240

Asn Pro Ala Val Gln Glu Ala Met Leu Asp Val Leu Arg Phe Trp Leu
245 250 255

Asp Leu Gly Leu Asp Gly Phe Arg Leu Asp Ala Val Pro Tyr Leu Phe
260 265 270

Glu Arg Glu Gly Thr Asn Gly Glu Asn Leu Lys Glu Thr His Asp Phe
275 280 285

Leu Lys Leu Cys Arg Ser Val Ile Glu Lys Glu Tyr Pro Gly Arg Ile
290 295 300

```
Leu Leu Ala Glu Ala Asn Gln Trp Pro Gln Asp Val Val Glu Tyr Phe
305                 310                 315                 320

Gly Glu Lys Asp Lys Gly Asp Glu Cys His Met Ala Phe His
                325                 330


<210> 25
<211> 1386
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1363)
<223> RXA00534

<400> 25
ctgtgcagaa agaaaacact cctctggcta ggtagacaca gtttataaag gtagagttga 60

gcgggtaact gtcagcacgt agatcgaaag gtgcacaaag gtg gcc ctg gtc gta   115
                                           Val Ala Leu Val Val
                                           1               5

cag aaa tat ggc ggt tcc tcg ctt gag agt gcg gaa cgc att aga aac   163
Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala Glu Arg Ile Arg Asn
                10                  15                  20

gtc gct gaa cgg atc gtt gcc acc aag aag gct gga aat gat gtc gtg   211
Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala Gly Asn Asp Val Val
            25                  30                  35

gtt gtc tgc tcc gca atg gga gac acc acg gat gaa ctt cta gaa ctt   259
Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp Glu Leu Leu Glu Leu
        40                  45                  50

gca gcg gca gtg aat ccc gtt ccg cca gct cgt gaa atg gat atg ctc   307
Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg Glu Met Asp Met Leu
    55                  60                  65

ctg act gct ggt gag cgt att tct aac gct ctc gtc gcc atg gct att   355
Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu Val Ala Met Ala Ile
70                  75                  80                  85

gag tcc ctt ggc gca gaa gcc caa tct ttc acg ggc tct cag gct ggt   403
Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr Gly Ser Gln Ala Gly
                90                  95                  100

gtg ctc acc acc gag cgc cac gga aac gca cgc att gtt gat gtc act   451
Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg Ile Val Asp Val Thr
            105                 110                 115

cca ggt cgt gtg cgt gaa gca ctc gat gag ggc aag atc tgc att gtt   499
Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly Lys Ile Cys Ile Val
        120                 125                 130

gct ggt ttc cag ggt gtt aat aaa gaa acc cgc gat gtc acc acg ttg   547
Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg Asp Val Thr Thr Leu
    135                 140                 145

ggt cgt ggt ggt tct gac acc act gca gtt gcg ttg gca gct gct ttg   595
```

```
Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala Leu Ala Ala Ala Leu
150                 155                 160                 165

aac gct gat gtg tgt gag att tac tcg gac gtt gac ggt gtg tat acc    643
Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val Asp Gly Val Tyr Thr
                170                 175                 180

gct gac ccg cgc atc gtt cct aat gca cag aag ctg gaa aag ctc agc    691
Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys Leu Glu Lys Leu Ser
            185                 190                 195

ttc gaa gaa atg ctg gaa ctt gct gct gtt ggc tcc aag att ttg gtg    739
Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly Ser Lys Ile Leu Val
        200                 205                 210

ctg cgc agt gtt gaa tac gct cgt gca ttc aat gtg cca ctt cgc gta    787
Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn Val Pro Leu Arg Val
    215                 220                 225

cgc tcg tct tat agt aat gat ccc ggc act ttg att gcc ggc tct atg    835
Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu Ile Ala Gly Ser Met
230                 235                 240                 245

gag gat att cct gtg gaa gaa gca gtc ctt acc ggt gtc gca acc gac    883
Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr Gly Val Ala Thr Asp
                250                 255                 260

aag tcc gaa gcc aaa gta acc gtt ctg ggt att tcc gat aag cca ggc    931
Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile Ser Asp Lys Pro Gly
            265                 270                 275

gag gct gcg aag gtt ttc cgt gcg ttg gct gat gca gaa atc aac att    979
Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp Ala Glu Ile Asn Ile
        280                 285                 290

gac atg gtt ctg cag aac gtc tct tct gta gaa gac ggc acc acc gac
1027
Asp Met Val Leu Gln Asn Val Ser Ser Val Glu Asp Gly Thr Thr Asp
    295                 300                 305

atc acc ttc acc tgc cct cgt tcc gac ggc cgc cgc gcg atg gag atc
1075
Ile Thr Phe Thr Cys Pro Arg Ser Asp Gly Arg Arg Ala Met Glu Ile
310                 315                 320                 325

ttg aag aag ctt cag gtt cag ggc aac tgg acc aat gtg ctt tac gac
1123
Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr Asn Val Leu Tyr Asp
                330                 335                 340

gac cag gtc ggc aaa gtc tcc ctc gtg ggt gct ggc atg aag tct cac
1171
Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala Gly Met Lys Ser His
            345                 350                 355

cca ggt gtt acc gca gag ttc atg gaa gct ctg cgc gat gtc aac gtg
1219
Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu Arg Asp Val Asn Val
        360                 365                 370
```

```
aac atc gaa ttg att tcc acc tct gag att cgt att tcc gtg ctg atc
1267
Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg Ile Ser Val Leu Ile
    375                 380                 385

cgt gaa gat gat ctg gat gct gct gca cgt gca ttg cat gag cag ttc
1315
Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala Leu His Glu Gln Phe
390                 395                 400                 405

cag ctg ggc ggc gaa gac gaa gcc gtc gtt tat gca ggc acc gga cgc
1363
Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr Ala Gly Thr Gly Arg
                410                 415                 420

taaagtttta aaggagtagt ttt
1386


<210> 26
<211> 421
<212> PRT
<213> Corynebacterium glutamicum

<400> 26
Val Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala
  1               5                  10                  15

Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
             20                  25                  30

Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
         35                  40                  45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
     50                  55                  60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
 65                  70                  75                  80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
                 85                  90                  95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
            100                 105                 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
        115                 120                 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
    130                 135                 140

Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
145                 150                 155                 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
                165                 170                 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
            180                 185                 190
```

```
Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
        195                 200                 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
    210                 215                 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
225                 230                 235                 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
                245                 250                 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
            260                 265                 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
        275                 280                 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
    290                 295                 300

Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ser Asp Gly Arg
305                 310                 315                 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr
                325                 330                 335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
            340                 345                 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
        355                 360                 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
    370                 375                 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
385                 390                 395                 400

Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
                405                 410                 415

Ala Gly Thr Gly Arg
            420


<210> 27
<211> 1155
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1132)
<223> RXA00533

<400> 27
ctgcacgtgc attgcatgag cagttccagc tgggcggcga agacgaagcc gtcgtttatg 60

caggcaccgg acgctaaagt tttaaaggag tagttttaca atg acc acc atc gca   115
                                            Met Thr Thr Ile Ala
```

1 5

gtt gtt ggt gca acc ggc cag gtc ggc cag gtt atg cgc acc ctt ttg 163
Val Val Gly Ala Thr Gly Gln Val Gly Gln Val Met Arg Thr Leu Leu
10 15 20

gaa gag cgc aat ttc cca gct gac act gtt cgt ttc ttt gct tcc cca 211
Glu Glu Arg Asn Phe Pro Ala Asp Thr Val Arg Phe Phe Ala Ser Pro
25 30 35

cgt tcc gca ggc cgt aag att gaa ttc cgt ggc acg gaa atc gag gta 259
Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly Thr Glu Ile Glu Val
40 45 50

gaa gac att act cag gca acc gag gag tcc ctc aag gac atc gac gtt 307
Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu Lys Asp Ile Asp Val
55 60 65

gcg ttg ttc tcc gct gga ggc acc gct tcc aag cag tac gct cca ctg 355
Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys Gln Tyr Ala Pro Leu
70 75 80 85

ttc gct gct gca ggc gcg act gtt gtg gat aac tct tct gct tgg cgc 403
Phe Ala Ala Ala Gly Ala Thr Val Val Asp Asn Ser Ser Ala Trp Arg
90 95 100

aag gac gac gag gtt cca cta atc gtc tct gag gtg aac cct tcc gac 451
Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu Val Asn Pro Ser Asp
105 110 115

aag gat tcc ctg gtc aag ggc att att gcg aac cct aac tgc acc acc 499
Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn Pro Asn Cys Thr Thr
120 125 130

atg gct gcg atg cca gtg ctg aag cca ctt cac gat gcc gct ggt ctt 547
Met Ala Ala Met Pro Val Leu Lys Pro Leu His Asp Ala Ala Gly Leu
135 140 145

gta aag ctt cac gtt tcc tct tac cag gct gtt tcc ggt tct ggt ctt 595
Val Lys Leu His Val Ser Ser Tyr Gln Ala Val Ser Gly Ser Gly Leu
150 155 160 165

gca ggt gtg gaa acc ttg gca aag cag gtt gct gca gtt gga gac cac 643
Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala Ala Val Gly Asp His
170 175 180

aac gtt gag ttc gtc cat gat gga cag gct gct gac gca ggc gat gtc 691
Asn Val Glu Phe Val His Asp Gly Gln Ala Ala Asp Ala Gly Asp Val
185 190 195

gga cct tat gtt tca cca atc gct tac aac gtg ctg cca ttc gcc gga 739
Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val Leu Pro Phe Ala Gly
200 205 210

aac ctc gtc gat gac ggc acc ttc gaa acc gat gaa gag cag aag ctg 787
Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp Glu Glu Gln Lys Leu
215 220 225

cgc aac gaa tcc cgc aag att ctc ggt ctc cca gac ctc aag gtc tca 835
Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro Asp Leu Lys Val Ser
230 235 240 245

ggc acc tgc gtc cgc gtg ccg gtt ttc acc ggc cac acg ctg acc att 883
Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly His Thr Leu Thr Ile
250 255 260

cac gcc gaa ttc gac aag gca atc acc gtg gac cag gcg cag gag atc 931
His Ala Glu Phe Asp Lys Ala Ile Thr Val Asp Gln Ala Gln Glu Ile
265 270 275

ttg ggt gcc gct tca ggc gtc aag ctt gtc gac gtc cca acc cca ctt 979
Leu Gly Ala Ala Ser Gly Val Lys Leu Val Asp Val Pro Thr Pro Leu
280 285 290

gca gct gcc ggc att gac gaa tcc ctc gtt gga cgc atc cgt cag gac
1027
Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly Arg Ile Arg Gln Asp
295 300 305

tcc act gtc gac gat aac cgc ggt ctg gtt ctc gtc gta tct ggc gac
1075
Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu Val Val Ser Gly Asp
310 315 320 325

aac ctc cgc aag ggt gct gcg cta aac acc atc cag atc gct gag ctg
1123
Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile Gln Ile Ala Glu Leu
330 335 340

ctg gtt aag taaaaacccg ccattaaaaa ctc
1155
Leu Val Lys

<210> 28
<211> 344
<212> PRT
<213> Corynebacterium glutamicum

<400> 28
Met Thr Thr Ile Ala Val Val Gly Ala Thr Gly Gln Val Gly Gln Val
1 5 10 15

Met Arg Thr Leu Leu Glu Glu Arg Asn Phe Pro Ala Asp Thr Val Arg
20 25 30

Phe Phe Ala Ser Pro Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly
35 40 45

Thr Glu Ile Glu Val Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu
50 55 60

Lys Asp Ile Asp Val Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys
65 70 75 80

Gln Tyr Ala Pro Leu Phe Ala Ala Ala Gly Ala Thr Val Val Asp Asn
85 90 95

Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu
100 105 110

```
Val Asn Pro Ser Asp Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn
        115                 120                 125

Pro Asn Cys Thr Thr Met Ala Ala Met Pro Val Leu Lys Pro Leu His
    130                 135                 140

Asp Ala Ala Gly Leu Val Lys Leu His Val Ser Ser Tyr Gln Ala Val
145                 150                 155                 160

Ser Gly Ser Gly Leu Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala
                165                 170                 175

Ala Val Gly Asp His Asn Val Glu Phe Val His Asp Gly Gln Ala Ala
            180                 185                 190

Asp Ala Gly Asp Val Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val
        195                 200                 205

Leu Pro Phe Ala Gly Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp
    210                 215                 220

Glu Glu Gln Lys Leu Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro
225                 230                 235                 240

Asp Leu Lys Val Ser Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly
                245                 250                 255

His Thr Leu Thr Ile His Ala Glu Phe Asp Lys Ala Ile Thr Val Asp
            260                 265                 270

Gln Ala Gln Glu Ile Leu Gly Ala Ala Ser Gly Val Lys Leu Val Asp
        275                 280                 285

Val Pro Thr Pro Leu Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly
    290                 295                 300

Arg Ile Arg Gln Asp Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu
305                 310                 315                 320

Val Val Ser Gly Asp Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile
                325                 330                 335

Gln Ile Ala Glu Leu Leu Val Lys
            340


<210> 29
<211> 608
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (69)..(608)
<223> RXA02843

<400> 29
cccattgcgc ggaggtcgca ccccttccga cttgaactga taggccgata gaaattattc 60

tggacgtcatg act act gct tcc gca acc gga att gca aca ctg acc tcc   110
            Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser
```

1 5 10

acc ggc gac gtc ctg gac gtg tgg tat cca gaa atc ggg tcc acc gac 158
Thr Gly Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp
15 20 25 30

cag tcc gcg ctc aca cct cta gaa ggc gtc gat gaa gat cga aac gtc 206
Gln Ser Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val
35 40 45

acc cgc aaa atc gtg acg aca act atc gac acc gac gca gcc ccc acc 254
Thr Arg Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr
50 55 60

gac acc tac gat gca tgg ctg cgc ctt cac ctc ctc tcc cac cgc gtt 302
Asp Thr Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val
65 70 75

ttc cgc cct cac acc atc aac cta gac ggc att ttc ggc ctc ctc aac 350
Phe Arg Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn
80 85 90

aat gtc gtg tgg acc aac ttc gga ccg tgc gca gtt gac ggt ttc gca 398
Asn Val Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala
95 100 105 110

ctc acc cgc gcg cgc ctg tca cgc cga ggc caa gtt acg gtt tat agc 446
Leu Thr Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser
115 120 125

gtc gac aag ttc cca cgc atg gtc gac tat gtg gtt ccc tcg ggc gtg 494
Val Asp Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val
130 135 140

cgc atc ggt gac gcc gac cgc gtc cga ctt ggc gcg tac ctg gca gat 542
Arg Ile Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp
145 150 155

ggc acc acc gtg atg cat gag ggc ttc gtg aac ttc aac gct ggc acg 590
Gly Thr Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr
160 165 170

ctc ggc gct tcc atg gtt 608
Leu Gly Ala Ser Met Val
175 180

<210> 30
<211> 180
<212> PRT
<213> Corynebacterium glutamicum

<400> 30
Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser Thr Gly
1 5 10 15

Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp Gln Ser
20 25 30

Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val Thr Arg
35 40 45

```
Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr Asp Thr
    50                  55                  60

Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val Phe Arg
65                  70                  75                  80

Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn Asn Val
                85                  90                  95

Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala Leu Thr
            100                 105                 110

Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser Val Asp
        115                 120                 125

Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val Arg Ile
    130                 135                 140

Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp Gly Thr
145                 150                 155                 160

Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr Leu Gly
                165                 170                 175

Ala Ser Met Val
            180


<210> 31
<211> 1230
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1207)
<223> RXA02022

<400> 31
tatttgcgat tccaactgct tgggctccgc gaatgttttc actcattttt taatcgaccg 60

cttccatcat gttttaacta aggtttgtag gcttaaacct gtg aac tct gaa ctc    115
                                          Val Asn Ser Glu Leu
                                          1               5

aaa cca gga tta gat ctc ctc ggc gac cca att gtc ctt act caa cgt    163
Lys Pro Gly Leu Asp Leu Leu Gly Asp Pro Ile Val Leu Thr Gln Arg
                10                  15                  20

ttg gta gat ata ccg agt ccg tcg ggt cag gaa aag cag att gct gat    211
Leu Val Asp Ile Pro Ser Pro Ser Gly Gln Glu Lys Gln Ile Ala Asp
            25                  30                  35

gaa att gaa gat gcc ctt cgg aac ctt aat cta cct ggt gta gag gtc    259
Glu Ile Glu Asp Ala Leu Arg Asn Leu Asn Leu Pro Gly Val Glu Val
        40                  45                  50

ttc cgc ttc aac aac aac gtt ctt gct cgc acg aac agg gga ttg gcc    307
Phe Arg Phe Asn Asn Asn Val Leu Ala Arg Thr Asn Arg Gly Leu Ala
    55                  60                  65
```

```
tcg agg gtc atg ctt gct ggt cat atc gat aca gtg ccg atc gcg gac    355
Ser Arg Val Met Leu Ala Gly His Ile Asp Thr Val Pro Ile Ala Asp
 70                 75                  80                  85

aat ctg cca agc cgt gtg gaa gac ggc atc atg tat ggc tgt ggc acc    403
Asn Leu Pro Ser Arg Val Glu Asp Gly Ile Met Tyr Gly Cys Gly Thr
                90                  95                  100

gtc gat atg aaa tct ggg ttg gcg gtg tat ttg cat act ttt gcc acc    451
Val Asp Met Lys Ser Gly Leu Ala Val Tyr Leu His Thr Phe Ala Thr
            105                 110                 115

ttg gcc acg tcg act gag ctt aaa cat gat ctg acg ctg att gcg tat    499
Leu Ala Thr Ser Thr Glu Leu Lys His Asp Leu Thr Leu Ile Ala Tyr
        120                 125                 130

gag tgc gag gaa gtt gct gat cac ctc aat ggt ttg ggc cac att cgc    547
Glu Cys Glu Glu Val Ala Asp His Leu Asn Gly Leu Gly His Ile Arg
    135                 140                 145

gat gag cat ccg gag tgg ttg gcg gct gat ttg gcg ttg ttg ggt gag    595
Asp Glu His Pro Glu Trp Leu Ala Ala Asp Leu Ala Leu Leu Gly Glu
150                 155                 160                 165

cct act ggc ggc tgg att gag gcg ggc tgc cag ggc aat ctg cgc atc    643
Pro Thr Gly Gly Trp Ile Glu Ala Gly Cys Gln Gly Asn Leu Arg Ile
                170                 175                 180

aag gtg acg gcg cat ggt gtg cgt gcc cat tcg gcg aga agc tgg ttg    691
Lys Val Thr Ala His Gly Val Arg Ala His Ser Ala Arg Ser Trp Leu
            185                 190                 195

ggt gat aat gcg atg cat aag ttg tcg ccg atc att tcg aag gtt gct    739
Gly Asp Asn Ala Met His Lys Leu Ser Pro Ile Ile Ser Lys Val Ala
        200                 205                 210

gcg tat aag gcc gca gaa gtc aac att gat ggc ttg acc tac cgt gaa    787
Ala Tyr Lys Ala Ala Glu Val Asn Ile Asp Gly Leu Thr Tyr Arg Glu
    215                 220                 225

ggc ctc aac atc gtt ttc tgc gaa tcg ggc gtg gca aac aac gtc att    835
Gly Leu Asn Ile Val Phe Cys Glu Ser Gly Val Ala Asn Asn Val Ile
230                 235                 240                 245

cca gac ctc gcg tgg atg aac ctc aac ttc cgt ttc gcg ccg aat cgc    883
Pro Asp Leu Ala Trp Met Asn Leu Asn Phe Arg Phe Ala Pro Asn Arg
                250                 255                 260

gat ctc aac gag gcg atc gag cat gtc gtc gaa acg ctt gag ctt gac    931
Asp Leu Asn Glu Ala Ile Glu His Val Val Glu Thr Leu Glu Leu Asp
            265                 270                 275

ggt caa gac ggc atc gaa tgg gcc gta gaa gac ggg gca ggc ggt gcc    979
Gly Gln Asp Gly Ile Glu Trp Ala Val Glu Asp Gly Ala Gly Gly Ala
        280                 285                 290

ctt cca ggc ttg ggg cag cag gtg aca agc ggg ctt atc gac gcc gtc
1027
Leu Pro Gly Leu Gly Gln Gln Val Thr Ser Gly Leu Ile Asp Ala Val
    295                 300                 305
```

180 185 190

Ile Leu Thr Gly Ser Glu Thr Thr Val Asp Phe Ala Tyr Leu Ala Gly
195 200 205

Ala Asp Gly Val Val Pro Gly Leu Gly Asn Val Asp Pro Ala Ala Tyr
210 215 220

Ala Ala Leu Ala Lys Leu Cys Leu Asp Gly Lys Trp Ala Glu Ala Ala
225 230 235 240

Ala Leu Gln Lys Arg Ile Asn His Leu Phe His Ile Val Phe Val Gly
245 250 255

Asp Thr Ser His Met Ser Gly Ser Ser Ala Gly Leu Gly Gly Phe Lys
260 265 270

Thr Ala Leu Ala His Leu Gly Ile Ile Glu Ser Asn Ala Met Ala Val
275 280 285

Pro His Gln Ser Leu Ser Asp Glu Glu Thr Ala Arg Ile His Ala Ile
290 295 300

Val Asp Glu Phe Leu Tyr Thr Ala
305 310

<210> 35
<211> 867
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(844)
<223> RXA00863

<400> 35
aacggtcagt taggtatgga tatcagcacc ttctgaacgg gtacgtctag actggtgggc 60

gtttgaaaaa ctcttcgccc cacgaaaatg aaggagcata atg gga atc aag gtt 115
Met Gly Ile Lys Val
1 5

ggc gtt ctc gga gcc aaa ggc cgt gtt ggt caa act att gtg gca gca 163
Gly Val Leu Gly Ala Lys Gly Arg Val Gly Gln Thr Ile Val Ala Ala
10 15 20

gtc aat gag tcc gac gat ctg gag ctt gtt gca gag atc ggc gtc gac 211
Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala Glu Ile Gly Val Asp
25 30 35

gat gat ttg agc ctt ctg gta gac aac ggc gct gaa gtt gtc gtt gac 259
Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala Glu Val Val Val Asp
40 45 50

ttc acc act cct aac gct gtg atg ggc aac ctg gag ttc tgc atc aac 307
Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu Glu Phe Cys Ile Asn
55 60 65

aac ggc att tct gcg gtt gtt gga acc acg ggc ttc gat gat gct cgt 355

```
Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly Phe Asp Asp Ala Arg
 70                 75                  80                  85

ttg gag cag gtt cgc gac tgg ctt gaa gga aaa gac aat gtc ggt gtt     403
Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys Asp Asn Val Gly Val
                90                  95                 100

ctg atc gca cct aac ttt gct atc tct gcg gtg ttg acc atg gtc ttt     451
Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val Leu Thr Met Val Phe
            105                 110                 115

tcc aag cag gct gcc cgc ttc ttc gaa tca gct gaa gtt att gag ctg     499
Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala Glu Val Ile Glu Leu
        120                 125                 130

cac cac ccc aac aag ctg gat gca cct tca ggc acc gcg atc cac act     547
His His Pro Asn Lys Leu Asp Ala Pro Ser Gly Thr Ala Ile His Thr
    135                 140                 145

gct cag ggc att gct gcg gca cgc aaa gaa gca ggc atg gac gca cag     595
Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala Gly Met Asp Ala Gln
150                 155                 160                 165

cca gat gcg acc gag cag gca ctt gag ggt tcc cgt ggc gca agc gta     643
Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser Arg Gly Ala Ser Val
                170                 175                 180

gat gga atc ccg gtt cat gca gtc cgc atg tcc ggc atg gtt gct cac     691
Asp Gly Ile Pro Val His Ala Val Arg Met Ser Gly Met Val Ala His
            185                 190                 195

gag caa gtt atc ttt ggc acc cag ggt cag acc ttg acc atc aag cag     739
Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr Leu Thr Ile Lys Gln
        200                 205                 210

gac tcc tat gat cgc aac tca ttt gca cca ggt gtc ttg gtg ggt gtg     787
Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly Val Leu Val Gly Val
    215                 220                 225

cgc aac att gca cag cac cca ggc cta gtc gta gga ctt gag cat tac     835
Arg Asn Ile Ala Gln His Pro Gly Leu Val Val Gly Leu Glu His Tyr
230                 235                 240                 245

cta ggc ctg taaaggctca tttcagcagc ggg                               867
Leu Gly Leu


<210> 36
<211> 248
<212> PRT
<213> Corynebacterium glutamicum

<400> 36
Met Gly Ile Lys Val Gly Val Leu Gly Ala Lys Gly Arg Val Gly Gln
  1               5                  10                  15

Thr Ile Val Ala Ala Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala
            20                  25                  30

Glu Ile Gly Val Asp Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala
```

```
Phe Thr Gly Val Ile Pro Pro Val Met Thr Pro Leu His Ala Asp Gly
                10                  15                  20

agt gtg gat gta gaa agc ctc cgc aag ctc gtt gac cac ctc atc aat    211
Ser Val Asp Val Glu Ser Leu Arg Lys Leu Val Asp His Leu Ile Asn
            25                  30                  35

ggt ggc gtc gac gga ctt ttc gca ctg ggc tcc tca ggc gaa gcg gca    259
Gly Gly Val Asp Gly Leu Phe Ala Leu Gly Ser Ser Gly Glu Ala Ala
        40                  45                  50

ttc ctc acc cgc gcc cag cgc aaa ctc gca ctg acc acc atc atc gag    307
Phe Leu Thr Arg Ala Gln Arg Lys Leu Ala Leu Thr Thr Ile Ile Glu
    55                  60                  65

cac acc gca ggc cgc gtt ccc gta act gct ggt gtc att gaa acc acc    355
His Thr Ala Gly Arg Val Pro Val Thr Ala Gly Val Ile Glu Thr Thr
70                  75                  80                  85

act gct cgc gtg att gag ctc gtg gaa gat gcc ctg gag gct ggt gcc    403
Thr Ala Arg Val Ile Glu Leu Val Glu Asp Ala Leu Glu Ala Gly Ala
                90                  95                  100

gaa ggc ctc gtt gcc act gca cct ttc tac acc cgc acc cac gat gtg    451
Glu Gly Leu Val Ala Thr Ala Pro Phe Tyr Thr Arg Thr His Asp Val
            105                 110                 115

gaa att gaa gaa cac ttc cgc aag atc cac gcc gcc gct cca gag ctt    499
Glu Ile Glu Glu His Phe Arg Lys Ile His Ala Ala Ala Pro Glu Leu
        120                 125                 130

cca ctg ttt gcc tac aac atc cca gtg tcg gtg cac tcc aac ctc aac    547
Pro Leu Phe Ala Tyr Asn Ile Pro Val Ser Val His Ser Asn Leu Asn
    135                 140                 145

cca gtc atg ctt ttg acg ctg gcc aag gat ggc gtt ctt gca ggc acc    595
Pro Val Met Leu Leu Thr Leu Ala Lys Asp Gly Val Leu Ala Gly Thr
150                 155                 160                 165

aag gat tcc agt ggc aat gat ggc gca atc cgc tca ctg atc gaa gct    643
Lys Asp Ser Ser Gly Asn Asp Gly Ala Ile Arg Ser Leu Ile Glu Ala
                170                 175                 180

cgt gat gat gct gga ctc act gag cag ttc aag atc ctc acc ggc agc    691
Arg Asp Asp Ala Gly Leu Thr Glu Gln Phe Lys Ile Leu Thr Gly Ser
            185                 190                 195

gaa acc acc gtt gat ttc gcc tac ctt gcg ggt gcc gat gga gtt gtc    739
Glu Thr Thr Val Asp Phe Ala Tyr Leu Ala Gly Ala Asp Gly Val Val
        200                 205                 210

cca ggc ctg ggc aat gtt gat cct gca gca tac gca gct tta gca aaa    787
Pro Gly Leu Gly Asn Val Asp Pro Ala Ala Tyr Ala Ala Leu Ala Lys
    215                 220                 225

ctc tgc ctc gat gga aag tgg gca gaa gct gct gct ttg cag aag cgc    835
Leu Cys Leu Asp Gly Lys Trp Ala Glu Ala Ala Ala Leu Gln Lys Arg
230                 235                 240                 245

atc aac cac ctc ttc cac atc gtc ttc gtg gga gac acc tcc cat atg    883
Ile Asn His Leu Phe His Ile Val Phe Val Gly Asp Thr Ser His Met
```

```
                250                 255                 260

tcc gga tcc agc gct ggt ttg ggc ggt ttc aag aca gca ctc gca cac    931
Ser Gly Ser Ser Ala Gly Leu Gly Gly Phe Lys Thr Ala Leu Ala His
            265                 270                 275

ctt ggc att att gaa tcc aat gcg atg gca gtt cct cac cag agc ctc    979
Leu Gly Ile Ile Glu Ser Asn Ala Met Ala Val Pro His Gln Ser Leu
        280                 285                 290

agc gac gaa gaa act gct cgc att cac gcc att gtt gat gaa ttc ctg
1027
Ser Asp Glu Glu Thr Ala Arg Ile His Ala Ile Val Asp Glu Phe Leu
    295                 300                 305

tac acc gct taaggcccac acctcatgac tga
1059
Tyr Thr Ala
310


<210> 34
<211> 312
<212> PRT
<213> Corynebacterium glutamicum

<400> 34
Met Ala Ser Ala Thr Phe Thr Gly Val Ile Pro Pro Val Met Thr Pro
  1               5                  10                  15

Leu His Ala Asp Gly Ser Val Asp Val Glu Ser Leu Arg Lys Leu Val
            20                  25                  30

Asp His Leu Ile Asn Gly Gly Val Asp Gly Leu Phe Ala Leu Gly Ser
        35                  40                  45

Ser Gly Glu Ala Ala Phe Leu Thr Arg Ala Gln Arg Lys Leu Ala Leu
    50                  55                  60

Thr Thr Ile Ile Glu His Thr Ala Gly Arg Val Pro Val Thr Ala Gly
 65                  70                  75                  80

Val Ile Glu Thr Thr Thr Ala Arg Val Ile Glu Leu Val Glu Asp Ala
                85                  90                  95

Leu Glu Ala Gly Ala Glu Gly Leu Val Ala Thr Ala Pro Phe Tyr Thr
            100                 105                 110

Arg Thr His Asp Val Glu Ile Glu Glu His Phe Arg Lys Ile His Ala
        115                 120                 125

Ala Ala Pro Glu Leu Pro Leu Phe Ala Tyr Asn Ile Pro Val Ser Val
    130                 135                 140

His Ser Asn Leu Asn Pro Val Met Leu Leu Thr Leu Ala Lys Asp Gly
145                 150                 155                 160

Val Leu Ala Gly Thr Lys Asp Ser Ser Gly Asn Asp Gly Ala Ile Arg
                165                 170                 175

Ser Leu Ile Glu Ala Arg Asp Asp Ala Gly Leu Thr Glu Gln Phe Lys
```

ggc cgc gaa aaa atc cgc gca aaa ttc ggc tgg acc gat gtc tca cgt
1075
Gly Arg Glu Lys Ile Arg Ala Lys Phe Gly Trp Thr Asp Val Ser Arg
310 315 320 325

ttt tca gcc atg gga att cca gcc cta aac ttt ggc gct ggt gat cca
1123
Phe Ser Ala Met Gly Ile Pro Ala Leu Asn Phe Gly Ala Gly Asp Pro
330 335 340

agt ttc gcg cat aaa cgc gac gag cag tgc cca gtg gag caa atc acg
1171
Ser Phe Ala His Lys Arg Asp Glu Gln Cys Pro Val Glu Gln Ile Thr
345 350 355

gat gtg gca gca att ttg aag cag tac ctg agc gag taaccgcatt
1217
Asp Val Ala Ala Ile Leu Lys Gln Tyr Leu Ser Glu
360 365

cggggttatc gtg
1230

<210> 32
<211> 369
<212> PRT
<213> Corynebacterium glutamicum

<400> 32
Val Asn Ser Glu Leu Lys Pro Gly Leu Asp Leu Leu Gly Asp Pro Ile
1 5 10 15

Val Leu Thr Gln Arg Leu Val Asp Ile Pro Ser Pro Ser Gly Gln Glu
20 25 30

Lys Gln Ile Ala Asp Glu Ile Glu Asp Ala Leu Arg Asn Leu Asn Leu
35 40 45

Pro Gly Val Glu Val Phe Arg Phe Asn Asn Asn Val Leu Ala Arg Thr
50 55 60

Asn Arg Gly Leu Ala Ser Arg Val Met Leu Ala Gly His Ile Asp Thr
65 70 75 80

Val Pro Ile Ala Asp Asn Leu Pro Ser Arg Val Glu Asp Gly Ile Met
85 90 95

Tyr Gly Cys Gly Thr Val Asp Met Lys Ser Gly Leu Ala Val Tyr Leu
100 105 110

His Thr Phe Ala Thr Leu Ala Thr Ser Thr Glu Leu Lys His Asp Leu
115 120 125

Thr Leu Ile Ala Tyr Glu Cys Glu Glu Val Ala Asp His Leu Asn Gly
130 135 140

Leu Gly His Ile Arg Asp Glu His Pro Glu Trp Leu Ala Ala Asp Leu
145 150 155 160

```
Ala Leu Leu Gly Glu Pro Thr Gly Gly Trp Ile Glu Ala Gly Cys Gln
                165                 170                 175

Gly Asn Leu Arg Ile Lys Val Thr Ala His Gly Val Arg Ala His Ser
            180                 185                 190

Ala Arg Ser Trp Leu Gly Asp Asn Ala Met His Lys Leu Ser Pro Ile
        195                 200                 205

Ile Ser Lys Val Ala Ala Tyr Lys Ala Ala Glu Val Asn Ile Asp Gly
    210                 215                 220

Leu Thr Tyr Arg Glu Gly Leu Asn Ile Val Phe Cys Glu Ser Gly Val
225                 230                 235                 240

Ala Asn Asn Val Ile Pro Asp Leu Ala Trp Met Asn Leu Asn Phe Arg
                245                 250                 255

Phe Ala Pro Asn Arg Asp Leu Asn Glu Ala Ile Glu His Val Val Glu
            260                 265                 270

Thr Leu Glu Leu Asp Gly Gln Asp Gly Ile Glu Trp Ala Val Glu Asp
        275                 280                 285

Gly Ala Gly Gly Ala Leu Pro Gly Leu Gly Gln Gln Val Thr Ser Gly
    290                 295                 300

Leu Ile Asp Ala Val Gly Arg Glu Lys Ile Arg Ala Lys Phe Gly Trp
305                 310                 315                 320

Thr Asp Val Ser Arg Phe Ser Ala Met Gly Ile Pro Ala Leu Asn Phe
                325                 330                 335

Gly Ala Gly Asp Pro Ser Phe Ala His Lys Arg Asp Glu Gln Cys Pro
            340                 345                 350

Val Glu Gln Ile Thr Asp Val Ala Ala Ile Leu Lys Gln Tyr Leu Ser
        355                 360                 365

Glu


<210> 33
<211> 1059
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1036)
<223> RXA00044

<400> 33
attacctcag ccttccaagc tgatgatgca ttacttaaaa actgcagaca cttgaaaaac 60

ttctcacccg cactcgttcc ctcaacccac aaggagcacc atg gct tcc gca act   115
                                          Met Ala Ser Ala Thr
                                          1               5

ttc acc ggc gtg atc cca ccc gta atg acc cca ctc cac gcc gac ggc   163
```

```
            35                  40                  45

Glu Val Val Val Asp Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu
    50                  55                  60

Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly
65                  70                  75                  80

Phe Asp Asp Ala Arg Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys
                85                  90                  95

Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val
            100                 105                 110

Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala
        115                 120                 125

Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala Pro Ser Gly
    130                 135                 140

Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala
145                 150                 155                 160

Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser
                165                 170                 175

Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val Arg Met Ser
            180                 185                 190

Gly Met Val Ala His Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr
        195                 200                 205

Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly
    210                 215                 220

Val Leu Val Gly Val Arg Asn Ile Ala Gln His Pro Gly Leu Val Val
225                 230                 235                 240

Gly Leu Glu His Tyr Leu Gly Leu
                245


<210> 37
<211> 873
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(850)
<223> RXA00864

<400> 37
acagcaccca ggcctagtcg taggacttga gcattaccta ggcctgtaaa ggctcatttc 60

agcagcgggt ggaattttt aaaaggagcg tttaaaggct gtg gcc gaa caa gtt    115
                                          Val Ala Glu Gln Val
                                          1               5

aaa ttg agc gtg gag ttg ata gcg tgc agt tct ttt act cca ccc gct    163
Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser Phe Thr Pro Pro Ala
```

```
                    10                            15                            20

gat gtt gag tgg tca act gat gtt gag ggc gcg gaa gca ctc gtc gag   211
Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala Glu Ala Leu Val Glu
                 25                  30                  35

ttt gcg ggt cgt gcc tgc tac gaa act ttt gat aag ccg aac cct cga   259
Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp Lys Pro Asn Pro Arg
         40                  45                  50

act gct tcc aat gct gcg tat ctg cgc cac atc atg gaa gtg ggg cac   307
Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile Met Glu Val Gly His
     55                  60                  65

act gct ttg ctt gag cat gcc aat gcc acg atg tat atc cga ggc att   355
Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met Tyr Ile Arg Gly Ile
 70                  75                  80                  85

tct cgg tcc gcg acc cat gaa ttg gtc cga cac cgc cat ttt tcc ttc   403
Ser Arg Ser Ala Thr His Glu Leu Val Arg His Arg His Phe Ser Phe
                 90                  95                 100

tct caa ctg tct cag cgt ttc gtg cac agc gga gaa tcg gaa gta gtg   451
Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly Glu Ser Glu Val Val
            105                 110                 115

gtg ccc act ctc atc gat gaa gat ccg cag ttg cgt gaa ctt ttc atg   499
Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu Arg Glu Leu Phe Met
        120                 125                 130

cac gcc atg gat gag tct cgg ttc gct ttc aat gag ctg ctt aat gcg   547
His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn Glu Leu Leu Asn Ala
    135                 140                 145

ctg gaa gaa aaa ctt ggc gat gaa ccg aat gca ctt tta agg aaa aag   595
Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala Leu Leu Arg Lys Lys
150                 155                 160                 165

cag gct cgt caa gca gct cgc gct gtg ctg ccc aac gct aca gag tcc   643
Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro Asn Ala Thr Glu Ser
                170                 175                 180

aga atc gtg gtg tct gga aac ttc cgc acc tgg agg cat ttc att ggc   691
Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp Arg His Phe Ile Gly
            185                 190                 195

atg cga gcc agt gaa cat gca gac gtc gaa atc cgc gaa gta gcg gta   739
Met Arg Ala Ser Glu His Ala Asp Val Glu Ile Arg Glu Val Ala Val
        200                 205                 210

gaa tgt tta aga aag ctg cag gta gca gcg cca act gtt ttc ggt gat   787
Glu Cys Leu Arg Lys Leu Gln Val Ala Ala Pro Thr Val Phe Gly Asp
    215                 220                 225

ttt gag att gaa act ttg gca gac gga tcg caa atg gca aca agc ccg   835
Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln Met Ala Thr Ser Pro
230                 235                 240                 245

tat gtc atg gac ttt taacgcaaag ctcacaccca cga                     873
Tyr Val Met Asp Phe
                250
```

<210> 38
<211> 250
<212> PRT
<213> Corynebacterium glutamicum

<400> 38
Val Ala Glu Gln Val Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser
1 5 10 15

Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala
20 25 30

Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp
35 40 45

Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile
50 55 60

Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met
65 70 75 80

Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His
85 90 95

Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly
100 105 110

Glu Ser Glu Val Val Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu
115 120 125

Arg Glu Leu Phe Met His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn
130 135 140

Glu Leu Leu Asn Ala Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala
145 150 155 160

Leu Leu Arg Lys Lys Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro
165 170 175

Asn Ala Thr Glu Ser Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp
180 185 190

Arg His Phe Ile Gly Met Arg Ala Ser Glu His Ala Asp Val Glu Ile
195 200 205

Arg Glu Val Ala Val Glu Cys Leu Arg Lys Leu Gln Val Ala Ala Pro
210 215 220

Thr Val Phe Gly Asp Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln
225 230 235 240

Met Ala Thr Ser Pro Tyr Val Met Asp Phe
245 250

<210> 39
<211> 608
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (69)..(608)
<223> RXA02843

<400> 39
cccattgcgc ggaggtcgca ccccttccga cttgaactga taggccgata gaaattattc 60

tggacgtcatg act act gct tcc gca acc gga att gca aca ctg acc tcc 110
Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser
1 5 10

acc ggc gac gtc ctg gac gtg tgg tat cca gaa atc ggg tcc acc gac 158
Thr Gly Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp
15 20 25 30

cag tcc gcg ctc aca cct cta gaa ggc gtc gat gaa gat cga aac gtc 206
Gln Ser Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val
35 40 45

acc cgc aaa atc gtg acg aca act atc gac acc gac gca gcc ccc acc 254
Thr Arg Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr
50 55 60

gac acc tac gat gca tgg ctg cgc ctt cac ctc ctc tcc cac cgc gtt 302
Asp Thr Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val
65 70 75

ttc cgc cct cac acc atc aac cta gac ggc att ttc ggc ctc ctc aac 350
Phe Arg Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn
80 85 90

aat gtc gtg tgg acc aac ttc gga ccg tgc gca gtt gac ggt ttc gca 398
Asn Val Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala
95 100 105 110

ctc acc cgc gcg cgc ctg tca cgc cga ggc caa gtt acg gtt tat agc 446
Leu Thr Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser
115 120 125

gtc gac aag ttc cca cgc atg gtc gac tat gtg gtt ccc tcg ggc gtg 494
Val Asp Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val
130 135 140

cgc atc ggt gac gcc gac cgc gtc cga ctt ggc gcg tac ctg gca gat 542
Arg Ile Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp
145 150 155

ggc acc acc gtg atg cat gag ggc ttc gtg aac ttc aac gct ggc acg 590
Gly Thr Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr
160 165 170

ctc ggc gct tcc atg gtt 608
Leu Gly Ala Ser Met Val
175 180

<210> 40
<211> 180
<212> PRT

<213> Corynebacterium glutamicum

<400> 40
Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser Thr Gly
1 5 10 15

Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp Gln Ser
20 25 30

Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val Thr Arg
35 40 45

Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr Asp Thr
50 55 60

Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val Phe Arg
65 70 75 80

Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn Asn Val
85 90 95

Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala Leu Thr
100 105 110

Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser Val Asp
115 120 125

Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val Arg Ile
130 135 140

Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp Gly Thr
145 150 155 160

Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr Leu Gly
165 170 175

Ala Ser Met Val
180

<210> 41
<211> 1143
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1120)
<223> RXN00355

<400> 41
aatagatcag cgcatccgtg gtggaaccaa aaggctcaac aatacgaaac gttcgctttc 60

ggtcctgatg aaagagatgt ccctgaatca tcatctaagt atg cat ctc ggt aag 115
Met His Leu Gly Lys
1 5

ctc gac cag gac agt gcc acc aca att ttg gag gat tac aag aac atg 163
Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu Asp Tyr Lys Asn Met
10 15 20

```
acc aac atc cgc gta gct atc gtg ggc tac gga aac ctg gga cgc agc    211
Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Arg Ser
            25                  30                  35

gtc gaa aag ctt att gcc aag cag ccc gac atg gac ctt gta gga atc    259
Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met Asp Leu Val Gly Ile
        40                  45                  50

ttc tcg cgc cgg gcc acc ctc gac aca aag acg cca gtc ttt gat gtc    307
Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr Pro Val Phe Asp Val
    55                  60                  65

gcc gac gtg gac aag cac gcc gac gac gtg gac gtg ctg ttc ctg tgc    355
Ala Asp Val Asp Lys His Ala Asp Asp Val Asp Val Leu Phe Leu Cys
70                  75                  80                  85

atg ggc tcc gcc acc gac atc cct gag cag gca cca aag ttc gcg cag    403
Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala Pro Lys Phe Ala Gln
                90                  95                  100

ttc gcc tgc acc gta gac acc tac gac aac cac cgc gac atc cca cgc    451
Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His Arg Asp Ile Pro Arg
            105                 110                 115

cac cgc cag gtc atg aac gaa gcc gcc acc gca gcc ggc aac gtt gca    499
His Arg Gln Val Met Asn Glu Ala Ala Thr Ala Ala Gly Asn Val Ala
        120                 125                 130

ctg gtc tct acc ggc tgg gat cca gga atg ttc tcc atc aac cgc gtc    547
Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe Ser Ile Asn Arg Val
    135                 140                 145

tac gca gcg gca gtc tta gcc gag cac cag cag cac acc ttc tgg ggc    595
Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln His Thr Phe Trp Gly
150                 155                 160                 165

cca ggt ttg tca cag ggc cac tcc gat gct ttg cga cgc atc cct ggc    643
Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu Arg Arg Ile Pro Gly
                170                 175                 180

gtt caa aag gca gtc cag tac acc ctc cca tcc gaa gac gcc ctg gaa    691
Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser Glu Asp Ala Leu Glu
            185                 190                 195

aag gcc cgc cgc ggc gaa gcc ggc gac ctt acc gga aag caa acc cac    739
Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr Gly Lys Gln Thr His
        200                 205                 210

aag cgc caa tgc ttc gtg gtt gcc gac gcg gcc gat cac gag cgc atc    787
Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala Asp His Glu Arg Ile
    215                 220                 225

gaa aac gac atc cgc acc atg cct gat tac ttc gtt ggc tac gaa gtc    835
Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe Val Gly Tyr Glu Val
230                 235                 240                 245

gaa gtc aac ttc atc gac gaa gca acc ttc gac tcc gag cac acc ggc    883
Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp Ser Glu His Thr Gly
                250                 255                 260

atg cca cac ggt ggc cac gtg att acc acc ggc gac acc ggt ggc ttc    931
```

Met Pro His Gly Gly His Val Ile Thr Thr Gly Asp Thr Gly Gly Phe
265 270 275

aac cac acc gtg gaa tac atc ctc aag ctg gac cga aac cca gat ttc 979
Asn His Thr Val Glu Tyr Ile Leu Lys Leu Asp Arg Asn Pro Asp Phe
280 285 290

acc gct tcc tca cag atc gct ttc ggt cgc gca gct cac cgc atg aag
1027
Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala Ala His Arg Met Lys
295 300 305

cag cag ggc caa agc gga gct ttc acc gtc ctc gaa gtt gct cca tac
1075
Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu Glu Val Ala Pro Tyr
310 315 320 325

ctg ctc tcc cca gag aac ttg gac gat ctg atc gca cgc gac gtc
1120
Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile Ala Arg Asp Val
330 335 340

taatttagct cgaggggcaa gga
1143

<210> 42
<211> 340
<212> PRT
<213> Corynebacterium glutamicum

<400> 42
Met His Leu Gly Lys Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu
1 5 10 15

Asp Tyr Lys Asn Met Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly
20 25 30

Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met
35 40 45

Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr
50 55 60

Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp
65 70 75 80

Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala
85 90 95

Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His
100 105 110

Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala
115 120 125

Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe
130 135 140

Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln
145 150 155 160

```
His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu
                165                 170                 175

Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser
            180                 185                 190

Glu Asp Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr
        195                 200                 205

Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala
    210                 215                 220

Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe
225                 230                 235                 240

Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp
                245                 250                 255

Ser Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly
            260                 265                 270

Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys Leu Asp
        275                 280                 285

Arg Asn Pro Asp Phe Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala
    290                 295                 300

Ala His Arg Met Lys Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu
305                 310                 315                 320

Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile
                325                 330                 335

Ala Arg Asp Val
            340


<210> 43
<211> 958
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(958)
<223> FRXA00352

<400> 43
aatagatcag cgcatccgtg gtggaaccaa aaggctcaac aatacgaaac gttcgctttc 60

ggtcctgatg aaagagatgt ccctgaatca tcatctaagt atg cat ctc ggt aag   115
                                          Met His Leu Gly Lys
                                           1               5

ctc gac cag gac agt gcc acc aca att ttg gag gat tac aag aac atg   163
Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu Asp Tyr Lys Asn Met
                10                  15                  20

acc aac atc cgc gta gct atc gtg ggc tac gga aac ctg gga cgc agc   211
Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Arg Ser
```

```
            25                      30                      35

gtc gaa aag ctt att gcc aag cag ccc gac atg gac ctt gta gga atc    259
Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met Asp Leu Val Gly Ile
        40                      45                      50

ttc tcg cgc cgg gcc acc ctc gac aca aag acg cca gtc ttt gat gtc    307
Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr Pro Val Phe Asp Val
    55                      60                      65

gcc gac gtg gac aag cac gcc gac gac gtg gac gtg ctg ttc ctg tgc    355
Ala Asp Val Asp Lys His Ala Asp Asp Val Asp Val Leu Phe Leu Cys
70                      75                      80                      85

atg ggc tcc gcc acc gac atc cct gag cag gca cca aag ttc gcg cag    403
Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala Pro Lys Phe Ala Gln
                90                      95                      100

ttc gcc tgc acc gta gac acc tac gac aac cac cgc gac atc cca cgc    451
Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His Arg Asp Ile Pro Arg
            105                     110                     115

cac cgc cag gtc atg aac gaa gcc gcc acc gca gcc ggc aac gtt gca    499
His Arg Gln Val Met Asn Glu Ala Ala Thr Ala Ala Gly Asn Val Ala
        120                     125                     130

ctg gtc tct acc ggc tgg gat cca gga atg ttc tcc atc aac cgc gtc    547
Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe Ser Ile Asn Arg Val
    135                     140                     145

tac gca gcg gca gtc tta gcc gag cac cag cag cac acc ttc tgg ggc    595
Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln His Thr Phe Trp Gly
150                     155                     160                     165

cca ggt ttg tca cag ggc cac tcc gat gct ttg cga cgc atc cct ggc    643
Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu Arg Arg Ile Pro Gly
                170                     175                     180

gtt caa aag gca gtc cag tac acc ctc cca tcc gaa gac gcc ctg gaa    691
Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser Glu Asp Ala Leu Glu
            185                     190                     195

aag gcc cgc cgc ggc gaa gcc ggc gac ctt acc gga aag caa acc cac    739
Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr Gly Lys Gln Thr His
        200                     205                     210

aag cgc caa tgc ttc gtg gtt gcc gac gcg gcc gat cac gag cgc atc    787
Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala Asp His Glu Arg Ile
    215                     220                     225

gaa aac gac atc cgc acc atg cct gat tac ttc gtt ggc tac gaa gtc    835
Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe Val Gly Tyr Glu Val
230                     235                     240                     245

gaa gtc aac ttc atc gac gaa gca acc ttc gac tcc gag cac acc ggc    883
Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp Ser Glu His Thr Gly
                250                     255                     260

atg cca cac ggt ggc cac gtg att acc acc ggc gac acc ggt ggc ttc    931
Met Pro His Gly Gly His Val Ile Thr Thr Gly Asp Thr Gly Gly Phe
            265                     270                     275
```

```
aac cac acc gtg gaa tac atc ctc aag                              958
Asn His Thr Val Glu Tyr Ile Leu Lys
        280                     285


<210> 44
<211> 286
<212> PRT
<213> Corynebacterium glutamicum

<400> 44
Met His Leu Gly Lys Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu
  1               5                  10                  15

Asp Tyr Lys Asn Met Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly
             20                  25                  30

Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met
         35                  40                  45

Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr
     50                  55                  60

Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp
 65                  70                  75                  80

Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala
                 85                  90                  95

Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His
            100                 105                 110

Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala
        115                 120                 125

Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe
    130                 135                 140

Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln
145                 150                 155                 160

His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu
                165                 170                 175

Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser
            180                 185                 190

Glu Asp Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr
        195                 200                 205

Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala
    210                 215                 220

Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe
225                 230                 235                 240

Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp
                245                 250                 255

Ser Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly
```

260 265 270

Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys
275 280 285

<210> 45
<211> 1400
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1377)
<223> RXA00972

<400> 45
cct gca cct ggt tgg cgt ttc cgc acc gga gaa gat gta aca atg gct 48
Pro Ala Pro Gly Trp Arg Phe Arg Thr Gly Glu Asp Val Thr Met Ala
1 5 10 15

aca gtt gaa aat ttc aat gaa ctt ccc gca cac gta tgg cca cgc aat 96
Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro Arg Asn
20 25 30

gcc gtg cgc caa gaa gac ggc gtt gtc acc gtc gct ggt gtg cct ctg 144
Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val Pro Leu
35 40 45

cct gac ctc gct gaa gaa tac gga acc cca ctg ttc gta gtc gac gag 192
Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val Asp Glu
50 55 60

gac gat ttc cgt tcc cgc tgt cgc gac atg gct acc gca ttc ggt gga 240
Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe Gly Gly
65 70 75 80

cca ggc aat gtg cac tac gca tct aaa gcg ttc ctg acc aag acc att 288
Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys Thr Ile
85 90 95

gca cgt tgg gtt gat gaa gag ggg ctg gca ctg gac att gca tcc atc 336
Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala Ser Ile
100 105 110

aac gaa ctg ggc att gcc ctg gcc gct ggt ttc ccc gcc agc cgt atc 384
Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser Arg Ile
115 120 125

acc gcg cac ggc aac aac aaa ggc gta gag ttc ctg cgc gcg ttg gtt 432
Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala Leu Val
130 135 140

caa aac ggt gtg gga cac gtg gtg ctg gac tcc gca cag gaa cta gaa 480
Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu Leu Glu
145 150 155 160

ctg ttg gat tac gtt gcc gct ggt gaa ggc aag att cag gac gtg ttg 528
Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp Val Leu
165 170 175

```
atc cgc gta aag cca ggc atc gaa gca cac acc cac gag ttc atc gcc     576
Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe Ile Ala
            180                 185                 190

act agc cac gaa gac cag aag ttc gga ttc tcc ctg gca tcc ggt tcc     624
Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser Gly Ser
        195                 200                 205

gca ttc gaa gca gca aaa gcc gcc aac aac gca gaa aac ctg aac ctg     672
Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu Asn Leu
    210                 215                 220

gtt ggc ctg cac tgc cac gtt ggt tcc cag gtg ttc gac gcc gaa ggc     720
Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala Glu Gly
225                 230                 235                 240

ttc aag ctg gca gca gaa cgc gtg ttg ggc ctg tac tca cag atc cac     768
Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln Ile His
                245                 250                 255

agc gaa ctg ggc gtt gcc ctt cct gaa ctg gat ctc ggt ggc gga tac     816
Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly Gly Tyr
            260                 265                 270

ggc att gcc tat acc gca gct gaa gaa cca ctc aac gtc gca gaa gtt     864
Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala Glu Val
        275                 280                 285

gcc tcc gac ctg ctc acc gca gtc gga aaa atg gca gcg gaa cta ggc     912
Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu Leu Gly
    290                 295                 300

atc gac gca cca acc gtg ctt gtt gag ccc ggc cgc gct atc gca ggc     960
Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile Ala Gly
305                 310                 315                 320

ccc tcc acc gtg acc atc tac gaa gtc ggc acc acc aaa gac gtc cac
1008
Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp Val His
                325                 330                 335

gta gac gac gac aaa acc cgc cgt tac atc gcc gtg gac gga ggc atg
1056
Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly Gly Met
            340                 345                 350

tcc gac aac atc cgc cca gca ctc tac ggg tcc gaa tac gac gcc cgc
1104
Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp Ala Arg
        355                 360                 365

gta gta tcc cgc ttc gcc gaa gga gac cca gta agc acc cgc atc gtg
1152
Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg Ile Val
    370                 375                 380

ggc tcc cac tgc gaa tcc ggc gat atc ctg atc aac gat gaa atc tac
1200
Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu Ile Tyr
385                 390                 395                 400
```

cca tct gac atc acc agc ggc gac ttc ctt gca ctc gca gcc acc ggc
1248
Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala Thr Gly
405 410 415

gca tac tgc tac gcc atg agc tcc cgc tac aac gcc ttc aca cgg ccc
1296
Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr Arg Pro
420 425 430

gcc gtc gtg tcc gtc cgc gct ggc agc tcc cgc ctc atg ctg cgc cgc
1344
Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu Arg Arg
435 440 445

gaa acg ctc gac gac atc ctc tca cta gag gca taacgctttt cgacgcctga
1397
Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala
450 455

ccc
1400

<210> 46
<211> 459
<212> PRT
<213> Corynebacterium glutamicum

<400> 46
Pro Ala Pro Gly Trp Arg Phe Arg Thr Gly Glu Asp Val Thr Met Ala
1 5 10 15

Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro Arg Asn
20 25 30

Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val Pro Leu
35 40 45

Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val Asp Glu
50 55 60

Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe Gly Gly
65 70 75 80

Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys Thr Ile
85 90 95

Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala Ser Ile
100 105 110

Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser Arg Ile
115 120 125

Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala Leu Val
130 135 140

Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu Leu Glu
145 150 155 160

Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp Val Leu

165 170 175

Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe Ile Ala
180 185 190

Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser Gly Ser
195 200 205

Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu Asn Leu
210 215 220

Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala Glu Gly
225 230 235 240

Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln Ile His
245 250 255

Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly Gly Tyr
260 265 270

Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala Glu Val
275 280 285

Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu Leu Gly
290 295 300

Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile Ala Gly
305 310 315 320

Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp Val His
325 330 335

Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly Gly Met
340 345 350

Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp Ala Arg
355 360 365

Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg Ile Val
370 375 380

Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu Ile Tyr
385 390 395 400

Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala Thr Gly
405 410 415

Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr Arg Pro
420 425 430

Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu Arg Arg
435 440 445

Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala
450 455

<210> 47
<211> 2121
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2098)
<223> RXA02653

<400> 47
agacagagtg ttagtgcgtg gggcagctct cactttcatc gacatcactc gagtatgctc 60

accggccgta ttcattccaa taacccgcac agggaaacta atg ata ccg aag ccc 115
Met Ile Pro Lys Pro
1 5

gac gtg acc gac tta tat tta gag gac ctc tta aat gag ggt tcg gaa 163
Asp Val Thr Asp Leu Tyr Leu Glu Asp Leu Leu Asn Glu Gly Ser Glu
10 15 20

aag att cgg tcc gcc aag gat ctt tcc gaa ctt agg aca gtt cta aaa 211
Lys Ile Arg Ser Ala Lys Asp Leu Ser Glu Leu Arg Thr Val Leu Lys
25 30 35

gag gtt tcc tcc caa att cag gaa cga gct ggg aaa aaa gat gaa gaa 259
Glu Val Ser Ser Gln Ile Gln Glu Arg Ala Gly Lys Lys Asp Glu Glu
40 45 50

tgg gga atg ggg gcc act tgg cgg gag ctg tac ccc agc atc gtg gaa 307
Trp Gly Met Gly Ala Thr Trp Arg Glu Leu Tyr Pro Ser Ile Val Glu
55 60 65

cgc gct tcc tac gaa ggg cgt gac agc cta atc gga ttt gat cac tta 355
Arg Ala Ser Tyr Glu Gly Arg Asp Ser Leu Ile Gly Phe Asp His Leu
70 75 80 85

gcc cgg gaa atg gaa aga tta gcc ttc ggc cca cca tcc gaa agt ttt 403
Ala Arg Glu Met Glu Arg Leu Ala Phe Gly Pro Pro Ser Glu Ser Phe
90 95 100

gaa tac ctc caa gaa ctc gta aaa tcc gga gtg gta gac atc act cac 451
Glu Tyr Leu Gln Glu Leu Val Lys Ser Gly Val Val Asp Ile Thr His
105 110 115

ctg cat cgt ggc cgg gaa cca ctg aca gat tta gtt cgt gaa ctt gaa 499
Leu His Arg Gly Arg Glu Pro Leu Thr Asp Leu Val Arg Glu Leu Glu
120 125 130

ata act gtg gtg ata gac gct gtt ctt ccc ccg ccg gga gta gtg cca 547
Ile Thr Val Val Ile Asp Ala Val Leu Pro Pro Pro Gly Val Val Pro
135 140 145

ggc aca ttg gtg cac aat ttg gta aaa gag gga tat gcc aga atg cgt 595
Gly Thr Leu Val His Asn Leu Val Lys Glu Gly Tyr Ala Arg Met Arg
150 155 160 165

cct ggg act cgg ggg tta gat gta gcg gct gac ggc acc gtt caa ggg 643
Pro Gly Thr Arg Gly Leu Asp Val Ala Ala Asp Gly Thr Val Gln Gly
170 175 180

caa cga cat ttg gct gca gtc gga cgg atg acg gaa gat gtg gtt ttg 691
Gln Arg His Leu Ala Ala Val Gly Arg Met Thr Glu Asp Val Val Leu
185 190 195

```
ggt aat gac aca ttg tcg cga tca tta cat gac ata atc ccg aag tgg     739
Gly Asn Asp Thr Leu Ser Arg Ser Leu His Asp Ile Ile Pro Lys Trp
        200                 205                 210

gct cgt cga gtt atc cgc gac gcg agc acg tat ccc gat agg gta cat     787
Ala Arg Arg Val Ile Arg Asp Ala Ser Thr Tyr Pro Asp Arg Val His
    215                 220                 225

ggt act cca ccg ctt ccg gca cgg ttg gaa ccc tgg gcg gaa aag ctc     835
Gly Thr Pro Pro Leu Pro Ala Arg Leu Glu Pro Trp Ala Glu Lys Leu
230                 235                 240                 245

act tca gat ccg gcc aca tgc cgc cac ctg att gaa gaa ttc ggg agt     883
Thr Ser Asp Pro Ala Thr Cys Arg His Leu Ile Glu Glu Phe Gly Ser
                250                 255                 260

cct gtg aat gta ctc cat tca ggt tct atg cct cgt aat ata aat gag     931
Pro Val Asn Val Leu His Ser Gly Ser Met Pro Arg Asn Ile Asn Glu
            265                 270                 275

ttg gtt gac gcc ggc att cag atg ggg gtg gat act cga ata ttt ttt     979
Leu Val Asp Ala Gly Ile Gln Met Gly Val Asp Thr Arg Ile Phe Phe
        280                 285                 290

gcc cgc aaa gcg aat aag ggt ctt acc ttc gtt gat gcc gtt aaa gac
1027
Ala Arg Lys Ala Asn Lys Gly Leu Thr Phe Val Asp Ala Val Lys Asp
    295                 300                 305

acc ggt cat ggt gta gat gta gcc agt gaa cga gag tta tct cag gtg
1075
Thr Gly His Gly Val Asp Val Ala Ser Glu Arg Glu Leu Ser Gln Val
310                 315                 320                 325

ctt aat cgt gga gtc cca gga gag cgg atc att cta tcc gca gct atc
1123
Leu Asn Arg Gly Val Pro Gly Glu Arg Ile Ile Leu Ser Ala Ala Ile
                330                 335                 340

aaa ccg gac aga cta ttg gca tta gcg atc gaa aat ggc gtg atc atc
1171
Lys Pro Asp Arg Leu Leu Ala Leu Ala Ile Glu Asn Gly Val Ile Ile
            345                 350                 355

tct gtg gat tcg cgt gat gaa tta gat cgc att tcg gct ttg gtt ggt
1219
Ser Val Asp Ser Arg Asp Glu Leu Asp Arg Ile Ser Ala Leu Val Gly
        360                 365                 370

gac cgc gtt gca cga gtt gcg cct aga gta gct cca gat cct gca gtc
1267
Asp Arg Val Ala Arg Val Ala Pro Arg Val Ala Pro Asp Pro Ala Val
    375                 380                 385

tta cct cca act aga ttt ggt gag cgt gct gca gac tgg ggt aat cgg
1315
Leu Pro Pro Thr Arg Phe Gly Glu Arg Ala Ala Asp Trp Gly Asn Arg
390                 395                 400                 405

ctt acc gag gtg ata ccc ggc gtg gat att gtg ggt ctt cac gtt cac
1363
```

Leu Thr Glu Val Ile Pro Gly Val Asp Ile Val Gly Leu His Val His
410 415 420

ctc cat ggc tat gct gca aaa gac cgt gct ctg gct ctg cag gaa tgt
1411
Leu His Gly Tyr Ala Ala Lys Asp Arg Ala Leu Ala Leu Gln Glu Cys
425 430 435

tgc caa ctc gtc gat tct ctc aga gaa tgc ggg cat tcc cca cag ttt
1459
Cys Gln Leu Val Asp Ser Leu Arg Glu Cys Gly His Ser Pro Gln Phe
440 445 450

att gac ctt gga gga ggg gtg cct atg agc tac att gaa tct gag gaa
1507
Ile Asp Leu Gly Gly Gly Val Pro Met Ser Tyr Ile Glu Ser Glu Glu
455 460 465

gat tgg atc cgt tat caa tcc gct aaa tct gcg act tca gcc ggg tat
1555
Asp Trp Ile Arg Tyr Gln Ser Ala Lys Ser Ala Thr Ser Ala Gly Tyr
470 475 480 485

gcc gaa tcc ttt acg tgg aaa gac gat ccg tta tct aat acg tac ccg
1603
Ala Glu Ser Phe Thr Trp Lys Asp Asp Pro Leu Ser Asn Thr Tyr Pro
490 495 500

ttc tat cag acc cca gtg cgc ggt aat tgg ttg aaa gac gtg ctt tct
1651
Phe Tyr Gln Thr Pro Val Arg Gly Asn Trp Leu Lys Asp Val Leu Ser
505 510 515

aag ggg gta gct cag atg ctc att gac cgg gga ttg cgg tta cac ata
1699
Lys Gly Val Ala Gln Met Leu Ile Asp Arg Gly Leu Arg Leu His Ile
520 525 530

gag cct ggt cga agt tta cta gat ggg tgt ggc gtc act ctt gcc gaa
1747
Glu Pro Gly Arg Ser Leu Leu Asp Gly Cys Gly Val Thr Leu Ala Glu
535 540 545

gtt gct ttt gtg aaa acc cga agt gac ggg ttg cct cta gtg gga ctg
1795
Val Ala Phe Val Lys Thr Arg Ser Asp Gly Leu Pro Leu Val Gly Leu
550 555 560 565

gct atg aac cga acg cag tgc cgg act aca tcc gat gat ttt ctc att
1843
Ala Met Asn Arg Thr Gln Cys Arg Thr Thr Ser Asp Asp Phe Leu Ile
570 575 580

gat ccc ctg cat atc act gac ggt gat gta ggc gag gaa atc gaa gca
1891
Asp Pro Leu His Ile Thr Asp Gly Asp Val Gly Glu Glu Ile Glu Ala
585 590 595

tat cta gtg ggt gcc tac tgc atc gaa gat gag ctg att tta cgc cgg
1939
Tyr Leu Val Gly Ala Tyr Cys Ile Glu Asp Glu Leu Ile Leu Arg Arg

600 605 610

cga atc cgc ttc ccg aga gga gtc aaa cca gga gat atc atc gga att 1987
Arg Ile Arg Phe Pro Arg Gly Val Lys Pro Gly Asp Ile Ile Gly Ile
615 620 625

cct aac acc gca gga tac ttc atg cat atc ttg gaa agt gca tcg cac 2035
Pro Asn Thr Ala Gly Tyr Phe Met His Ile Leu Glu Ser Ala Ser His
630 635 640 645

caa atc ccg ttg gcg aaa aat gta gtg tgg ccg gag ggg cag tta gac 2083
Gln Ile Pro Leu Ala Lys Asn Val Val Trp Pro Glu Gly Gln Leu Asp
650 655 660

gat atc gat gcg gat taagacataa ccattcgcta atc 2121
Asp Ile Asp Ala Asp
665

<210> 48
<211> 666
<212> PRT
<213> Corynebacterium glutamicum

<400> 48
Met Ile Pro Lys Pro Asp Val Thr Asp Leu Tyr Leu Glu Asp Leu Leu
1 5 10 15

Asn Glu Gly Ser Glu Lys Ile Arg Ser Ala Lys Asp Leu Ser Glu Leu
20 25 30

Arg Thr Val Leu Lys Glu Val Ser Ser Gln Ile Gln Glu Arg Ala Gly
35 40 45

Lys Lys Asp Glu Glu Trp Gly Met Gly Ala Thr Trp Arg Glu Leu Tyr
50 55 60

Pro Ser Ile Val Glu Arg Ala Ser Tyr Glu Gly Arg Asp Ser Leu Ile
65 70 75 80

Gly Phe Asp His Leu Ala Arg Glu Met Glu Arg Leu Ala Phe Gly Pro
85 90 95

Pro Ser Glu Ser Phe Glu Tyr Leu Gln Glu Leu Val Lys Ser Gly Val
100 105 110

Val Asp Ile Thr His Leu His Arg Gly Arg Glu Pro Leu Thr Asp Leu
115 120 125

Val Arg Glu Leu Glu Ile Thr Val Val Ile Asp Ala Val Leu Pro Pro
130 135 140

Pro Gly Val Val Pro Gly Thr Leu Val His Asn Leu Val Lys Glu Gly
145 150 155 160

Tyr Ala Arg Met Arg Pro Gly Thr Arg Gly Leu Asp Val Ala Ala Asp
165 170 175

Gly Thr Val Gln Gly Gln Arg His Leu Ala Ala Val Gly Arg Met Thr
180 185 190

Glu Asp Val Val Leu Gly Asn Asp Thr Leu Ser Arg Ser Leu His Asp
195 200 205

Ile Ile Pro Lys Trp Ala Arg Arg Val Ile Arg Asp Ala Ser Thr Tyr
210 215 220

Pro Asp Arg Val His Gly Thr Pro Pro Leu Pro Ala Arg Leu Glu Pro
225 230 235 240

Trp Ala Glu Lys Leu Thr Ser Asp Pro Ala Thr Cys Arg His Leu Ile
245 250 255

Glu Glu Phe Gly Ser Pro Val Asn Val Leu His Ser Gly Ser Met Pro
260 265 270

Arg Asn Ile Asn Glu Leu Val Asp Ala Gly Ile Gln Met Gly Val Asp
275 280 285

Thr Arg Ile Phe Phe Ala Arg Lys Ala Asn Lys Gly Leu Thr Phe Val
290 295 300

Asp Ala Val Lys Asp Thr Gly His Gly Val Asp Val Ala Ser Glu Arg
305 310 315 320

Glu Leu Ser Gln Val Leu Asn Arg Gly Val Pro Gly Glu Arg Ile Ile
325 330 335

Leu Ser Ala Ala Ile Lys Pro Asp Arg Leu Leu Ala Leu Ala Ile Glu
340 345 350

Asn Gly Val Ile Ile Ser Val Asp Ser Arg Asp Glu Leu Asp Arg Ile
355 360 365

Ser Ala Leu Val Gly Asp Arg Val Ala Arg Val Ala Pro Arg Val Ala
370 375 380

Pro Asp Pro Ala Val Leu Pro Pro Thr Arg Phe Gly Glu Arg Ala Ala
385 390 395 400

Asp Trp Gly Asn Arg Leu Thr Glu Val Ile Pro Gly Val Asp Ile Val
405 410 415

Gly Leu His Val His Leu His Gly Tyr Ala Ala Lys Asp Arg Ala Leu
420 425 430

Ala Leu Gln Glu Cys Cys Gln Leu Val Asp Ser Leu Arg Glu Cys Gly
435 440 445

His Ser Pro Gln Phe Ile Asp Leu Gly Gly Gly Val Pro Met Ser Tyr
450 455 460

Ile Glu Ser Glu Glu Asp Trp Ile Arg Tyr Gln Ser Ala Lys Ser Ala
465 470 475 480

Thr Ser Ala Gly Tyr Ala Glu Ser Phe Thr Trp Lys Asp Asp Pro Leu
485 490 495

Ser Asn Thr Tyr Pro Phe Tyr Gln Thr Pro Val Arg Gly Asn Trp Leu
500 505 510

Lys Asp Val Leu Ser Lys Gly Val Ala Gln Met Leu Ile Asp Arg Gly
515 520 525

Leu Arg Leu His Ile Glu Pro Gly Arg Ser Leu Leu Asp Gly Cys Gly
530 535 540

Val Thr Leu Ala Glu Val Ala Phe Val Lys Thr Arg Ser Asp Gly Leu
545 550 555 560

Pro Leu Val Gly Leu Ala Met Asn Arg Thr Gln Cys Arg Thr Thr Ser
565 570 575

Asp Asp Phe Leu Ile Asp Pro Leu His Ile Thr Asp Gly Asp Val Gly
580 585 590

Glu Glu Ile Glu Ala Tyr Leu Val Gly Ala Tyr Cys Ile Glu Asp Glu
595 600 605

Leu Ile Leu Arg Arg Arg Ile Arg Phe Pro Arg Gly Val Lys Pro Gly
610 615 620

Asp Ile Ile Gly Ile Pro Asn Thr Ala Gly Tyr Phe Met His Ile Leu
625 630 635 640

Glu Ser Ala Ser His Gln Ile Pro Leu Ala Lys Asn Val Val Trp Pro
645 650 655

Glu Gly Gln Leu Asp Asp Ile Asp Ala Asp
660 665

<210> 49
<211> 993
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(970)
<223> RXA01393

<400> 49
caaaagcaga cctgtaatga agatttccat gatcaccatc gtgacctatg gaagtactta 60

agtaaaatga ttggttctta acatggttta atatagcttc atg aac ccc att caa 115
Met Asn Pro Ile Gln
1 5

ctg gac act ttg ctc tca atc att gat gaa ggc agc ttc gaa ggc gcc 163
Leu Asp Thr Leu Leu Ser Ile Ile Asp Glu Gly Ser Phe Glu Gly Ala
10 15 20

tcc tta gcc ctt tcc att tcc ccc tcg gcg gtg agt cag cgc gtt aaa 211
Ser Leu Ala Leu Ser Ile Ser Pro Ser Ala Val Ser Gln Arg Val Lys
25 30 35

gct ctc gag cat cac gtg ggt cga gtg ttg gta tcg cgc acc caa ccg 259
Ala Leu Glu His His Val Gly Arg Val Leu Val Ser Arg Thr Gln Pro

40 45 50

gcc aaa gca acc gaa gcg ggt gaa gtc ctt gtg caa gca gcg cgg aaa 307
Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val Gln Ala Ala Arg Lys
55 60 65

atg gtg ttg ctg caa gca gaa act aaa gcg caa cta tct gga cgc ctt 355
Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln Leu Ser Gly Arg Leu
70 75 80 85

gct gaa atc ccg tta acc atc gcc atc aac gca gat tcg cta tcc aca 403
Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala Asp Ser Leu Ser Thr
90 95 100

tgg ttt cct ccc gtg ttc aac gag gta gct tct tgg ggt gga gca acg 451
Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser Trp Gly Gly Ala Thr
105 110 115

ctc acg ctg cgc ttg gaa gat gaa gcg cac aca tta tcc ttg ctg cgg 499
Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr Leu Ser Leu Leu Arg
120 125 130

cgt gga gat gtt tta gga gcg gta acc cgt gaa gct aat ccc gtg gcg 547
Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu Ala Asn Pro Val Ala
135 140 145

gga tgt gaa gta gta gaa ctt gga acc atg cgc cac ttg gcc att gca 595
Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg His Leu Ala Ile Ala
150 155 160 165

acc ccc tca ttg cgg gat gcc tac atg gtt gat ggg aaa cta gat tgg 643
Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp Gly Lys Leu Asp Trp
170 175 180

gct gcg atg ccc gtc tta cgc ttc ggt ccc aaa gat gtg ctt caa gac 691
Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys Asp Val Leu Gln Asp
185 190 195

cgt gac ctg gac ggg cgc gtc gat ggt cct gtg ggg cgc agg cgc gta 739
Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val Gly Arg Arg Arg Val
200 205 210

tcc att gtc ccg tcg gcg gaa ggt ttt ggt gag gca att cgc cga ggc 787
Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu Ala Ile Arg Arg Gly
215 220 225

ctt ggt tgg gga ctt ctt ccc gaa acc caa gct gct ccc atg cta aaa 835
Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala Ala Pro Met Leu Lys
230 235 240 245

gca gga gaa gtg atc ctc ctc gat gag ata ccc att gac aca ccg atg 883
Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro Ile Asp Thr Pro Met
250 255 260

tat tgg caa cga tgg cgc ctg gaa tct aga tct cta gct aga ctc aca 931
Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser Leu Ala Arg Leu Thr
265 270 275

gac gcc gtc gtt gat gca gca atc gag gga ttg cgg cct tagttacttc 980
Asp Ala Val Val Asp Ala Ala Ile Glu Gly Leu Arg Pro
280 285 290

tgaaaaggtt cag 993

<210> 50
<211> 290
<212> PRT
<213> Corynebacterium glutamicum

<400> 50
Met Asn Pro Ile Gln Leu Asp Thr Leu Leu Ser Ile Ile Asp Glu Gly
1 5 10 15

Ser Phe Glu Gly Ala Ser Leu Ala Leu Ser Ile Ser Pro Ser Ala Val
20 25 30

Ser Gln Arg Val Lys Ala Leu Glu His His Val Gly Arg Val Leu Val
35 40 45

Ser Arg Thr Gln Pro Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val
50 55 60

Gln Ala Ala Arg Lys Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln
65 70 75 80

Leu Ser Gly Arg Leu Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala
85 90 95

Asp Ser Leu Ser Thr Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser
100 105 110

Trp Gly Gly Ala Thr Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr
115 120 125

Leu Ser Leu Leu Arg Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu
130 135 140

Ala Asn Pro Val Ala Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg
145 150 155 160

His Leu Ala Ile Ala Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp
165 170 175

Gly Lys Leu Asp Trp Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys
180 185 190

Asp Val Leu Gln Asp Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val
195 200 205

Gly Arg Arg Arg Val Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu
210 215 220

Ala Ile Arg Arg Gly Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala
225 230 235 240

Ala Pro Met Leu Lys Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro
245 250 255

Ile Asp Thr Pro Met Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser
260 265 270

```
Leu Ala Arg Leu Thr Asp Ala Val Val Asp Ala Ala Ile Glu Gly Leu
        275                 280                 285

Arg Pro
    290


<210> 51
<211> 1626
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1603)
<223> RXA00241

<400> 51
ggtctccagc ctttctaaac aattcatctg cacttgatta attggcccca agattacgcg 60

aagtttagcg acttcgccgt acgtcaacta cgttaaatga gtg aat act caa tca   115
                                           Val Asn Thr Gln Ser
                                           1               5

gat tct gcg ggg tct caa ggt gca gcg gcc aca agt cgt act gta tct   163
Asp Ser Ala Gly Ser Gln Gly Ala Ala Ala Thr Ser Arg Thr Val Ser
                10                  15                  20

att aga acc ctc atc gcg ctg atc atc gga tcg acc gtc ggc gcg gga   211
Ile Arg Thr Leu Ile Ala Leu Ile Ile Gly Ser Thr Val Gly Ala Gly
            25                  30                  35

att ttc tcc atc cct caa aac atc ggc tca gtc gca ggt ccc ggc gcg   259
Ile Phe Ser Ile Pro Gln Asn Ile Gly Ser Val Ala Gly Pro Gly Ala
        40                  45                  50

atg ctc atc ggc tgg ctg atc gcc ggt gtg ggc atg ttg tcc gta gcg   307
Met Leu Ile Gly Trp Leu Ile Ala Gly Val Gly Met Leu Ser Val Ala
    55                  60                  65

ttc gtg ttc cat gtt ctt gcc cgc cgt aaa cct cac ctc gat tct ggc   355
Phe Val Phe His Val Leu Ala Arg Arg Lys Pro His Leu Asp Ser Gly
70                  75                  80                  85

gtc tac gca tat gcg cgt gtt gga ttg ggc gat tat gta ggt ttc tcc   403
Val Tyr Ala Tyr Ala Arg Val Gly Leu Gly Asp Tyr Val Gly Phe Ser
                90                  95                  100

tcc gct tgg ggt tat tgg ctg ggt tca gtc atc gcc caa gtt ggc tac   451
Ser Ala Trp Gly Tyr Trp Leu Gly Ser Val Ile Ala Gln Val Gly Tyr
            105                 110                 115

gca acg tta ttt ttc tcc acg ttg ggc cac tac gta ccg ctg ttt tcc   499
Ala Thr Leu Phe Phe Ser Thr Leu Gly His Tyr Val Pro Leu Phe Ser
        120                 125                 130

caa gat cat cca ttt gtg tca gcg ttg gca gtt agc gct ttg acc tgg   547
Gln Asp His Pro Phe Val Ser Ala Leu Ala Val Ser Ala Leu Thr Trp
    135                 140                 145

ctg gtg ttt gga gtt gtt tcc cga gga att agc caa gct gct ttc ttg   595
```

```
Leu Val Phe Gly Val Val Ser Arg Gly Ile Ser Gln Ala Ala Phe Leu
150                 155                 160                 165

aca acg gtc acc acc gtg gcc aaa att ctg cct ctg ttg tgc ttc atc     643
Thr Thr Val Thr Thr Val Ala Lys Ile Leu Pro Leu Leu Cys Phe Ile
                170                 175                 180

atc ctt gtt gca ttc ttg ggc ttt agc tgg gag aag ttc act gtt gat     691
Ile Leu Val Ala Phe Leu Gly Phe Ser Trp Glu Lys Phe Thr Val Asp
            185                 190                 195

tta tgg gcg cgt gat ggt ggc gtg ggc agc att ttt gat cag gtg cgc     739
Leu Trp Ala Arg Asp Gly Gly Val Gly Ser Ile Phe Asp Gln Val Arg
        200                 205                 210

ggc atc atg gtg tac acc gtg tgg gtg ttc atc ggt atc gaa ggt gca     787
Gly Ile Met Val Tyr Thr Val Trp Val Phe Ile Gly Ile Glu Gly Ala
    215                 220                 225

tcg gta tat tcc cgc cag gca cgc tca cgc agt gat gtc agc cga gct     835
Ser Val Tyr Ser Arg Gln Ala Arg Ser Arg Ser Asp Val Ser Arg Ala
230                 235                 240                 245

acc gtg att ggt ttt gtg gct gtt ctc ctt ttg ctg gtg tcg att tct     883
Thr Val Ile Gly Phe Val Ala Val Leu Leu Leu Leu Val Ser Ile Ser
                250                 255                 260

tcg ctg agc ttc ggt gta ctg acc caa caa gag ctc gct gcg tta cca     931
Ser Leu Ser Phe Gly Val Leu Thr Gln Gln Glu Leu Ala Ala Leu Pro
            265                 270                 275

gat aat tcc atg gcg tcg gtg ctc gaa gct gtt gtt ggt cca tgg ggt     979
Asp Asn Ser Met Ala Ser Val Leu Glu Ala Val Val Gly Pro Trp Gly
        280                 285                 290

gcc gca ttg att tcg ttg ggt ctg tgt ctt tcg gtt ctt ggg gcc tat
1027
Ala Ala Leu Ile Ser Leu Gly Leu Cys Leu Ser Val Leu Gly Ala Tyr
    295                 300                 305

gtg tcc tgg cag atg ctc tgc gca gaa cca ctg gcg ttg atg gca atg
1075
Val Ser Trp Gln Met Leu Cys Ala Glu Pro Leu Ala Leu Met Ala Met
310                 315                 320                 325

gat ggc ctc att cca agc aaa atc ggg gcc atc aac agc cgc ggt gct
1123
Asp Gly Leu Ile Pro Ser Lys Ile Gly Ala Ile Asn Ser Arg Gly Ala
                330                 335                 340

gcc tgg atg gct cag ctg atc tcc acc atc gtg att cag att ttc atc
1171
Ala Trp Met Ala Gln Leu Ile Ser Thr Ile Val Ile Gln Ile Phe Ile
            345                 350                 355

atc att ttc ttc ctc aac gag acc acc tac gtc tcc atg gtg caa ttg
1219
Ile Ile Phe Phe Leu Asn Glu Thr Thr Tyr Val Ser Met Val Gln Leu
        360                 365                 370
```

gct acc aac cta tac ttg gtg cct tac ctg ttc tct gcc ttt tat ctg
1267
Ala Thr Asn Leu Tyr Leu Val Pro Tyr Leu Phe Ser Ala Phe Tyr Leu
375 380 385

gtc atg ctg gca aca cgt gga aaa gga atc acc cac cca cat gcc ggc
1315
Val Met Leu Ala Thr Arg Gly Lys Gly Ile Thr His Pro His Ala Gly
390 395 400 405

aca cgt ttt gat gat tcc ggt cca gag ata tcc cgc cga gaa aac cgc
1363
Thr Arg Phe Asp Asp Ser Gly Pro Glu Ile Ser Arg Arg Glu Asn Arg
410 415 420

aaa cac ctc atc gtc ggt tta gta gca acg gtg tat tca gtg tgg ctg
1411
Lys His Leu Ile Val Gly Leu Val Ala Thr Val Tyr Ser Val Trp Leu
425 430 435

ttt tac gct gca gaa ccg cag ttt gtc ctc ttc gga gcc atg gcg atg
1459
Phe Tyr Ala Ala Glu Pro Gln Phe Val Leu Phe Gly Ala Met Ala Met
440 445 450

ctt ccc ggc tta atc ccc tat gtg tgg aca agg att tat cgt ggc gaa
1507
Leu Pro Gly Leu Ile Pro Tyr Val Trp Thr Arg Ile Tyr Arg Gly Glu
455 460 465

cag gtg ttt aac cgc ttt gaa atc ggc gtg gtt gtt gtc ctg gtc gtt
1555
Gln Val Phe Asn Arg Phe Glu Ile Gly Val Val Val Val Leu Val Val
470 475 480 485

gct gcc agc gcg ggc gtt att ggt ttg gtc aac gga tca cta tcg ctt
1603
Ala Ala Ser Ala Gly Val Ile Gly Leu Val Asn Gly Ser Leu Ser Leu
490 495 500

taaacaccga aaccttcctg cta
1626

<210> 52
<211> 501
<212> PRT
<213> Corynebacterium glutamicum

<400> 52
Val Asn Thr Gln Ser Asp Ser Ala Gly Ser Gln Gly Ala Ala Ala Thr
1 5 10 15

Ser Arg Thr Val Ser Ile Arg Thr Leu Ile Ala Leu Ile Ile Gly Ser
20 25 30

Thr Val Gly Ala Gly Ile Phe Ser Ile Pro Gln Asn Ile Gly Ser Val
35 40 45

Ala Gly Pro Gly Ala Met Leu Ile Gly Trp Leu Ile Ala Gly Val Gly
50 55 60

Met Leu Ser Val Ala Phe Val Phe His Val Leu Ala Arg Arg Lys Pro
65 70 75 80

His Leu Asp Ser Gly Val Tyr Ala Tyr Ala Arg Val Gly Leu Gly Asp
85 90 95

Tyr Val Gly Phe Ser Ser Ala Trp Gly Tyr Trp Leu Gly Ser Val Ile
100 105 110

Ala Gln Val Gly Tyr Ala Thr Leu Phe Phe Ser Thr Leu Gly His Tyr
115 120 125

Val Pro Leu Phe Ser Gln Asp His Pro Phe Val Ser Ala Leu Ala Val
130 135 140

Ser Ala Leu Thr Trp Leu Val Phe Gly Val Val Ser Arg Gly Ile Ser
145 150 155 160

Gln Ala Ala Phe Leu Thr Thr Val Thr Thr Val Ala Lys Ile Leu Pro
165 170 175

Leu Leu Cys Phe Ile Ile Leu Val Ala Phe Leu Gly Phe Ser Trp Glu
180 185 190

Lys Phe Thr Val Asp Leu Trp Ala Arg Asp Gly Gly Val Gly Ser Ile
195 200 205

Phe Asp Gln Val Arg Gly Ile Met Val Tyr Thr Val Trp Val Phe Ile
210 215 220

Gly Ile Glu Gly Ala Ser Val Tyr Ser Arg Gln Ala Arg Ser Arg Ser
225 230 235 240

Asp Val Ser Arg Ala Thr Val Ile Gly Phe Val Ala Val Leu Leu Leu
245 250 255

Leu Val Ser Ile Ser Ser Leu Ser Phe Gly Val Leu Thr Gln Gln Glu
260 265 270

Leu Ala Ala Leu Pro Asp Asn Ser Met Ala Ser Val Leu Glu Ala Val
275 280 285

Val Gly Pro Trp Gly Ala Ala Leu Ile Ser Leu Gly Leu Cys Leu Ser
290 295 300

Val Leu Gly Ala Tyr Val Ser Trp Gln Met Leu Cys Ala Glu Pro Leu
305 310 315 320

Ala Leu Met Ala Met Asp Gly Leu Ile Pro Ser Lys Ile Gly Ala Ile
325 330 335

Asn Ser Arg Gly Ala Ala Trp Met Ala Gln Leu Ile Ser Thr Ile Val
340 345 350

Ile Gln Ile Phe Ile Ile Ile Phe Phe Leu Asn Glu Thr Thr Tyr Val
355 360 365

Ser Met Val Gln Leu Ala Thr Asn Leu Tyr Leu Val Pro Tyr Leu Phe
370 375 380

Ser Ala Phe Tyr Leu Val Met Leu Ala Thr Arg Gly Lys Gly Ile Thr
385 390 395 400

His Pro His Ala Gly Thr Arg Phe Asp Asp Ser Gly Pro Glu Ile Ser
405 410 415

Arg Arg Glu Asn Arg Lys His Leu Ile Val Gly Leu Val Ala Thr Val
420 425 430

Tyr Ser Val Trp Leu Phe Tyr Ala Ala Glu Pro Gln Phe Val Leu Phe
435 440 445

Gly Ala Met Ala Met Leu Pro Gly Leu Ile Pro Tyr Val Trp Thr Arg
450 455 460

Ile Tyr Arg Gly Glu Gln Val Phe Asn Arg Phe Glu Ile Gly Val Val
465 470 475 480

Val Val Leu Val Val Ala Ala Ser Ala Gly Val Ile Gly Leu Val Asn
485 490 495

Gly Ser Leu Ser Leu
500

<210> 53
<211> 822
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(799)
<223> RXA01394

<400> 53
gagcaaagtg tccagttgaa tggggttcat gaagctatat taaaccatgt taagaaccaa 60

tcattttact taagtacttc cataggtcac gatggtgatc atg gaa atc ttc att 115
Met Glu Ile Phe Ile
1 5

aca ggt ctg ctt ttg ggg gcc agt ctt tta ctg tcc atc gga ccg cag 163
Thr Gly Leu Leu Leu Gly Ala Ser Leu Leu Leu Ser Ile Gly Pro Gln
10 15 20

aat gta ctg gtg att aaa caa gga att aag cgc gaa gga ctc att gcg 211
Asn Val Leu Val Ile Lys Gln Gly Ile Lys Arg Glu Gly Leu Ile Ala
25 30 35

gtt ctt ctc gtg tgt tta att tct gac gtc ttt ttg ttc atc gcc ggc 259
Val Leu Leu Val Cys Leu Ile Ser Asp Val Phe Leu Phe Ile Ala Gly
40 45 50

acc ttg ggc gtt gat ctt ttg tcc aat gcc gcg ccg atc gtg ctc gat 307
Thr Leu Gly Val Asp Leu Leu Ser Asn Ala Ala Pro Ile Val Leu Asp
55 60 65

att atg cgc tgg ggt ggc atc gct tac ctg tta tgg ttt gcc gtc atg 355
Ile Met Arg Trp Gly Gly Ile Ala Tyr Leu Leu Trp Phe Ala Val Met
70 75 80 85

```
gca gcg aaa gac gcc atg aca aac aag gtg gaa gcg cca cag atc att     403
Ala Ala Lys Asp Ala Met Thr Asn Lys Val Glu Ala Pro Gln Ile Ile
                 90                  95                 100

gaa gaa aca gaa cca acc gtg ccc gat gac acg cct ttg ggc ggt tcg     451
Glu Glu Thr Glu Pro Thr Val Pro Asp Asp Thr Pro Leu Gly Gly Ser
            105                 110                 115

gcg gtg gcc act gac acg cgc aac cgg gtg cgg gtg gag gtg agc gtc     499
Ala Val Ala Thr Asp Thr Arg Asn Arg Val Arg Val Glu Val Ser Val
        120                 125                 130

gat aag cag cgg gtt tgg gta aag ccc atg ttg atg gca atc gtg ctg     547
Asp Lys Gln Arg Val Trp Val Lys Pro Met Leu Met Ala Ile Val Leu
    135                 140                 145

acc tgg ttg aac ccg aat gcg tat ttg gac gcg ttt gtg ttt atc ggc     595
Thr Trp Leu Asn Pro Asn Ala Tyr Leu Asp Ala Phe Val Phe Ile Gly
150                 155                 160                 165

ggc gtc ggc gcg caa tac ggc gac acc gga cgg tgg att ttc gcc gct     643
Gly Val Gly Ala Gln Tyr Gly Asp Thr Gly Arg Trp Ile Phe Ala Ala
                170                 175                 180

ggc gcg ttc gcg gca agc ctg atc tgg ttc ccg ctg gtg ggt ttc ggc     691
Gly Ala Phe Ala Ala Ser Leu Ile Trp Phe Pro Leu Val Gly Phe Gly
            185                 190                 195

gca gca gca ttg tca cgc ccg ctg tcc agc ccc aag gtg tgg cgc tgg     739
Ala Ala Ala Leu Ser Arg Pro Leu Ser Ser Pro Lys Val Trp Arg Trp
        200                 205                 210

atc aac gtc gtc gtg gca gtt gtg atg acc gca ttg gcc atc aaa ctg     787
Ile Asn Val Val Val Ala Val Val Met Thr Ala Leu Ala Ile Lys Leu
    215                 220                 225

atg ttg atg ggt tagttttcgc gggttttgga atc                           822
Met Leu Met Gly
230


<210> 54
<211> 233
<212> PRT
<213> Corynebacterium glutamicum

<400> 54
Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser Leu Leu Leu
  1               5                  10                  15

Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly Ile Lys Arg
            20                  25                  30

Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser Asp Val Phe
        35                  40                  45

Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser Asn Ala Ala
    50                  55                  60

Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala Tyr Leu Leu
```

```
 65                  70                  75                  80

Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn Lys Val Glu
                85                  90                  95

Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro Asp Asp Thr
            100                 105                 110

Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn Arg Val Arg
        115                 120                 125

Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys Pro Met Leu
    130                 135                 140

Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr Leu Asp Ala
145                 150                 155                 160

Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp Thr Gly Arg
                165                 170                 175

Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile Trp Phe Pro
            180                 185                 190

Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu Ser Ser Pro
        195                 200                 205

Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val Met Thr Ala
    210                 215                 220

Leu Ala Ile Lys Leu Met Leu Met Gly
225                 230


<210> 55
<211> 1026
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1003)
<223> RXA00865

<400> 55
ttatcggaat gtggcttggg cgattgttat gcaaaagttg ttaggttttt tgcggggttg 60

tttaaccccc aaatgaggga agaaggtaac cttgaactct atg agc aca ggt tta   115
                                          Met Ser Thr Gly Leu
                                           1               5

aca gct aag acc gga gta gag cac ttc ggc acc gtt gga gta gca atg   163
Thr Ala Lys Thr Gly Val Glu His Phe Gly Thr Val Gly Val Ala Met
                10                  15                  20

gtt act cca ttc acg gaa tcc gga gac atc gat atc gct gct ggc cgc   211
Val Thr Pro Phe Thr Glu Ser Gly Asp Ile Asp Ile Ala Ala Gly Arg
            25                  30                  35

gaa gtc gcg gct tat ttg gtt gat aag ggc ttg gat tct ttg gtt ctc   259
Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu Asp Ser Leu Val Leu
        40                  45                  50
```

gcg ggc acc act ggt gaa tcc cca acg aca acc gcc gct gaa aaa cta 307
Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr Ala Ala Glu Lys Leu
55 60 65

gaa ctg ctc aag gcc gtt cgt gag gaa gtt ggg gat cgg gcg aag ctc 355
Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly Asp Arg Ala Lys Leu
70 75 80 85

atc gcc ggt gtc gga acc aac aac acg cgg aca tct gtg gaa ctt gcg 403
Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr Ser Val Glu Leu Ala
90 95 100

gaa gct gct gct tct gct ggc gca gac ggc ctt tta gtt gta act cct 451
Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly Leu Leu Val Val Thr Pro
105 110 115

tat tac tcc aag ccg agc caa gag gga ttg ctg gcg cac ttc ggt gca 499
Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu Ala His Phe Gly Ala
120 125 130

att gct gca gca aca gag gtt cca att tgt ctc tat gac att cct ggt 547
Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu Tyr Asp Ile Pro Gly
135 140 145

cgg tca ggt att cca att gag tct gat acc atg aga cgc ctg agt gaa 595
Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met Arg Arg Leu Ser Glu
150 155 160 165

tta cct acg att ttg gcg gtc aag gac gcc aag ggt gac ctc gtt gca 643
Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys Gly Asp Leu Val Ala
170 175 180

gcc acg tca ttg atc aaa gaa acg gga ctt gcc tgg tat tca ggc gat 691
Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala Trp Tyr Ser Gly Asp
185 190 195

gac cca cta aac ctt gtt tgg ctt gct ttg ggc gga tca ggt ttc att 739
Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly Gly Ser Gly Phe Ile
200 205 210

tcc gta att gga cat gca gcc ccc aca gca tta cgt gag ttg tac aca 787
Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu Arg Glu Leu Tyr Thr
215 220 225

agc ttc gag gaa ggc gac ctc gtc cgt gcg cgg gaa atc aac gcc aaa 835
Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg Glu Ile Asn Ala Lys
230 235 240 245

cta tca ccg ctg gta gct gcc caa ggt cgc ttg ggt gga gtc agc ttg 883
Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu Gly Gly Val Ser Leu
250 255 260

gca aaa gct gct ctg cgt ctg cag ggc atc aac gta gga gat cct cga 931
Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn Val Gly Asp Pro Arg
265 270 275

ctt cca att atg gct cca aat gag cag gaa ctt gag gct ctc cga gaa 979
Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu Glu Ala Leu Arg Glu
280 285 290

gac atg aaa aaa gct gga gtt cta taaatatgaa tgattcccga aat
1026
Asp Met Lys Lys Ala Gly Val Leu
295 300

<210> 56
<211> 301
<212> PRT
<213> Corynebacterium glutamicum

<400> 56
Met Ser Thr Gly Leu Thr Ala Lys Thr Gly Val Glu His Phe Gly Thr
1 5 10 15

Val Gly Val Ala Met Val Thr Pro Phe Thr Glu Ser Gly Asp Ile Asp
20 25 30

Ile Ala Ala Gly Arg Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu
35 40 45

Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr
50 55 60

Ala Ala Glu Lys Leu Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly
65 70 75 80

Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr
85 90 95

Ser Val Glu Leu Ala Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly Leu
100 105 110

Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu
115 120 125

Ala His Phe Gly Ala Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu
130 135 140

Tyr Asp Ile Pro Gly Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met
145 150 155 160

Arg Arg Leu Ser Glu Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys
165 170 175

Gly Asp Leu Val Ala Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala
180 185 190

Trp Tyr Ser Gly Asp Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly
195 200 205

Gly Ser Gly Phe Ile Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu
210 215 220

Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg
225 230 235 240

Glu Ile Asn Ala Lys Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu
245 250 255

Gly Gly Val Ser Leu Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn

```
            260                 265                 270

Val Gly Asp Pro Arg Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu
        275                 280                 285

Glu Ala Leu Arg Glu Asp Met Lys Lys Ala Gly Val Leu
    290                 295                 300


<210> 57
<211> 1071
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1048)
<223> RXS02021

<400> 57
ttgggtcgcc gaggagatct aatcctggtt tgagttcaga gttcacaggt ttaagcctac 60

aaaccttagt taaaacatga tggaagcggt cgattaaaaa atg agt gaa aac att   115
                                           Met Ser Glu Asn Ile
                                           1               5

cgc gga gcc caa gca gtt gga atc gca aat atc gcc atg gac ggg acc   163
Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile Ala Met Asp Gly Thr
                10                  15                  20

atc ctg gac acg tgg tac cca gaa ccc caa att ttc aac ccg gat cag   211
Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile Phe Asn Pro Asp Gln
            25                  30                  35

tgg gct gaa cgc tac cca ttg gaa gtg ggc acc aca cgc ctc gga gca   259
Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr Thr Arg Leu Gly Ala
        40                  45                  50

aac gaa ctc acc cca cgg atg ctg cag ttg gta aaa ctg gac caa gat   307
Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val Lys Leu Asp Gln Asp
    55                  60                  65

cgc ctc gtc gaa cag gta gca gtc cgc acc gtt atc ccc gat ctg tct   355
Arg Leu Val Glu Gln Val Ala Val Arg Thr Val Ile Pro Asp Leu Ser
70                  75                  80                  85

caa cct cca gta gac gcg cac gat gtt tac ctg cgc ctc cac ctg ctt   403
Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu Arg Leu His Leu Leu
                90                  95                  100

tcc cac cgg ctg gtc cgc ccc cac gaa atg cac atg caa aac acc ttg   451
Ser His Arg Leu Val Arg Pro His Glu Met His Met Gln Asn Thr Leu
            105                 110                 115

gag ctg ctg tcc gac gtg gtg tgg aca aac aag ggc cct tgc ctt cct   499
Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys Gly Pro Cys Leu Pro
        120                 125                 130

gaa aac ttt gag tgg gtg cgt ggt gct ctg cgg tcc cgc gga ctc atc   547
Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg Ser Arg Gly Leu Ile
    135                 140                 145
```

cac gtc tac tgt gtg gac cgt ctt ccc cgc atg gtc gac tat gtg gtt 595
His Val Tyr Cys Val Asp Arg Leu Pro Arg Met Val Asp Tyr Val Val
150 155 160 165

ccc cct gga gtc cgc atc tcc gaa gca gaa cgc gtg cgc cta ggt gca 643
Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg Val Arg Leu Gly Ala
170 175 180

tac ctt gct ccg ggt acc tct gtg ctg cgt gaa ggt ttc gtg tct ttc 691
Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu Gly Phe Val Ser Phe
185 190 195

aac tcc ggc acc ttg ggt gcc gca aag gtg gaa ggc cgc ctg agt tcc 739
Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu Gly Arg Leu Ser Ser
200 205 210

ggt gtg gtc atc ggt gaa ggt tcc gag att gga ctg tct tct act att 787
Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly Leu Ser Ser Thr Ile
215 220 225

cag tcc ccg aga gat gaa cag cgc cgc cgt ttg ccg ttg agc atc ggc 835
Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu Pro Leu Ser Ile Gly
230 235 240 245

caa aac tgc aac ttt ggt gtc agc tcc gga atc atc gga gtc agt ctg 883
Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile Ile Gly Val Ser Leu
250 255 260

gga gac aat tgc gac atc gga aat aac att gtc ttg gat gga gat acc 931
Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val Leu Asp Gly Asp Thr
265 270 275

ccc att tgg ttc gca gcc gat gag gag tta cgc act atc gac tcc atc 979
Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg Thr Ile Asp Ser Ile
280 285 290

gaa ggc caa gca aat tgg tca atc aag cgt gaa tcc ggc ttc cat gag
1027
Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu Ser Gly Phe His Glu
295 300 305

cca gtt gcc cgc ctc aaa gct tgacccattt tcataaccag tgc
1071
Pro Val Ala Arg Leu Lys Ala
310 315

<210> 58
<211> 316
<212> PRT
<213> Corynebacterium glutamicum

<400> 58
Met Ser Glu Asn Ile Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile
1 5 10 15

Ala Met Asp Gly Thr Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile
20 25 30

Phe Asn Pro Asp Gln Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr

35 40 45

Thr Arg Leu Gly Ala Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val
50 55 60

Lys Leu Asp Gln Asp Arg Leu Val Glu Gln Val Ala Val Arg Thr Val
65 70 75 80

Ile Pro Asp Leu Ser Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu
85 90 95

Arg Leu His Leu Leu Ser His Arg Leu Val Arg Pro His Glu Met His
100 105 110

Met Gln Asn Thr Leu Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys
115 120 125

Gly Pro Cys Leu Pro Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg
130 135 140

Ser Arg Gly Leu Ile His Val Tyr Cys Val Asp Arg Leu Pro Arg Met
145 150 155 160

Val Asp Tyr Val Val Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg
165 170 175

Val Arg Leu Gly Ala Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu
180 185 190

Gly Phe Val Ser Phe Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu
195 200 205

Gly Arg Leu Ser Ser Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly
210 215 220

Leu Ser Ser Thr Ile Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu
225 230 235 240

Pro Leu Ser Ile Gly Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile
245 250 255

Ile Gly Val Ser Leu Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val
260 265 270

Leu Asp Gly Asp Thr Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg
275 280 285

Thr Ile Asp Ser Ile Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu
290 295 300

Ser Gly Phe His Glu Pro Val Ala Arg Leu Lys Ala
305 310 315

<210> 59
<211> 1296
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

```
<222> (101)..(1273)
<223> RXS02157

<400> 59
gggtggaatt ggcacgatgg tgctgccgga tgtttttgat cgggagaatt atcctgaagg 60

caccgttttt agaaaagacg acaaggatgg ggaactgtaa atg agc acg ctg gaa   115
                                            Met Ser Thr Leu Glu
                                            1               5

act tgg cca cag gtc att att aat acg tac ggc acc cca cca gtt gag   163
Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly Thr Pro Pro Val Glu
                10                  15                  20

ctg gtg tcc ggc aag ggc gca acc gtc act gat gac cag ggc aat gtc   211
Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp Asp Gln Gly Asn Val
            25                  30                  35

tac atc gac ttg ctc gcg ggc atc gca gtc aac gcg ttg ggc cac gcc   259
Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn Ala Leu Gly His Ala
        40                  45                  50

cac ccg gcg atc atc gag gcg gtc acc aac cag atc ggc caa ctt ggt   307
His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln Ile Gly Gln Leu Gly
    55                  60                  65

cac gtc tca aac ttg ttc gca tcc agg ccc gtc gtc gag gtc gcc gag   355
His Val Ser Asn Leu Phe Ala Ser Arg Pro Val Val Glu Val Ala Glu
70                  75                  80                  85

gag ctc atc aag cgt ttt tcg ctt gac gac gcc acc ctc gcc gcg caa   403
Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala Thr Leu Ala Ala Gln
                90                  95                  100

acc cgg gtt ttc ttc tgc aac tcg ggc gcc gaa gca aac gag gct gct   451
Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala
            105                 110                 115

ttc aag att gca cgc ttg act ggt cgt tcc cgg att ctg gct gca gtt   499
Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg Ile Leu Ala Ala Val
        120                 125                 130

cat ggt ttc cac ggc cgc acc atg ggt tcc ctc gcg ctg act ggc cag   547
His Gly Phe His Gly Arg Thr Met Gly Ser Leu Ala Leu Thr Gly Gln
    135                 140                 145

cca gac aag cgt gaa gcg ttc ctg cca atg cca agc ggt gtg gag ttc   595
Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro Ser Gly Val Glu Phe
150                 155                 160                 165

tac cct tac ggc gac acc gat tac ttg cgc aaa atg gta gaa acc aac   643
Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys Met Val Glu Thr Asn
                170                 175                 180

cca acg gat gtg gct gct atc ttc ctc gag cca atc cag ggt gaa acg   691
Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro Ile Gln Gly Glu Thr
            185                 190                 195

ggc gtt gtt cca gca cct gaa gga ttc ctc aag gca gtg cgc gag ctg   739
Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys Ala Val Arg Glu Leu
        200                 205                 210
```

tgc gat gag tac ggc atc ttg atg atc acc gat gaa gtc cag act ggc 787
Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp Glu Val Gln Thr Gly
215 220 225

gtt ggc cgt acc ggc gat ttc ttt gca cat cag cac gat ggc gtt gtt 835
Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln His Asp Gly Val Val
230 235 240 245

ccc gat gtg gtg acc atg gcc aag gga ctt ggc ggc ggt ctt ccc atc 883
Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly Gly Gly Leu Pro Ile
250 255 260

ggt gct tgt ttg gcc act ggc cgt gca gct gaa ttg atg acc cca ggc 931
Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu Leu Met Thr Pro Gly
265 270 275

aag cac ggc acc act ttc ggt ggc aac cca gtt gct tgt gca gct gcc 979
Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val Ala Cys Ala Ala Ala
280 285 290

aag gca gtg ctg tct gtt gtc gat gac gct ttc tgc gca gaa gtt gcc
1027
Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe Cys Ala Glu Val Ala
295 300 305

cgc aag ggc gag ctg ttc aag gaa ctt ctt gcc aag gtt gac ggc gtt
1075
Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val
310 315 320 325

gta gac gtc cgt ggc agg ggc ttg atg ttg ggc gtg gtg ctg gag cgc
1123
Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg
330 335 340

gac gtc gca aag caa gct gtt ctt gat ggt ttt aag cac ggc gtt att
1171
Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile
345 350 355

ttg aat gca ccg gcg gac aac att atc cgt ttg acc ccg ccg ctg gtg
1219
Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val
360 365 370

atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca
1267
Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys Ala Ile Ala Glu Thr
375 380 385

atc gca taaaggactc aaacttatga ctt
1296
Ile Ala
390

<210> 60
<211> 391
<212> PRT
<213> Corynebacterium glutamicum

<400> 60
Met Ser Thr Leu Glu Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly
1   5   10   15

Thr Pro Pro Val Glu Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp
            20   25   30

Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn
        35   40   45

Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln
    50   55   60

Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val
65   70   75   80

Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala
                85   90   95

Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu
            100   105   110

Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg
        115   120   125

Ile Leu Ala Ala Val His Gly Phe His Gly Arg Thr Met Gly Ser Leu
    130   135   140

Ala Leu Thr Gly Gln Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro
145   150   155   160

Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys
                165   170   175

Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro
            180   185   190

Ile Gln Gly Glu Thr Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys
        195   200   205

Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp
    210   215   220

Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln
225   230   235   240

His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly
                245   250   255

Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu
            260   265   270

Leu Met Thr Pro Gly Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val
        275   280   285

Ala Cys Ala Ala Ala Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe
    290   295   300

Cys Ala Glu Val Ala Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala
305   310   315   320

Lys Val Asp Gly Val Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly
325 330 335

Val Val Leu Glu Arg Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe
340 345 350

Lys His Gly Val Ile Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu
355 360 365

Thr Pro Pro Leu Val Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys
370 375 380

Ala Ile Ala Glu Thr Ile Ala
385 390

<210> 61
<211> 1008
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(985)
<223> RXC00733

<400> 61
acggcgaggt tgtcggtatt ggaacgcaca cgaatttgct gaacacgtgc ggtacctacc 60

gtgaaattgt tgaatcccaa gagactgcgc aggcgcaatc atg agt aat act gca 115
Met Ser Asn Thr Ala
1 5

ggc ccc cgc ggg cgt tcc cat cag gca gac gcc gcg ccg aat caa aag 163
Gly Pro Arg Gly Arg Ser His Gln Ala Asp Ala Ala Pro Asn Gln Lys
10 15 20

gca cag aat ttc gga cca tct gcc aaa agg ctt ttc gga att cta ggc 211
Ala Gln Asn Phe Gly Pro Ser Ala Lys Arg Leu Phe Gly Ile Leu Gly
25 30 35

cat gac cgt aac acc tta att ttt gtt atc ttc cta gcc gtc ctg agc 259
His Asp Arg Asn Thr Leu Ile Phe Val Ile Phe Leu Ala Val Leu Ser
40 45 50

gtt gga ctt acc gtc ttg ggc cca tgg ttg ctg ggt aaa gcc acc aac 307
Val Gly Leu Thr Val Leu Gly Pro Trp Leu Leu Gly Lys Ala Thr Asn
55 60 65

gtg gtg ttt gaa gga ttc cta tct aag cgc atg ccg gct ggt gcg tca 355
Val Val Phe Glu Gly Phe Leu Ser Lys Arg Met Pro Ala Gly Ala Ser
70 75 80 85

aag gaa gat atc atc gcg cag ttg cag gct gca ggt aaa cat aat cag 403
Lys Glu Asp Ile Ile Ala Gln Leu Gln Ala Ala Gly Lys His Asn Gln
90 95 100

gct tcc atg atg gaa gac atg aac ctt gtt cca ggc tca ggc att gat 451
Ala Ser Met Met Glu Asp Met Asn Leu Val Pro Gly Ser Gly Ile Asp
105 110 115

```
ttt gaa aaa tta gcc atg atc ctc gga ctg gtg atc ggt gct tat ctc      499
Phe Glu Lys Leu Ala Met Ile Leu Gly Leu Val Ile Gly Ala Tyr Leu
        120                 125                 130

atc ggt agc ctg ttg tcg ttg ttc cag gcg cgg atg ctc aac cgc atc      547
Ile Gly Ser Leu Leu Ser Leu Phe Gln Ala Arg Met Leu Asn Arg Ile
    135                 140                 145

gtg caa agt gcc atg cac cgg ctg cgc atg gag gtg gag gaa aaa atc      595
Val Gln Ser Ala Met His Arg Leu Arg Met Glu Val Glu Glu Lys Ile
150                 155                 160                 165

cac cgc cta ccg ctg agc tat ttc gat tcc atc aaa cgt ggt gat ctg      643
His Arg Leu Pro Leu Ser Tyr Phe Asp Ser Ile Lys Arg Gly Asp Leu
                170                 175                 180

ctt agc cgt gtg acc aac gat gtg gat aat atc ggt caa tcc ctg caa      691
Leu Ser Arg Val Thr Asn Asp Val Asp Asn Ile Gly Gln Ser Leu Gln
            185                 190                 195

caa acc ttg tca cag gcg atc act tcc cta ctg acc gtc atc ggt gtg      739
Gln Thr Leu Ser Gln Ala Ile Thr Ser Leu Leu Thr Val Ile Gly Val
        200                 205                 210

ttg gtg atg atg ttt atc atc tcc cca ctg ctc gca ctc gtg gcg ctg      787
Leu Val Met Met Phe Ile Ile Ser Pro Leu Leu Ala Leu Val Ala Leu
    215                 220                 225

gta tcc att ccg gtc acc atc gtg gtc act gtg gtg gtt gcg agc cgt      835
Val Ser Ile Pro Val Thr Ile Val Val Thr Val Val Val Ala Ser Arg
230                 235                 240                 245

tcc cag aaa ctc ttt gcg gaa cag tgg aag cag acc ggt att ttg aat      883
Ser Gln Lys Leu Phe Ala Glu Gln Trp Lys Gln Thr Gly Ile Leu Asn
                250                 255                 260

gcg cgc ctg gag gaa acc tac tct ggc cac gcc gtg gtt aag gtt ttc      931
Ala Arg Leu Glu Glu Thr Tyr Ser Gly His Ala Val Val Lys Val Phe
            265                 270                 275

gga cac caa aag gat gtt caa gaa gca ttc gag gaa gaa aat caa gct      979
Gly His Gln Lys Asp Val Gln Glu Ala Phe Glu Glu Glu Asn Gln Ala
        280                 285                 290

tgt gta taaggccagc tttggtgccc agt
1008
Cys Val
    295
```

<210> 62
<211> 295
<212> PRT
<213> Corynebacterium glutamicum

<400> 62

```
Met Ser Asn Thr Ala Gly Pro Arg Gly Arg Ser His Gln Ala Asp Ala
  1               5                  10                  15

Ala Pro Asn Gln Lys Ala Gln Asn Phe Gly Pro Ser Ala Lys Arg Leu
```

```
            20                  25                  30

Phe Gly Ile Leu Gly His Asp Arg Asn Thr Leu Ile Phe Val Ile Phe
        35                  40                  45

Leu Ala Val Leu Ser Val Gly Leu Thr Val Leu Gly Pro Trp Leu Leu
    50                  55                  60

Gly Lys Ala Thr Asn Val Val Phe Glu Gly Phe Leu Ser Lys Arg Met
65                  70                  75                  80

Pro Ala Gly Ala Ser Lys Glu Asp Ile Ile Ala Gln Leu Gln Ala Ala
                85                  90                  95

Gly Lys His Asn Gln Ala Ser Met Met Glu Asp Met Asn Leu Val Pro
            100                 105                 110

Gly Ser Gly Ile Asp Phe Glu Lys Leu Ala Met Ile Leu Gly Leu Val
        115                 120                 125

Ile Gly Ala Tyr Leu Ile Gly Ser Leu Leu Ser Leu Phe Gln Ala Arg
    130                 135                 140

Met Leu Asn Arg Ile Val Gln Ser Ala Met His Arg Leu Arg Met Glu
145                 150                 155                 160

Val Glu Glu Lys Ile His Arg Leu Pro Leu Ser Tyr Phe Asp Ser Ile
                165                 170                 175

Lys Arg Gly Asp Leu Leu Ser Arg Val Thr Asn Asp Val Asp Asn Ile
            180                 185                 190

Gly Gln Ser Leu Gln Gln Thr Leu Ser Gln Ala Ile Thr Ser Leu Leu
        195                 200                 205

Thr Val Ile Gly Val Leu Val Met Met Phe Ile Ile Ser Pro Leu Leu
    210                 215                 220

Ala Leu Val Ala Leu Val Ser Ile Pro Val Thr Ile Val Val Thr Val
225                 230                 235                 240

Val Val Ala Ser Arg Ser Gln Lys Leu Phe Ala Glu Gln Trp Lys Gln
                245                 250                 255

Thr Gly Ile Leu Asn Ala Arg Leu Glu Glu Thr Tyr Ser Gly His Ala
            260                 265                 270

Val Val Lys Val Phe Gly His Gln Lys Asp Val Gln Glu Ala Phe Glu
        275                 280                 285

Glu Glu Asn Gln Ala Cys Val
    290                 295
```

<210> 63
<211> 426
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (1)..(426)
<223> RXC00861

<400> 63
atg gct cct cac aag gtc atg ctg att acc act ggt act cag ggt gag 48
Met Ala Pro His Lys Val Met Leu Ile Thr Thr Gly Thr Gln Gly Glu
1 5 10 15

cct atg gct gcg ctg tct cgc atg gcg cgt cgt gag cac cga cag atc 96
Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile
20 25 30

act gtc cgt gat gga gac ttg att atc ctt tct tcc tcc ctg gtt cca 144
Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro
35 40 45

ggt aac gaa gaa gca gtg ttc ggt gtc atc aac atg ctg gct cag atc 192
Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile
50 55 60

ggt gca act gtt gtt acc ggt cgc gac gcc aag gtg cac acc tcg ggc 240
Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly
65 70 75 80

cac ggc tac tcc gga gag ctg ttg ttc ttg tac aac gcc gct cgt ccg 288
His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro
85 90 95

aag aac gct atg cct gtc cac ggc gag tgg cgc cac ctg cgc gcc aac 336
Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn
100 105 110

aag gaa ctg gct atc tcc act ggt gtt aac cgc gac aac gtt gtg ctt 384
Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu
115 120 125

gca caa aac ggt gtt gtg gtt gat atg gtc aac ggt cgc gca 426
Ala Gln Asn Gly Val Val Val Asp Met Val Asn Gly Arg Ala
130 135 140

<210> 64
<211> 142
<212> PRT
<213> Corynebacterium glutamicum

<400> 64
Met Ala Pro His Lys Val Met Leu Ile Thr Thr Gly Thr Gln Gly Glu
1 5 10 15

Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile
20 25 30

Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro
35 40 45

Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile
50 55 60

Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly
65 70 75 80

```
His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro
                85                  90                  95

Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn
            100                 105                 110

Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu
        115                 120                 125

Ala Gln Asn Gly Val Val Val Asp Met Val Asn Gly Arg Ala
    130                 135                 140


<210> 65
<211> 1066
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1066)
<223> RXC00866

<400> 65
gcatcaacgt aggagatcct cgacttccaa ttatggctcc aaatgagcag gaacttgagg 60

ctctccgaga agacatgaaa aaagctggag ttctataaat atg aat gat tcc cga    115
                                           Met Asn Asp Ser Arg
                                           1               5

aat cgc ggc cgg aag gtt acc cgc aag gcg ggc cca cca gaa gct ggt    163
Asn Arg Gly Arg Lys Val Thr Arg Lys Ala Gly Pro Pro Glu Ala Gly
                10                  15                  20

cag gaa aac cat ctg gat acc cct gtc ttt cag gca cca gat gct tcc    211
Gln Glu Asn His Leu Asp Thr Pro Val Phe Gln Ala Pro Asp Ala Ser
            25                  30                  35

tct aac cag agc gct gta aaa gct gag acc gcc gga aac gac aat cgg    259
Ser Asn Gln Ser Ala Val Lys Ala Glu Thr Ala Gly Asn Asp Asn Arg
        40                  45                  50

gat gct gcg caa ggt gct caa gga tcc caa gat tct cag ggt tcc cag    307
Asp Ala Ala Gln Gly Ala Gln Gly Ser Gln Asp Ser Gln Gly Ser Gln
    55                  60                  65

aac gct caa ggt tcc cag aac cgc gag tcc gga aac aac aac cgc aac    355
Asn Ala Gln Gly Ser Gln Asn Arg Glu Ser Gly Asn Asn Asn Arg Asn
70                  75                  80                  85

cgt tcc aac aac aac cgt cgc ggt ggt cgt gga cgt cgt gga tcc gga    403
Arg Ser Asn Asn Asn Arg Arg Gly Gly Arg Gly Arg Arg Gly Ser Gly
                90                  95                  100

aac gcc aat gag ggc gcg aac aac aac agc ggt aac cag aac cgt cag    451
Asn Ala Asn Glu Gly Ala Asn Asn Asn Ser Gly Asn Gln Asn Arg Gln
            105                 110                 115

ggc gga aac cgt ggc aac cgc ggt ggc gga cgc cga aac gtt gtt aag    499
Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg Arg Asn Val Val Lys
```

```
        120                 125                 130

tcg atg cag ggt gcg gat ctg acc cag cgc ctg cca gag cca cca aag     547
Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu Pro Glu Pro Pro Lys
    135                 140                 145

gca ccg gca aac ggt ctg cgt att tac gca ctt ggt ggc att tcc gaa     595
Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu Gly Gly Ile Ser Glu
150                 155                 160                 165

atc ggt cgc aac atg acc gtg ttt gag tac aac aac cgt ctg ctc atc     643
Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn Asn Arg Leu Leu Ile
                170                 175                 180

gtg gac tgt ggt gtg ctc ttc cca tct tca ggt gag cca ggc gtt gac     691
Val Asp Cys Gly Val Leu Phe Pro Ser Ser Gly Glu Pro Gly Val Asp
            185                 190                 195

ctg att ctt cct gac ttc ggc cca att gag gat cac ctg cac cgc gtc     739
Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp His Leu His Arg Val
        200                 205                 210

gat gca ttg gtg gtt act cac gga cac gaa gac cac att ggt gct att     787
Asp Ala Leu Val Val Thr His Gly His Glu Asp His Ile Gly Ala Ile
    215                 220                 225

ccc tgg ctg ctg aag ctg cgc aac gat atc cca atc ttg gca tcc cgt     835
Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro Ile Leu Ala Ser Arg
230                 235                 240                 245

ttc acc ttg gct ctg att gca gct aag tgt aag gaa cac cgt cag cgt     883
Phe Thr Leu Ala Leu Ile Ala Ala Lys Cys Lys Glu His Arg Gln Arg
                250                 255                 260

ccg aag ctg atc gag gtc aac gag cag tcc aat gag gac cgc gga ccg     931
Pro Lys Leu Ile Glu Val Asn Glu Gln Ser Asn Glu Asp Arg Gly Pro
            265                 270                 275

ttc aac att cgc ttc tgg gct gtt aac cac tcc atc cca gac tgc ctt     979
Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser Ile Pro Asp Cys Leu
        280                 285                 290

ggt ctt gct atc aag act cct gct ggt ttg gtc atc cac acc ggt gac
1027
Gly Leu Ala Ile Lys Thr Pro Ala Gly Leu Val Ile His Thr Gly Asp
    295                 300                 305

atc aag ctg gat cag act cct cct gat gga cgc cca act
1066
Ile Lys Leu Asp Gln Thr Pro Pro Asp Gly Arg Pro Thr
310                 315                 320


<210> 66
<211> 322
<212> PRT
<213> Corynebacterium glutamicum

<400> 66
Met Asn Asp Ser Arg Asn Arg Gly Arg Lys Val Thr Arg Lys Ala Gly
  1               5                  10                  15
```

```
Pro Pro Glu Ala Gly Gln Glu Asn His Leu Asp Thr Pro Val Phe Gln
            20                  25                  30

Ala Pro Asp Ala Ser Ser Asn Gln Ser Ala Val Lys Ala Glu Thr Ala
        35                  40                  45

Gly Asn Asp Asn Arg Asp Ala Ala Gln Gly Ala Gln Gly Ser Gln Asp
    50                  55                  60

Ser Gln Gly Ser Gln Asn Ala Gln Gly Ser Gln Asn Arg Glu Ser Gly
65                  70                  75                  80

Asn Asn Asn Arg Asn Arg Ser Asn Asn Asn Arg Arg Gly Gly Arg Gly
                85                  90                  95

Arg Arg Gly Ser Gly Asn Ala Asn Glu Gly Ala Asn Asn Asn Ser Gly
            100                 105                 110

Asn Gln Asn Arg Gln Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg
        115                 120                 125

Arg Asn Val Val Lys Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu
    130                 135                 140

Pro Glu Pro Pro Lys Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu
145                 150                 155                 160

Gly Gly Ile Ser Glu Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn
                165                 170                 175

Asn Arg Leu Leu Ile Val Asp Cys Gly Val Leu Phe Pro Ser Ser Gly
            180                 185                 190

Glu Pro Gly Val Asp Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp
        195                 200                 205

His Leu His Arg Val Asp Ala Leu Val Val Thr His Gly His Glu Asp
    210                 215                 220

His Ile Gly Ala Ile Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro
225                 230                 235                 240

Ile Leu Ala Ser Arg Phe Thr Leu Ala Leu Ile Ala Ala Lys Cys Lys
                245                 250                 255

Glu His Arg Gln Arg Pro Lys Leu Ile Glu Val Asn Glu Gln Ser Asn
            260                 265                 270

Glu Asp Arg Gly Pro Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser
        275                 280                 285

Ile Pro Asp Cys Leu Gly Leu Ala Ile Lys Thr Pro Ala Gly Leu Val
    290                 295                 300

Ile His Thr Gly Asp Ile Lys Leu Asp Gln Thr Pro Pro Asp Gly Arg
305                 310                 315                 320

Pro Thr
```

<210> 67
<211> 1527
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1504)
<223> RXC02095

<400> 67
ctctcttggt cctctcccca cccattttta agtactcaag acccttccaa cagaaaggat 60

tactccccca acaggctcaa aaatactgaa aggctcacgc atg aaa act gag caa 115
Met Lys Thr Glu Gln
1 5

tcc caa aaa gca caa tta gcc cct aag aaa gca cct gaa aag cca caa 163
Ser Gln Lys Ala Gln Leu Ala Pro Lys Lys Ala Pro Glu Lys Pro Gln
10 15 20

cgc atc cgc caa ctt att tcc gtg gcg tgg cag cga cct tgg ctc acc 211
Arg Ile Arg Gln Leu Ile Ser Val Ala Trp Gln Arg Pro Trp Leu Thr
25 30 35

tca ttc acc gta atc agc gct tta gct gca acg ttg ttt gaa ctt aca 259
Ser Phe Thr Val Ile Ser Ala Leu Ala Ala Thr Leu Phe Glu Leu Thr
40 45 50

ctt cct ctt ttg acc ggt ggc gcc atc gat atc gcg ctc gga aat acc 307
Leu Pro Leu Leu Thr Gly Gly Ala Ile Asp Ile Ala Leu Gly Asn Thr
55 60 65

gga gat act tta acc act gac ctg ctg gac cgg ttc act ccg agt gga 355
Gly Asp Thr Leu Thr Thr Asp Leu Leu Asp Arg Phe Thr Pro Ser Gly
70 75 80 85

tta agc gtg ttg acc agc gtc att gcc ctt atc gtg ctt ctc gcg ttg 403
Leu Ser Val Leu Thr Ser Val Ile Ala Leu Ile Val Leu Leu Ala Leu
90 95 100

ctt cgc tat gcc agt caa ttt gga cgg cga tac acc gca ggc aag ctc 451
Leu Arg Tyr Ala Ser Gln Phe Gly Arg Arg Tyr Thr Ala Gly Lys Leu
105 110 115

agc atg ggg gta cag cat gat gtc cgg ctt aaa acg atg cgc tca ttg 499
Ser Met Gly Val Gln His Asp Val Arg Leu Lys Thr Met Arg Ser Leu
120 125 130

cag aac ctc gat ggg cca ggt cag gac tct att cgc aca ggc caa gta 547
Gln Asn Leu Asp Gly Pro Gly Gln Asp Ser Ile Arg Thr Gly Gln Val
135 140 145

gtc agt cgg tcc att tcg gat atc aac atg gtg caa agc ctt gtg gcg 595
Val Ser Arg Ser Ile Ser Asp Ile Asn Met Val Gln Ser Leu Val Ala
150 155 160 165

atg ttg ccg atg ttg atc gga aat gtg gtc aag ctt gtg ctc act ttg 643
Met Leu Pro Met Leu Ile Gly Asn Val Val Lys Leu Val Leu Thr Leu
170 175 180

gtg atc atg ctg gct att tcc ccg ccg ctg acc atc atc gct gca gtg 691
Val Ile Met Leu Ala Ile Ser Pro Pro Leu Thr Ile Ile Ala Ala Val
185 190 195

ttg gtg cct ttg ctg ttg tgg gcc gtg gcc tat tcg cga aaa gcg ctt 739
Leu Val Pro Leu Leu Leu Trp Ala Val Ala Tyr Ser Arg Lys Ala Leu
200 205 210

ttt gcg tcc acg tgg tcg gcc cag caa aag gct gcg gat ctg acc act 787
Phe Ala Ser Thr Trp Ser Ala Gln Gln Lys Ala Ala Asp Leu Thr Thr
215 220 225

cat gtg gaa gaa act gtc acg ggt atc cgc gtg gtc aag gca ttt gcg 835
His Val Glu Glu Thr Val Thr Gly Ile Arg Val Val Lys Ala Phe Ala
230 235 240 245

cag gaa gac cgc gag acc gac aaa ttg gat ctc acc gca cgt gag tta 883
Gln Glu Asp Arg Glu Thr Asp Lys Leu Asp Leu Thr Ala Arg Glu Leu
250 255 260

ttt gcc cag cgc atg cgc act gca cgt ctg acg gca aag ttc atc ccc 931
Phe Ala Gln Arg Met Arg Thr Ala Arg Leu Thr Ala Lys Phe Ile Pro
265 270 275

atg gtt gag cag ctt ccg cag ctt gct ttg gtg gtc aac att gtt ggc 979
Met Val Glu Gln Leu Pro Gln Leu Ala Leu Val Val Asn Ile Val Gly
280 285 290

ggt ggc tat ttg gcc atg act ggt cac atc acg gtg ggc acg ttt gtg
1027
Gly Gly Tyr Leu Ala Met Thr Gly His Ile Thr Val Gly Thr Phe Val
295 300 305

gcg ttt tct tcc tat ctc act agc ttg tcg gcg gtg gct agg tcc ctg
1075
Ala Phe Ser Ser Tyr Leu Thr Ser Leu Ser Ala Val Ala Arg Ser Leu
310 315 320 325

tcg ggc atg ctc atg cgc gtg cag ttg gcg ctg tct tct gtg gag cgc
1123
Ser Gly Met Leu Met Arg Val Gln Leu Ala Leu Ser Ser Val Glu Arg
330 335 340

atc ttt gaa gtc att gat ctt cag cct gaa cgc acc gat cct gca cac
1171
Ile Phe Glu Val Ile Asp Leu Gln Pro Glu Arg Thr Asp Pro Ala His
345 350 355

ccc ctg tca ctt ccc gac act ccc ctg ggt ctg tcg ttc aac aac gta
1219
Pro Leu Ser Leu Pro Asp Thr Pro Leu Gly Leu Ser Phe Asn Asn Val
360 365 370

gat ttc cgt ggg att ctc aac ggt ttt gag ctg ggt gtt cag gcc ggt
1267
Asp Phe Arg Gly Ile Leu Asn Gly Phe Glu Leu Gly Val Gln Ala Gly
375 380 385

gaa acc gtt gtg ttg gtg ggc cct cca ggt tca ggc aag acc atg gct
1315

Glu Thr Val Val Leu Val Gly Pro Pro Gly Ser Gly Lys Thr Met Ala
390 395 400 405

gtg cag ctt gct gga aac ttt tat caa cca gac agc ggc cac atc gcc
1363
Val Gln Leu Ala Gly Asn Phe Tyr Gln Pro Asp Ser Gly His Ile Ala
410 415 420

ttt gat agc aac ggc cat cgc act cgc ttc gac gac ctc acc cac agc
1411
Phe Asp Ser Asn Gly His Arg Thr Arg Phe Asp Asp Leu Thr His Ser
425 430 435

gat atc cgc agg aat ctc atc gcg gtt ttt gat gag ccg ttc ttg tac
1459
Asp Ile Arg Arg Asn Leu Ile Ala Val Phe Asp Glu Pro Phe Leu Tyr
440 445 450

tcc tcc tcc ata ccg cga gaa cat ctc gat ggg ttt gga tgt cag
1504
Ser Ser Ser Ile Pro Arg Glu His Leu Asp Gly Phe Gly Cys Gln
455 460 465

tgatgagcag atcgaacacg cag
1527

<210> 68
<211> 468
<212> PRT
<213> Corynebacterium glutamicum

<400> 68
Met Lys Thr Glu Gln Ser Gln Lys Ala Gln Leu Ala Pro Lys Lys Ala
1 5 10 15

Pro Glu Lys Pro Gln Arg Ile Arg Gln Leu Ile Ser Val Ala Trp Gln
20 25 30

Arg Pro Trp Leu Thr Ser Phe Thr Val Ile Ser Ala Leu Ala Ala Thr
35 40 45

Leu Phe Glu Leu Thr Leu Pro Leu Leu Thr Gly Gly Ala Ile Asp Ile
50 55 60

Ala Leu Gly Asn Thr Gly Asp Thr Leu Thr Thr Asp Leu Leu Asp Arg
65 70 75 80

Phe Thr Pro Ser Gly Leu Ser Val Leu Thr Ser Val Ile Ala Leu Ile
85 90 95

Val Leu Leu Ala Leu Leu Arg Tyr Ala Ser Gln Phe Gly Arg Arg Tyr
100 105 110

Thr Ala Gly Lys Leu Ser Met Gly Val Gln His Asp Val Arg Leu Lys
115 120 125

Thr Met Arg Ser Leu Gln Asn Leu Asp Gly Pro Gly Gln Asp Ser Ile
130 135 140

Arg Thr Gly Gln Val Val Ser Arg Ser Ile Ser Asp Ile Asn Met Val

145 150 155 160

Gln Ser Leu Val Ala Met Leu Pro Met Leu Ile Gly Asn Val Val Lys
165 170 175

Leu Val Leu Thr Leu Val Ile Met Leu Ala Ile Ser Pro Pro Leu Thr
180 185 190

Ile Ile Ala Ala Val Leu Val Pro Leu Leu Leu Trp Ala Val Ala Tyr
195 200 205

Ser Arg Lys Ala Leu Phe Ala Ser Thr Trp Ser Ala Gln Gln Lys Ala
210 215 220

Ala Asp Leu Thr Thr His Val Glu Glu Thr Val Thr Gly Ile Arg Val
225 230 235 240

Val Lys Ala Phe Ala Gln Glu Asp Arg Glu Thr Asp Lys Leu Asp Leu
245 250 255

Thr Ala Arg Glu Leu Phe Ala Gln Arg Met Arg Thr Ala Arg Leu Thr
260 265 270

Ala Lys Phe Ile Pro Met Val Glu Gln Leu Pro Gln Leu Ala Leu Val
275 280 285

Val Asn Ile Val Gly Gly Gly Tyr Leu Ala Met Thr Gly His Ile Thr
290 295 300

Val Gly Thr Phe Val Ala Phe Ser Ser Tyr Leu Thr Ser Leu Ser Ala
305 310 315 320

Val Ala Arg Ser Leu Ser Gly Met Leu Met Arg Val Gln Leu Ala Leu
325 330 335

Ser Ser Val Glu Arg Ile Phe Glu Val Ile Asp Leu Gln Pro Glu Arg
340 345 350

Thr Asp Pro Ala His Pro Leu Ser Leu Pro Asp Thr Pro Leu Gly Leu
355 360 365

Ser Phe Asn Asn Val Asp Phe Arg Gly Ile Leu Asn Gly Phe Glu Leu
370 375 380

Gly Val Gln Ala Gly Glu Thr Val Val Leu Val Gly Pro Pro Gly Ser
385 390 395 400

Gly Lys Thr Met Ala Val Gln Leu Ala Gly Asn Phe Tyr Gln Pro Asp
405 410 415

Ser Gly His Ile Ala Phe Asp Ser Asn Gly His Arg Thr Arg Phe Asp
420 425 430

Asp Leu Thr His Ser Asp Ile Arg Arg Asn Leu Ile Ala Val Phe Asp
435 440 445

Glu Pro Phe Leu Tyr Ser Ser Ser Ile Pro Arg Glu His Leu Asp Gly
450 455 460

Phe Gly Cys Gln
465

<210> 69
<211> 295
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (84)..(272)
<223> RXC03185

<400> 69
```
agcgcccaac cgttcagacc agcggtttct ctgaggatgc aaagtccatg atgggtnagg 60

tcactgagct gtccgaaacc accatg aat gat ctt gca gct gaa ggt gaa aac  113
                             Met Asn Asp Leu Ala Ala Glu Gly Glu Asn
                              1               5                  10

gat cct tac cgc atg gtt cag cag ctg cgc cgc aag ctc tct cgc ttc   161
Asp Pro Tyr Arg Met Val Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe
                15                  20                  25

gtc gag cag aag tgg aag cgc cag ccg gtc atc atg cca acc gtc att   209
Val Glu Gln Lys Trp Lys Arg Gln Pro Val Ile Met Pro Thr Val Ile
            30                  35                  40

ccg atg act gcg gaa acc acg cac atc ggt gac gat gag gtt cgc gct   257
Pro Met Thr Ala Glu Thr Thr His Ile Gly Asp Asp Glu Val Arg Ala
        45                  50                  55

tca cgc gag tcc ctg taaaagcatt tcgcttttcg acg                     295
Ser Arg Glu Ser Leu
    60
```

<210> 70
<211> 63
<212> PRT
<213> Corynebacterium glutamicum

<400> 70
```
Met Asn Asp Leu Ala Ala Glu Gly Glu Asn Asp Pro Tyr Arg Met Val
 1               5                  10                  15

Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe Val Glu Gln Lys Trp Lys
            20                  25                  30

Arg Gln Pro Val Ile Met Pro Thr Val Ile Pro Met Thr Ala Glu Thr
        35                  40                  45

Thr His Ile Gly Asp Asp Glu Val Arg Ala Ser Arg Glu Ser Leu
    50                  55                  60
```

<210> 71
<211> 4653
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(4630)
<223> RXN00367

<400> 71
atcgaaagta accctttgt tacttgcgtt gcaggtagtg tccctgattt tcttattatc 60

gaacgattga tagaaacagg attaaagtga ggtatcccgc atg aaa cca caa gga 115
Met Lys Pro Gln Gly
1 5

ctc tac aac cct gcg cat gaa cat gac gcc tgc ggt gtg gcg ttt att 163
Leu Tyr Asn Pro Ala His Glu His Asp Ala Cys Gly Val Ala Phe Ile
10 15 20

gcg gat atc cac ggt cga ccc agc cgc agc att gtt gat cgt gca ctt 211
Ala Asp Ile His Gly Arg Pro Ser Arg Ser Ile Val Asp Arg Ala Leu
25 30 35

gag gcg ctt cgc aac att gac cac cga ggt gcc gcc ggt gca gag aag 259
Glu Ala Leu Arg Asn Ile Asp His Arg Gly Ala Ala Gly Ala Glu Lys
40 45 50

aac act ggc gat ggt gcg ggc atc ctc atg cag att ccg gac ggc ttt 307
Asn Thr Gly Asp Gly Ala Gly Ile Leu Met Gln Ile Pro Asp Gly Phe
55 60 65

tat cgt gaa gta tct ggc att gag ctt cct gag gca ggg gag tat gcc 355
Tyr Arg Glu Val Ser Gly Ile Glu Leu Pro Glu Ala Gly Glu Tyr Ala
70 75 80 85

act ggt att gcg ttc ttg cct cgc ggt cgc atg gcg atg atg gat gct 403
Thr Gly Ile Ala Phe Leu Pro Arg Gly Arg Met Ala Met Met Asp Ala
90 95 100

cag aag gaa att gag cgc atc gca aag caa gaa ggt gcc gat gtg ctt 451
Gln Lys Glu Ile Glu Arg Ile Ala Lys Gln Glu Gly Ala Asp Val Leu
105 110 115

ggt tgg cgc atg gtt cct ttt gat tct cgt gat ttg ggt tcc atg gct 499
Gly Trp Arg Met Val Pro Phe Asp Ser Arg Asp Leu Gly Ser Met Ala
120 125 130

gag gag gcg atg cct agt ttc gcg cag att ttc ctt act gtg cct gga 547
Glu Glu Ala Met Pro Ser Phe Ala Gln Ile Phe Leu Thr Val Pro Gly
135 140 145

aaa tct ggt gaa gat ctt gac cgt gtg atg ttc ttt atc cgt aag cgt 595
Lys Ser Gly Glu Asp Leu Asp Arg Val Met Phe Phe Ile Arg Lys Arg
150 155 160 165

tgt gag cgt gag ctg ggc acc acc aat ggt cgc gat acg gtg tat ttc 643
Cys Glu Arg Glu Leu Gly Thr Thr Asn Gly Arg Asp Thr Val Tyr Phe
170 175 180

ccg tcg cta tct tca cgc acc atc att tac aaa ggc atg ttg acc act 691
Pro Ser Leu Ser Ser Arg Thr Ile Ile Tyr Lys Gly Met Leu Thr Thr
185 190 195

ctg cag ctt gag ggc ttc ttt gag gat ctg ggt gat gct cgc ctg gag 739
Leu Gln Leu Glu Gly Phe Phe Glu Asp Leu Gly Asp Ala Arg Leu Glu

200 205 210

tcg gcc att gct att gtg cac tcg cgt ttc tcc acg aac act ttc cca 787
Ser Ala Ile Ala Ile Val His Ser Arg Phe Ser Thr Asn Thr Phe Pro
215 220 225

agc tgg ccg ctg gcg cac ccg tac cgt ttc gtt gcc cac aac ggt gag 835
Ser Trp Pro Leu Ala His Pro Tyr Arg Phe Val Ala His Asn Gly Glu
230 235 240 245

atc aac act gtg cgt ggc aat gaa aac tgg atg cgc gcc cgc gag gcg 883
Ile Asn Thr Val Arg Gly Asn Glu Asn Trp Met Arg Ala Arg Glu Ala
250 255 260

ctt atc aaa aac gac aag ctg ggc aat ttg agc agc gtg ctg cct atc 931
Leu Ile Lys Asn Asp Lys Leu Gly Asn Leu Ser Ser Val Leu Pro Ile
265 270 275

tgc acc ccg gag ggc tcg gat acc gcg cgt ttc gac gag gct ttg gag 979
Cys Thr Pro Glu Gly Ser Asp Thr Ala Arg Phe Asp Glu Ala Leu Glu
280 285 290

ctt ttg cac ctg ggc gga tac tca ctt ccg cat gct gtt gcg atg atg
1027
Leu Leu His Leu Gly Gly Tyr Ser Leu Pro His Ala Val Ala Met Met
295 300 305

atc cct cag gcg tgg gaa cac aac aag acg ctg agc cct gag ctg cgt
1075
Ile Pro Gln Ala Trp Glu His Asn Lys Thr Leu Ser Pro Glu Leu Arg
310 315 320 325

gat ttc tac gaa tac cac tct tgt ctg atg gag cca tgg gat ggt cct
1123
Asp Phe Tyr Glu Tyr His Ser Cys Leu Met Glu Pro Trp Asp Gly Pro
330 335 340

gca gcg ctg gca ttt act gac ggt cgt ttt gtg ggt gcc gtg ctg gac
1171
Ala Ala Leu Ala Phe Thr Asp Gly Arg Phe Val Gly Ala Val Leu Asp
345 350 355

cgt aat ggc ctg cga cct ggg cga atc acc att act gat tcg ggt ttg
1219
Arg Asn Gly Leu Arg Pro Gly Arg Ile Thr Ile Thr Asp Ser Gly Leu
360 365 370

gtt gtg atg gct tct gaa tcg gga gtg ttg gac ttg agg gag gag agc
1267
Val Val Met Ala Ser Glu Ser Gly Val Leu Asp Leu Arg Glu Glu Ser
375 380 385

gtc gta aag cgt act cgc gta cag cct gga cgc atg ttc ctt gtt gac
1315
Val Val Lys Arg Thr Arg Val Gln Pro Gly Arg Met Phe Leu Val Asp
390 395 400 405

act gcc gag ggc cgc atc gtt gaa gac gag gaa atc aag cag aaa tta
1363
Thr Ala Glu Gly Arg Ile Val Glu Asp Glu Glu Ile Lys Gln Lys Leu
410 415 420

agc gaa gcg cag cca tat ggt gag tgg att cgc gat aat ttt gtg cat 1411
Ser Glu Ala Gln Pro Tyr Gly Glu Trp Ile Arg Asp Asn Phe Val His
425 430 435

ctg gat cgt ctg cct cag aca cgc tac aac tac atg gcg cac tct cgt 1459
Leu Asp Arg Leu Pro Gln Thr Arg Tyr Asn Tyr Met Ala His Ser Arg
440 445 450

gct gtg ttg cgt cag cgt gtt ttc gga atc act gaa gaa gat gtg gat 1507
Ala Val Leu Arg Gln Arg Val Phe Gly Ile Thr Glu Glu Asp Val Asp
455 460 465

ttg ttg ctg ctg ccg atg gcc cgc cag ggt gct gag gcg att ggt tcc 1555
Leu Leu Leu Leu Pro Met Ala Arg Gln Gly Ala Glu Ala Ile Gly Ser
470 475 480 485

atg ggt tcg gat acg cca att gcg gcg cta tcc cag cga cca cgc atg 1603
Met Gly Ser Asp Thr Pro Ile Ala Ala Leu Ser Gln Arg Pro Arg Met
490 495 500

ctt tat gat ttc ttc gcg cag cgc ttt gct cag gtg aca aac cca ccg 1651
Leu Tyr Asp Phe Phe Ala Gln Arg Phe Ala Gln Val Thr Asn Pro Pro
505 510 515

ttg gac tct atc cgc gaa aag cct gtg acc agc atg ttc act ttg ttg 1699
Leu Asp Ser Ile Arg Glu Lys Pro Val Thr Ser Met Phe Thr Leu Leu
520 525 530

ggt gcg cag tct gac gtg ctc aat ccg ggt cct gat gcg gcg cga cgt 1747
Gly Ala Gln Ser Asp Val Leu Asn Pro Gly Pro Asp Ala Ala Arg Arg
535 540 545

atc cgt ttg gaa tcg ccg atc att gat aac cat gag ctg gcc acc ttg 1795
Ile Arg Leu Glu Ser Pro Ile Ile Asp Asn His Glu Leu Ala Thr Leu
550 555 560 565

atc aat gcc aac gcg cat ggt gag tgg gat tcc ttt ggt gct gct gta 1843
Ile Asn Ala Asn Ala His Gly Glu Trp Asp Ser Phe Gly Ala Ala Val
570 575 580

att tct ggt ttg tac cca gtg gct cac cat ggt gcc ggc atg aag gct 1891
Ile Ser Gly Leu Tyr Pro Val Ala His His Gly Ala Gly Met Lys Ala
585 590 595

gcg att gct cgt gtg cgc cgc gag gtt tct gaa gca atc cgc aat ggc 1939
Ala Ile Ala Arg Val Arg Arg Glu Val Ser Glu Ala Ile Arg Asn Gly
600 605 610

aag acg ttg atc gtg ctg tcg gat cgt gaa tct gat gag cgc atg gca
1987
Lys Thr Leu Ile Val Leu Ser Asp Arg Glu Ser Asp Glu Arg Met Ala
615 620 625

cct atc cct gcg ctg ctg ctg act tcc gct gtg cat cag tac ttg gtg
2035
Pro Ile Pro Ala Leu Leu Leu Thr Ser Ala Val His Gln Tyr Leu Val
630 635 640 645

cag caa cgt acc cgt acc cag tgc tcc ctg gtg gtg gaa tcc ggc gat
2083
Gln Gln Arg Thr Arg Thr Gln Cys Ser Leu Val Val Glu Ser Gly Asp
650 655 660

gcc cgc gag gtt cat cac ctg gcg atg ctc att ggt ttt ggt gcc gat
2131
Ala Arg Glu Val His His Leu Ala Met Leu Ile Gly Phe Gly Ala Asp
665 670 675

gcg atc aac ccg tac atg gca ttt gaa acc atc gat gag ctg cgc atg
2179
Ala Ile Asn Pro Tyr Met Ala Phe Glu Thr Ile Asp Glu Leu Arg Met
680 685 690

aag ggt cag ttg ggt gat ctt tct ttg gat gag gca tcc cga aac tac
2227
Lys Gly Gln Leu Gly Asp Leu Ser Leu Asp Glu Ala Ser Arg Asn Tyr
695 700 705

atc aag gca gcc acc act ggt gtg ctg aag gtg atg tcc aag atg ggc
2275
Ile Lys Ala Ala Thr Thr Gly Val Leu Lys Val Met Ser Lys Met Gly
710 715 720 725

att gca acg gtg tct tcg tac cgt ggc gcg cag ctt gcc gat gtc act
2323
Ile Ala Thr Val Ser Ser Tyr Arg Gly Ala Gln Leu Ala Asp Val Thr
730 735 740

ggt ctg cac cag gat ctc ctg gac aac tac ttc ggt ggt att gct tca
2371
Gly Leu His Gln Asp Leu Leu Asp Asn Tyr Phe Gly Gly Ile Ala Ser
745 750 755

cca att tct ggc atc ggt ctg gat gaa gtt gca gct gac gta gaa gct
2419
Pro Ile Ser Gly Ile Gly Leu Asp Glu Val Ala Ala Asp Val Glu Ala
760 765 770

cgt cac cgc agc gca ttt ttg cca cgc cct gaa gag cac gct cac cgt
2467
Arg His Arg Ser Ala Phe Leu Pro Arg Pro Glu Glu His Ala His Arg
775 780 785

gaa ttg gat ttg ggt ggt gaa tac aag tgg cgc cgc gaa ggt gaa tac
2515
Glu Leu Asp Leu Gly Gly Glu Tyr Lys Trp Arg Arg Glu Gly Glu Tyr
790 795 800 805

cac ctg ttc aac cca gaa acc atc ttc aag ctg cag cat gca acg cgt 2563
His Leu Phe Asn Pro Glu Thr Ile Phe Lys Leu Gln His Ala Thr Arg
810 815 820

tct ggc agc tac gag att ttc aag gat tac acc cgc aag gtt gat gat 2611
Ser Gly Ser Tyr Glu Ile Phe Lys Asp Tyr Thr Arg Lys Val Asp Asp
825 830 835

caa tcc act cgc ttg ggt act att cgt gga ctg ttt gag ttc agc acg 2659
Gln Ser Thr Arg Leu Gly Thr Ile Arg Gly Leu Phe Glu Phe Ser Thr
840 845 850

gac cgc aag cca att tcg gtg tct gag gtg gag ccg gtc agt gag atc 2707
Asp Arg Lys Pro Ile Ser Val Ser Glu Val Glu Pro Val Ser Glu Ile
855 860 865

gtg aag cgt ttc tcc act ggt gcg atg tct tat ggc tcg att tct gct 2755
Val Lys Arg Phe Ser Thr Gly Ala Met Ser Tyr Gly Ser Ile Ser Ala
870 875 880 885

gaa gcc cat gag gtc ttg gcc atc gcc atg aac cga ctg ggc ggt atg 2803
Glu Ala His Glu Val Leu Ala Ile Ala Met Asn Arg Leu Gly Gly Met
890 895 900

tcc aac tcc ggc gaa ggt ggc gag gac gcc cgc cga ttt gat gtg gaa 2851
Ser Asn Ser Gly Glu Gly Gly Glu Asp Ala Arg Arg Phe Asp Val Glu
905 910 915

ccc aac ggt gac tgg aag cgc tct gcc att aag cag gtg gcc tcg gga 2899
Pro Asn Gly Asp Trp Lys Arg Ser Ala Ile Lys Gln Val Ala Ser Gly
920 925 930

cgt ttc ggc gtg acc agc cac tac ttg aac aac tgc acc gat att cag 2947
Arg Phe Gly Val Thr Ser His Tyr Leu Asn Asn Cys Thr Asp Ile Gln
935 940 945

atc aag atg gca cag ggc gca aag ccc ggt gaa ggt ggc cag ctg cca 2995
Ile Lys Met Ala Gln Gly Ala Lys Pro Gly Glu Gly Gly Gln Leu Pro
950 955 960 965

cca aac aag gtg tac cca tgg gtt gca gaa gtc cgc atc acc acc cca 3043
Pro Asn Lys Val Tyr Pro Trp Val Ala Glu Val Arg Ile Thr Thr Pro
970 975 980

ggc gtt ggt ctg att tcc cct cca cca cac cac gat att tac tcc att 3091
Gly Val Gly Leu Ile Ser Pro Pro Pro His His Asp Ile Tyr Ser Ile
985 990 995

gag gat ctg gct cag ctg atc cac gac ctg aag aac gct aac cca cgc
3139
Glu Asp Leu Ala Gln Leu Ile His Asp Leu Lys Asn Ala Asn Pro Arg
1000 1005 1010

gca cga atc cac gtg aag cta gtg gca gaa caa ggc gtg ggc acc gtt
3187
Ala Arg Ile His Val Lys Leu Val Ala Glu Gln Gly Val Gly Thr Val
1015 1020 1025

gcc gca ggt gtg tcc aaa gca cac gct gat gtg gtg ctt att tcc ggc
3235
Ala Ala Gly Val Ser Lys Ala His Ala Asp Val Val Leu Ile Ser Gly
1030 1035 1040 1045

cac gat ggc gga act ggc gca tct cct ttg acc tcc ctg aag cat gcc
3283
His Asp Gly Gly Thr Gly Ala Ser Pro Leu Thr Ser Leu Lys His Ala
1050 1055 1060

ggt ggt cca tgg gag ttg ggc ttg gct gaa acc cag caa acg ttg ctg
3331
Gly Gly Pro Trp Glu Leu Gly Leu Ala Glu Thr Gln Gln Thr Leu Leu
1065 1070 1075

ctc aac ggc ctg cgc gat cgt att cgc gtg cag tgc gat ggt cag ctg
3379
Leu Asn Gly Leu Arg Asp Arg Ile Arg Val Gln Cys Asp Gly Gln Leu
1080 1085 1090

aaa act ggc cga gac gtg gtt atc gca gct ctt ctc ggt gcc gaa gaa
3427
Lys Thr Gly Arg Asp Val Val Ile Ala Ala Leu Leu Gly Ala Glu Glu
1095 1100 1105

ttc ggt ttt gcc acc gca ccg ctg gtg gtt gaa ggc tgc atc atg atg
3475
Phe Gly Phe Ala Thr Ala Pro Leu Val Val Glu Gly Cys Ile Met Met
1110 1115 1120 1125

cgc gtc tgc cac ctg gac acc tgc ccg gtg ggt atc gct acc cag aac
3523
Arg Val Cys His Leu Asp Thr Cys Pro Val Gly Ile Ala Thr Gln Asn
1130 1135 1140

ccg gat ttg cgt tcc aag ttc acc ggc aag gct gaa cac gtg gtc aac
3571
Pro Asp Leu Arg Ser Lys Phe Thr Gly Lys Ala Glu His Val Val Asn
1145 1150 1155

ttc ttc acc ttc atc gcc cag gaa gtc cgt gag tac ttg gca cag ctt
3619
Phe Phe Thr Phe Ile Ala Gln Glu Val Arg Glu Tyr Leu Ala Gln Leu
1160 1165 1170

ggt ttc cgc tct att gat gaa gcc gtc gga caa gcc cag gtg ctg cgc
3667
Gly Phe Arg Ser Ile Asp Glu Ala Val Gly Gln Ala Gln Val Leu Arg
1175 1180 1185

aag cgt tcc gga atc cca gct gat tcc cgc gca gca cac ctg gat ttg
3715
Lys Arg Ser Gly Ile Pro Ala Asp Ser Arg Ala Ala His Leu Asp Leu
1190 1195 1200 1205

agc cca att ttc cat cgc cca gaa act cca cac ttc cca act cag gat
3763
Ser Pro Ile Phe His Arg Pro Glu Thr Pro His Phe Pro Thr Gln Asp
1210 1215 1220

gtg cgt tgc acc aag acc cag gaa cac agc cta gaa aaa gcc ctg gac
3811
Val Arg Cys Thr Lys Thr Gln Glu His Ser Leu Glu Lys Ala Leu Asp
1225 1230 1235

aac gca ttt att gat aag gct tcg gac acg atc acc cgt gcc gca gcg
3859
Asn Ala Phe Ile Asp Lys Ala Ser Asp Thr Ile Thr Arg Ala Ala Ala
1240 1245 1250

ggt gtg gaa acc agc att gtt att gat agc tcc atc agc aac gtc aac
3907
Gly Val Glu Thr Ser Ile Val Ile Asp Ser Ser Ile Ser Asn Val Asn
1255 1260 1265

cgt tca gtt ggc acg atg ctg ggt tct gca gtc agc cgc gtg gct ggt
3955
Arg Ser Val Gly Thr Met Leu Gly Ser Ala Val Ser Arg Val Ala Gly
1270 1275 1280 1285

gcc caa ggt ttg cca gac ggc acc atc acc ttg aat ctt caa ggc tgc
4003
Ala Gln Gly Leu Pro Asp Gly Thr Ile Thr Leu Asn Leu Gln Gly Cys
1290 1295 1300

gcc ggt aac tcc ttt ggc gcg ttc atc cca cga ggc atc acc atc aac
4051
Ala Gly Asn Ser Phe Gly Ala Phe Ile Pro Arg Gly Ile Thr Ile Asn
1305 1310 1315

ctc acc ggc gat gcc aat gac ttt gtg ggc aag gga tta tct ggc gga
4099
Leu Thr Gly Asp Ala Asn Asp Phe Val Gly Lys Gly Leu Ser Gly Gly
1320 1325 1330

aag att gtg atc aag cct tcc gct cag gct ccg aag cag ctg aag aac
4147
Lys Ile Val Ile Lys Pro Ser Ala Gln Ala Pro Lys Gln Leu Lys Asn
1335 1340 1345

aat cca aat atc att gcc gga aac gtg ctt gga tac ggc gca acc agt
4195
Asn Pro Asn Ile Ile Ala Gly Asn Val Leu Gly Tyr Gly Ala Thr Ser
1350 1355 1360 1365

ggt gaa ttg ttc att cgt ggc cag gtc ggc gaa cgt ttc tgc gtc cgt
4243
Gly Glu Leu Phe Ile Arg Gly Gln Val Gly Glu Arg Phe Cys Val Arg
1370 1375 1380

aac tct ggc gcc acc gca gtg gtt gaa ggt atc gga aac cac ggt tgt
4291
Asn Ser Gly Ala Thr Ala Val Val Glu Gly Ile Gly Asn His Gly Cys
1385 1390 1395

gag tac atg act ggc ggc cga gtc ctg gtt ttg ggc ccg gtt ggt gag
4339
Glu Tyr Met Thr Gly Gly Arg Val Leu Val Leu Gly Pro Val Gly Glu
1400 1405 1410

aac ttt ggt gcc ggc atg tct ggt ggc att gca tac ctg gct aat tcc
4387
Asn Phe Gly Ala Gly Met Ser Gly Gly Ile Ala Tyr Leu Ala Asn Ser
1415 1420 1425

ccg gac cta aac cag aag atc aat ggc gaa ttg gtg gat gtt gtt cca
4435
Pro Asp Leu Asn Gln Lys Ile Asn Gly Glu Leu Val Asp Val Val Pro
1430 1435 1440 1445

ctg agc gct gac gat ctg acg tgg gct gat gag ctc att gct cgc cac
4483
Leu Ser Ala Asp Asp Leu Thr Trp Ala Asp Glu Leu Ile Ala Arg His
1450 1455 1460

cgc gaa ctc acc gga tcc gag acc aag ctg cgt gca caa gat ttg gtg
4531
Arg Glu Leu Thr Gly Ser Glu Thr Lys Leu Arg Ala Gln Asp Leu Val
1465 1470 1475

aaa atc atg ccg cgc gat ttc caa aaa gta ctc aac atc atc gaa acg
4579
Lys Ile Met Pro Arg Asp Phe Gln Lys Val Leu Asn Ile Ile Glu Thr
1480 1485 1490

gcc cac gct gag ggc caa gac cca gca atc aag atc atg gag gca gtg
4627
Ala His Ala Glu Gly Gln Asp Pro Ala Ile Lys Ile Met Glu Ala Val
1495 1500 1505

agc taatggccga cccacaagga ttc
4653
Ser
1510

<210> 72
<211> 1510
<212> PRT
<213> Corynebacterium glutamicum

<400> 72
Met Lys Pro Gln Gly Leu Tyr Asn Pro Ala His Glu His Asp Ala Cys
1 5 10 15

Gly Val Ala Phe Ile Ala Asp Ile His Gly Arg Pro Ser Arg Ser Ile
20 25 30

Val Asp Arg Ala Leu Glu Ala Leu Arg Asn Ile Asp His Arg Gly Ala
35 40 45

Ala Gly Ala Glu Lys Asn Thr Gly Asp Gly Ala Gly Ile Leu Met Gln
50 55 60

Ile Pro Asp Gly Phe Tyr Arg Glu Val Ser Gly Ile Glu Leu Pro Glu
65 70 75 80

Ala Gly Glu Tyr Ala Thr Gly Ile Ala Phe Leu Pro Arg Gly Arg Met
85 90 95

Ala Met Met Asp Ala Gln Lys Glu Ile Glu Arg Ile Ala Lys Gln Glu
100 105 110

Gly Ala Asp Val Leu Gly Trp Arg Met Val Pro Phe Asp Ser Arg Asp
115 120 125

Leu Gly Ser Met Ala Glu Glu Ala Met Pro Ser Phe Ala Gln Ile Phe
130 135 140

Leu Thr Val Pro Gly Lys Ser Gly Glu Asp Leu Asp Arg Val Met Phe
145 150 155 160

Phe Ile Arg Lys Arg Cys Glu Arg Glu Leu Gly Thr Thr Asn Gly Arg
165 170 175

Asp Thr Val Tyr Phe Pro Ser Leu Ser Ser Arg Thr Ile Ile Tyr Lys
180 185 190

Gly Met Leu Thr Thr Leu Gln Leu Glu Gly Phe Phe Glu Asp Leu Gly
195 200 205

Asp Ala Arg Leu Glu Ser Ala Ile Ala Ile Val His Ser Arg Phe Ser
210 215 220

Thr Asn Thr Phe Pro Ser Trp Pro Leu Ala His Pro Tyr Arg Phe Val
225 230 235 240

Ala His Asn Gly Glu Ile Asn Thr Val Arg Gly Asn Glu Asn Trp Met
245 250 255

Arg Ala Arg Glu Ala Leu Ile Lys Asn Asp Lys Leu Gly Asn Leu Ser
260 265 270

Ser Val Leu Pro Ile Cys Thr Pro Glu Gly Ser Asp Thr Ala Arg Phe
275 280 285

Asp Glu Ala Leu Glu Leu Leu His Leu Gly Gly Tyr Ser Leu Pro His
290 295 300

Ala Val Ala Met Met Ile Pro Gln Ala Trp Glu His Asn Lys Thr Leu
305 310 315 320

Ser Pro Glu Leu Arg Asp Phe Tyr Glu Tyr His Ser Cys Leu Met Glu
325 330 335

Pro Trp Asp Gly Pro Ala Ala Leu Ala Phe Thr Asp Gly Arg Phe Val
340 345 350

Gly Ala Val Leu Asp Arg Asn Gly Leu Arg Pro Gly Arg Ile Thr Ile
355 360 365

Thr Asp Ser Gly Leu Val Val Met Ala Ser Glu Ser Gly Val Leu Asp

370 375 380

Leu Arg Glu Glu Ser Val Val Lys Arg Thr Arg Val Gln Pro Gly Arg
385 390 395 400

Met Phe Leu Val Asp Thr Ala Glu Gly Arg Ile Val Glu Asp Glu Glu
405 410 415

Ile Lys Gln Lys Leu Ser Glu Ala Gln Pro Tyr Gly Glu Trp Ile Arg
420 425 430

Asp Asn Phe Val His Leu Asp Arg Leu Pro Gln Thr Arg Tyr Asn Tyr
435 440 445

Met Ala His Ser Arg Ala Val Leu Arg Gln Arg Val Phe Gly Ile Thr
450 455 460

Glu Glu Asp Val Asp Leu Leu Leu Leu Pro Met Ala Arg Gln Gly Ala
465 470 475 480

Glu Ala Ile Gly Ser Met Gly Ser Asp Thr Pro Ile Ala Ala Leu Ser
485 490 495

Gln Arg Pro Arg Met Leu Tyr Asp Phe Phe Ala Gln Arg Phe Ala Gln
500 505 510

Val Thr Asn Pro Pro Leu Asp Ser Ile Arg Glu Lys Pro Val Thr Ser
515 520 525

Met Phe Thr Leu Leu Gly Ala Gln Ser Asp Val Leu Asn Pro Gly Pro
530 535 540

Asp Ala Ala Arg Arg Ile Arg Leu Glu Ser Pro Ile Ile Asp Asn His
545 550 555 560

Glu Leu Ala Thr Leu Ile Asn Ala Asn Ala His Gly Glu Trp Asp Ser
565 570 575

Phe Gly Ala Ala Val Ile Ser Gly Leu Tyr Pro Val Ala His His Gly
580 585 590

Ala Gly Met Lys Ala Ala Ile Ala Arg Val Arg Arg Glu Val Ser Glu
595 600 605

Ala Ile Arg Asn Gly Lys Thr Leu Ile Val Leu Ser Asp Arg Glu Ser
610 615 620

Asp Glu Arg Met Ala Pro Ile Pro Ala Leu Leu Leu Thr Ser Ala Val
625 630 635 640

His Gln Tyr Leu Val Gln Gln Arg Thr Arg Thr Gln Cys Ser Leu Val
645 650 655

Val Glu Ser Gly Asp Ala Arg Glu Val His His Leu Ala Met Leu Ile
660 665 670

Gly Phe Gly Ala Asp Ala Ile Asn Pro Tyr Met Ala Phe Glu Thr Ile
675 680 685

Asp Glu Leu Arg Met Lys Gly Gln Leu Gly Asp Leu Ser Leu Asp Glu
690 695 700

Ala Ser Arg Asn Tyr Ile Lys Ala Ala Thr Thr Gly Val Leu Lys Val
705 710 715 720

Met Ser Lys Met Gly Ile Ala Thr Val Ser Ser Tyr Arg Gly Ala Gln
725 730 735

Leu Ala Asp Val Thr Gly Leu His Gln Asp Leu Leu Asp Asn Tyr Phe
740 745 750

Gly Gly Ile Ala Ser Pro Ile Ser Gly Ile Gly Leu Asp Glu Val Ala
755 760 765

Ala Asp Val Glu Ala Arg His Arg Ser Ala Phe Leu Pro Arg Pro Glu
770 775 780

Glu His Ala His Arg Glu Leu Asp Leu Gly Gly Glu Tyr Lys Trp Arg
785 790 795 800

Arg Glu Gly Glu Tyr His Leu Phe Asn Pro Glu Thr Ile Phe Lys Leu
805 810 815

Gln His Ala Thr Arg Ser Gly Ser Tyr Glu Ile Phe Lys Asp Tyr Thr
820 825 830

Arg Lys Val Asp Asp Gln Ser Thr Arg Leu Gly Thr Ile Arg Gly Leu
835 840 845

Phe Glu Phe Ser Thr Asp Arg Lys Pro Ile Ser Val Ser Glu Val Glu
850 855 860

Pro Val Ser Glu Ile Val Lys Arg Phe Ser Thr Gly Ala Met Ser Tyr
865 870 875 880

Gly Ser Ile Ser Ala Glu Ala His Glu Val Leu Ala Ile Ala Met Asn
885 890 895

Arg Leu Gly Gly Met Ser Asn Ser Gly Glu Gly Gly Glu Asp Ala Arg
900 905 910

Arg Phe Asp Val Glu Pro Asn Gly Asp Trp Lys Arg Ser Ala Ile Lys
915 920 925

Gln Val Ala Ser Gly Arg Phe Gly Val Thr Ser His Tyr Leu Asn Asn
930 935 940

Cys Thr Asp Ile Gln Ile Lys Met Ala Gln Gly Ala Lys Pro Gly Glu
945 950 955 960

Gly Gly Gln Leu Pro Pro Asn Lys Val Tyr Pro Trp Val Ala Glu Val
965 970 975

Arg Ile Thr Thr Pro Gly Val Gly Leu Ile Ser Pro Pro Pro His His
980 985 990

Asp Ile Tyr Ser Ile Glu Asp Leu Ala Gln Leu Ile His Asp Leu Lys
995 1000 1005

Asn Ala Asn Pro Arg Ala Arg Ile His Val Lys Leu Val Ala Glu Gln
1010 1015 1020

Gly Val Gly Thr Val Ala Ala Gly Val Ser Lys Ala His Ala Asp Val
1025 1030 1035 1040

Val Leu Ile Ser Gly His Asp Gly Gly Thr Gly Ala Ser Pro Leu Thr
1045 1050 1055

Ser Leu Lys His Ala Gly Gly Pro Trp Glu Leu Gly Leu Ala Glu Thr
1060 1065 1070

Gln Gln Thr Leu Leu Leu Asn Gly Leu Arg Asp Arg Ile Arg Val Gln
1075 1080 1085

Cys Asp Gly Gln Leu Lys Thr Gly Arg Asp Val Val Ile Ala Ala Leu
1090 1095 1100

Leu Gly Ala Glu Glu Phe Gly Phe Ala Thr Ala Pro Leu Val Val Glu
1105 1110 1115 1120

Gly Cys Ile Met Met Arg Val Cys His Leu Asp Thr Cys Pro Val Gly
1125 1130 1135

Ile Ala Thr Gln Asn Pro Asp Leu Arg Ser Lys Phe Thr Gly Lys Ala
1140 1145 1150

Glu His Val Val Asn Phe Phe Thr Phe Ile Ala Gln Glu Val Arg Glu
1155 1160 1165

Tyr Leu Ala Gln Leu Gly Phe Arg Ser Ile Asp Glu Ala Val Gly Gln
1170 1175 1180

Ala Gln Val Leu Arg Lys Arg Ser Gly Ile Pro Ala Asp Ser Arg Ala
1185 1190 1195 1200

Ala His Leu Asp Leu Ser Pro Ile Phe His Arg Pro Glu Thr Pro His
1205 1210 1215

Phe Pro Thr Gln Asp Val Arg Cys Thr Lys Thr Gln Glu His Ser Leu
1220 1225 1230

Glu Lys Ala Leu Asp Asn Ala Phe Ile Asp Lys Ala Ser Asp Thr Ile
1235 1240 1245

Thr Arg Ala Ala Ala Gly Val Glu Thr Ser Ile Val Ile Asp Ser Ser
1250 1255 1260

Ile Ser Asn Val Asn Arg Ser Val Gly Thr Met Leu Gly Ser Ala Val
1265 1270 1275 1280

Ser Arg Val Ala Gly Ala Gln Gly Leu Pro Asp Gly Thr Ile Thr Leu
1285 1290 1295

Asn Leu Gln Gly Cys Ala Gly Asn Ser Phe Gly Ala Phe Ile Pro Arg
1300 1305 1310

Gly Ile Thr Ile Asn Leu Thr Gly Asp Ala Asn Asp Phe Val Gly Lys
1315 1320 1325

Gly Leu Ser Gly Gly Lys Ile Val Ile Lys Pro Ser Ala Gln Ala Pro
1330 1335 1340

Lys Gln Leu Lys Asn Asn Pro Asn Ile Ile Ala Gly Asn Val Leu Gly

1345 1350 1355 1360

Tyr Gly Ala Thr Ser Gly Glu Leu Phe Ile Arg Gly Gln Val Gly Glu
1365 1370 1375

Arg Phe Cys Val Arg Asn Ser Gly Ala Thr Ala Val Val Glu Gly Ile
1380 1385 1390

Gly Asn His Gly Cys Glu Tyr Met Thr Gly Gly Arg Val Leu Val Leu
1395 1400 1405

Gly Pro Val Gly Glu Asn Phe Gly Ala Gly Met Ser Gly Gly Ile Ala
1410 1415 1420

Tyr Leu Ala Asn Ser Pro Asp Leu Asn Gln Lys Ile Asn Gly Glu Leu
1425 1430 1435 1440

Val Asp Val Val Pro Leu Ser Ala Asp Asp Leu Thr Trp Ala Asp Glu
1445 1450 1455

Leu Ile Ala Arg His Arg Glu Leu Thr Gly Ser Glu Thr Lys Leu Arg
1460 1465 1470

Ala Gln Asp Leu Val Lys Ile Met Pro Arg Asp Phe Gln Lys Val Leu
1475 1480 1485

Asn Ile Ile Glu Thr Ala His Ala Glu Gly Gln Asp Pro Ala Ile Lys
1490 1495 1500

Ile Met Glu Ala Val Ser
1505 1510

<210> 73
<211> 1906
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1906)
<223> FRXA00007

<400> 73
atcgaaagta acccttttgt tacttgcgtt gcaggtagtg tccctgattt tcttattatc 60

gaacgattga tagaaacagg attaaagtga ggtatcccgc atg aaa cca caa gga 115
Met Lys Pro Gln Gly
1 5

ctc tac aac cct gcg cat gaa cat gac gcc tgc ggt gtg gcg ttt att 163
Leu Tyr Asn Pro Ala His Glu His Asp Ala Cys Gly Val Ala Phe Ile
10 15 20

gcg gat atc cac ggt cga ccc agc cgc agc att gtt gat cgt gca ctt 211
Ala Asp Ile His Gly Arg Pro Ser Arg Ser Ile Val Asp Arg Ala Leu
25 30 35

gag gcg ctt cgc aac att gac cac cga ggt gcc gcc ggt gca gag aag 259
Glu Ala Leu Arg Asn Ile Asp His Arg Gly Ala Ala Gly Ala Glu Lys
40 45 50

```
aac act ggc gat ggt gcg ggc atc ctc atg cag att ccg gac ggc ttt   307
Asn Thr Gly Asp Gly Ala Gly Ile Leu Met Gln Ile Pro Asp Gly Phe
     55                  60                  65

tat cgt gaa gta tct ggc att gag ctt cct gag gca ggg gag tat gcc   355
Tyr Arg Glu Val Ser Gly Ile Glu Leu Pro Glu Ala Gly Glu Tyr Ala
 70                  75                  80                  85

act ggt att gcg ttc ttg cct cgc ggt cgc atg gcg atg atg gat gct   403
Thr Gly Ile Ala Phe Leu Pro Arg Gly Arg Met Ala Met Met Asp Ala
                 90                  95                 100

cag aag gaa att gag cgc atc gca aag caa gaa ggt gcc gat gtg ctt   451
Gln Lys Glu Ile Glu Arg Ile Ala Lys Gln Glu Gly Ala Asp Val Leu
            105                 110                 115

ggt tgg cgc atg gtt cct ttt gat tct cgt gat ttg ggt tcc atg gct   499
Gly Trp Arg Met Val Pro Phe Asp Ser Arg Asp Leu Gly Ser Met Ala
        120                 125                 130

gag gag gcg atg cct agt ttc gcg cag att ttc ctt act gtg cct gga   547
Glu Glu Ala Met Pro Ser Phe Ala Gln Ile Phe Leu Thr Val Pro Gly
    135                 140                 145

aaa tct ggt gaa gat ctt gac cgt gtg atg ttc ttt atc cgt aag cgt   595
Lys Ser Gly Glu Asp Leu Asp Arg Val Met Phe Phe Ile Arg Lys Arg
150                 155                 160                 165

tgt gag cgt gag ctg ggc acc acc aat ggt cgc gat acg gtg tat ttc   643
Cys Glu Arg Glu Leu Gly Thr Thr Asn Gly Arg Asp Thr Val Tyr Phe
                170                 175                 180

ccg tcg cta tct tca cgc acc atc att tac aaa ggc atg ttg acc act   691
Pro Ser Leu Ser Ser Arg Thr Ile Ile Tyr Lys Gly Met Leu Thr Thr
            185                 190                 195

ctg cag ctt gag ggc ttc ttt gag gat ctg ggt gat gct cgc ctg gag   739
Leu Gln Leu Glu Gly Phe Phe Glu Asp Leu Gly Asp Ala Arg Leu Glu
        200                 205                 210

tcg gcc att gct att gtg cac tcg cgt ttc tcc acg aac act ttc cca   787
Ser Ala Ile Ala Ile Val His Ser Arg Phe Ser Thr Asn Thr Phe Pro
    215                 220                 225

agc tgg ccg ctg gcg cac ccg tac cgt ttc gtt gcc cac aac ggt gag   835
Ser Trp Pro Leu Ala His Pro Tyr Arg Phe Val Ala His Asn Gly Glu
230                 235                 240                 245

atc aac act gtg cgt ggc aat gaa aac tgg atg cgc gcc cgc gag gcg   883
Ile Asn Thr Val Arg Gly Asn Glu Asn Trp Met Arg Ala Arg Glu Ala
                250                 255                 260

ctt atc aaa aac gac aag ctg ggc aat ttg agc agc gtg ctg cct atc   931
Leu Ile Lys Asn Asp Lys Leu Gly Asn Leu Ser Ser Val Leu Pro Ile
            265                 270                 275

tgc acc ccg gag ggc tcg gat acc gcg cgt ttc gac gag gct ttg gag   979
Cys Thr Pro Glu Gly Ser Asp Thr Ala Arg Phe Asp Glu Ala Leu Glu
        280                 285                 290
```

ctt ttg cac ctg ggc gga tac tca ctt ccg cat gct gtt gcg atg atg
1027
Leu Leu His Leu Gly Gly Tyr Ser Leu Pro His Ala Val Ala Met Met
295 300 305

atc cct cag gcg tgg gaa cac aac aag acg ctg agc cct gag ctg cgt
1075
Ile Pro Gln Ala Trp Glu His Asn Lys Thr Leu Ser Pro Glu Leu Arg
310 315 320 325

gat ttc tac gaa tac cac tct tgt ctg atg gag cca tgg gat ggt cct
1123
Asp Phe Tyr Glu Tyr His Ser Cys Leu Met Glu Pro Trp Asp Gly Pro
330 335 340

gca gcg ctg gca ttt act gac ggt cgt ttt gtg ggt gcc gtg ctg gac
1171
Ala Ala Leu Ala Phe Thr Asp Gly Arg Phe Val Gly Ala Val Leu Asp
345 350 355

cgt aat ggc ctg cga cct ggg cga atc acc att act gat tcg ggt ttg
1219
Arg Asn Gly Leu Arg Pro Gly Arg Ile Thr Ile Thr Asp Ser Gly Leu
360 365 370

gtt gtg atg gct tct gaa tcg gga gtg ttg gac ttg agg gag gag agc
1267
Val Val Met Ala Ser Glu Ser Gly Val Leu Asp Leu Arg Glu Glu Ser
375 380 385

gtc gta aag cgt act cgc gta cag cct gga cgc atg ttc ctt gtt gac
1315
Val Val Lys Arg Thr Arg Val Gln Pro Gly Arg Met Phe Leu Val Asp
390 395 400 405

act gcc gag ggc cgc atc gtt gaa gac gag gaa atc aag cag aaa tta
1363
Thr Ala Glu Gly Arg Ile Val Glu Asp Glu Glu Ile Lys Gln Lys Leu
410 415 420

agc gaa gcg cag cca tat ggt gag tgg att cgc gat aat ttt gtg cat
1411
Ser Glu Ala Gln Pro Tyr Gly Glu Trp Ile Arg Asp Asn Phe Val His
425 430 435

ctg gat cgt ctg cct cag aca cgc tac aac tac atg gcg cac tct cgt
1459
Leu Asp Arg Leu Pro Gln Thr Arg Tyr Asn Tyr Met Ala His Ser Arg
440 445 450

gct gtg ttg cgt cag cgt gtt ttc gga atc act gaa gaa gat gtg gat
1507
Ala Val Leu Arg Gln Arg Val Phe Gly Ile Thr Glu Glu Asp Val Asp
455 460 465

ttg ttg ctg ctg ccg atg gcc cgc cag ggt gct gag gcg att ggt tcc
1555
Leu Leu Leu Leu Pro Met Ala Arg Gln Gly Ala Glu Ala Ile Gly Ser
470 475 480 485

atg ggt tcg gat acg cca att gcg gcg cta tcc cag cga cca cgc atg
1603
Met Gly Ser Asp Thr Pro Ile Ala Ala Leu Ser Gln Arg Pro Arg Met
490 495 500

ctt tat gat ttc ttc gcg cag cgc ttt gct cag gtg aca aac cca ccg
1651
Leu Tyr Asp Phe Phe Ala Gln Arg Phe Ala Gln Val Thr Asn Pro Pro
505 510 515

ttg gac tct atc cgc gaa aag cct gtg acc agc atg ttc act ttg ttg
1699
Leu Asp Ser Ile Arg Glu Lys Pro Val Thr Ser Met Phe Thr Leu Leu
520 525 530

ggt gcg cag tct gac gtg ctc aat ccg ggt cct gat gcg gcg cga cgt
1747
Gly Ala Gln Ser Asp Val Leu Asn Pro Gly Pro Asp Ala Ala Arg Arg
535 540 545

att cgt ttg gaa tcg ccg atc att gat aac cat gag ctg gcc acc ttg
1795
Ile Arg Leu Glu Ser Pro Ile Ile Asp Asn His Glu Leu Ala Thr Leu
550 555 560 565

atc aat gcc aac gcg cat ggt gag tgg gat tcc ttt ggt gct gct gta
1843
Ile Asn Ala Asn Ala His Gly Glu Trp Asp Ser Phe Gly Ala Ala Val
570 575 580

att tct ggt ttg tac cca gtg gct cac cat ggt gcc ggc atg aag gct
1891
Ile Ser Gly Leu Tyr Pro Val Ala His His Gly Ala Gly Met Lys Ala
585 590 595

gcg att gct cgt gtg
1906
Ala Ile Ala Arg Val
600

<210> 74
<211> 602
<212> PRT
<213> Corynebacterium glutamicum

<400> 74
Met Lys Pro Gln Gly Leu Tyr Asn Pro Ala His Glu His Asp Ala Cys
1 5 10 15

Gly Val Ala Phe Ile Ala Asp Ile His Gly Arg Pro Ser Arg Ser Ile
20 25 30

Val Asp Arg Ala Leu Glu Ala Leu Arg Asn Ile Asp His Arg Gly Ala
35 40 45

Ala Gly Ala Glu Lys Asn Thr Gly Asp Gly Ala Gly Ile Leu Met Gln
50 55 60

Ile Pro Asp Gly Phe Tyr Arg Glu Val Ser Gly Ile Glu Leu Pro Glu
65 70 75 80

```
Ala Gly Glu Tyr Ala Thr Gly Ile Ala Phe Leu Pro Arg Gly Arg Met
                85                  90                  95

Ala Met Met Asp Ala Gln Lys Glu Ile Glu Arg Ile Ala Lys Gln Glu
            100                 105                 110

Gly Ala Asp Val Leu Gly Trp Arg Met Val Pro Phe Asp Ser Arg Asp
        115                 120                 125

Leu Gly Ser Met Ala Glu Glu Ala Met Pro Ser Phe Ala Gln Ile Phe
    130                 135                 140

Leu Thr Val Pro Gly Lys Ser Gly Glu Asp Leu Asp Arg Val Met Phe
145                 150                 155                 160

Phe Ile Arg Lys Arg Cys Glu Arg Glu Leu Gly Thr Thr Asn Gly Arg
                165                 170                 175

Asp Thr Val Tyr Phe Pro Ser Leu Ser Ser Arg Thr Ile Ile Tyr Lys
            180                 185                 190

Gly Met Leu Thr Thr Leu Gln Leu Glu Gly Phe Phe Glu Asp Leu Gly
        195                 200                 205

Asp Ala Arg Leu Glu Ser Ala Ile Ala Ile Val His Ser Arg Phe Ser
    210                 215                 220

Thr Asn Thr Phe Pro Ser Trp Pro Leu Ala His Pro Tyr Arg Phe Val
225                 230                 235                 240

Ala His Asn Gly Glu Ile Asn Thr Val Arg Gly Asn Glu Asn Trp Met
                245                 250                 255

Arg Ala Arg Glu Ala Leu Ile Lys Asn Asp Lys Leu Gly Asn Leu Ser
            260                 265                 270

Ser Val Leu Pro Ile Cys Thr Pro Glu Gly Ser Asp Thr Ala Arg Phe
        275                 280                 285

Asp Glu Ala Leu Glu Leu Leu His Leu Gly Gly Tyr Ser Leu Pro His
    290                 295                 300

Ala Val Ala Met Met Ile Pro Gln Ala Trp Glu His Asn Lys Thr Leu
305                 310                 315                 320

Ser Pro Glu Leu Arg Asp Phe Tyr Glu Tyr His Ser Cys Leu Met Glu
                325                 330                 335

Pro Trp Asp Gly Pro Ala Ala Leu Ala Phe Thr Asp Gly Arg Phe Val
            340                 345                 350

Gly Ala Val Leu Asp Arg Asn Gly Leu Arg Pro Gly Arg Ile Thr Ile
        355                 360                 365

Thr Asp Ser Gly Leu Val Val Met Ala Ser Glu Ser Gly Val Leu Asp
    370                 375                 380

Leu Arg Glu Glu Ser Val Val Lys Arg Thr Arg Val Gln Pro Gly Arg
385                 390                 395                 400
```

Met Phe Leu Val Asp Thr Ala Glu Gly Arg Ile Val Glu Asp Glu Glu
405 410 415

Ile Lys Gln Lys Leu Ser Glu Ala Gln Pro Tyr Gly Glu Trp Ile Arg
420 425 430

Asp Asn Phe Val His Leu Asp Arg Leu Pro Gln Thr Arg Tyr Asn Tyr
435 440 445

Met Ala His Ser Arg Ala Val Leu Arg Gln Arg Val Phe Gly Ile Thr
450 455 460

Glu Glu Asp Val Asp Leu Leu Leu Leu Pro Met Ala Arg Gln Gly Ala
465 470 475 480

Glu Ala Ile Gly Ser Met Gly Ser Asp Thr Pro Ile Ala Ala Leu Ser
485 490 495

Gln Arg Pro Arg Met Leu Tyr Asp Phe Phe Ala Gln Arg Phe Ala Gln
500 505 510

Val Thr Asn Pro Pro Leu Asp Ser Ile Arg Glu Lys Pro Val Thr Ser
515 520 525

Met Phe Thr Leu Leu Gly Ala Gln Ser Asp Val Leu Asn Pro Gly Pro
530 535 540

Asp Ala Ala Arg Arg Ile Arg Leu Glu Ser Pro Ile Ile Asp Asn His
545 550 555 560

Glu Leu Ala Thr Leu Ile Asn Ala Asn Ala His Gly Glu Trp Asp Ser
565 570 575

Phe Gly Ala Ala Val Ile Ser Gly Leu Tyr Pro Val Ala His His Gly
580 585 590

Ala Gly Met Lys Ala Ala Ile Ala Arg Val
595 600

<210> 75
<211> 1362
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (70)..(1362)
<223> FRXA00364

<400> 75
accaatttct ggcatcggtc tggatgaagt tgcagctgac gtagaaagct cgtcaccgca 60

gcgcattttttg cca cgc cct gaa gag cac gct cac cgt gaa ttg gat ttg 111
Leu Pro Arg Pro Glu Glu His Ala His Arg Glu Leu Asp Leu
1 5 10

ggt ggt gaa tac aag tgg cgc cgc gaa ggt gaa tac cac ctg ttc aac 159
Gly Gly Glu Tyr Lys Trp Arg Arg Glu Gly Glu Tyr His Leu Phe Asn
15 20 25 30

cca gaa acc atc ttc aag ctg cag cat gca acg cgt tct ggc agc tac 207
Pro Glu Thr Ile Phe Lys Leu Gln His Ala Thr Arg Ser Gly Ser Tyr
35 40 45

gag att ttc aag gat tac acc cgc aag gtt gat gat caa tcc act cgc 255
Glu Ile Phe Lys Asp Tyr Thr Arg Lys Val Asp Asp Gln Ser Thr Arg
50 55 60

ttg ggt act att cgt gga ctg ttt gag ttc agc acg gac cgc aag cca 303
Leu Gly Thr Ile Arg Gly Leu Phe Glu Phe Ser Thr Asp Arg Lys Pro
65 70 75

att tcg gtg tct gag gtg gag ccg gtc agt gag atc gtg aag cgt ttc 351
Ile Ser Val Ser Glu Val Glu Pro Val Ser Glu Ile Val Lys Arg Phe
80 85 90

tcc act ggt gcg atg tct tat ggc tcg att tct gct gaa gcc cat gag 399
Ser Thr Gly Ala Met Ser Tyr Gly Ser Ile Ser Ala Glu Ala His Glu
95 100 105 110

gtc ttg gcc atc gcc atg aac cga ctg ggc ggt atg tcc aac tcc ggc 447
Val Leu Ala Ile Ala Met Asn Arg Leu Gly Gly Met Ser Asn Ser Gly
115 120 125

gaa ggt ggc gag gac gcc cgc cga ttt gat gtg gaa ccc aac ggt gac 495
Glu Gly Gly Glu Asp Ala Arg Arg Phe Asp Val Glu Pro Asn Gly Asp
130 135 140

tgg aag cgc tct gcc att aag cag gtg gcc tcg gga cgt ttc ggc gtg 543
Trp Lys Arg Ser Ala Ile Lys Gln Val Ala Ser Gly Arg Phe Gly Val
145 150 155

acc agc cac tac ttg aac aac tgc acc gat att cag atc aag atg gca 591
Thr Ser His Tyr Leu Asn Asn Cys Thr Asp Ile Gln Ile Lys Met Ala
160 165 170

cag ggc gca aag ccc ggt gaa ggt ggc cag ctg cca cca aac aag gtg 639
Gln Gly Ala Lys Pro Gly Glu Gly Gly Gln Leu Pro Pro Asn Lys Val
175 180 185 190

tac cca tgg gtt gca gaa gtc cgc atc acc acc cca ggc gtt ggt ctg 687
Tyr Pro Trp Val Ala Glu Val Arg Ile Thr Thr Pro Gly Val Gly Leu
195 200 205

att tcc cct cca cca cac cac gat att tac tcc att gag gat ctg gct 735
Ile Ser Pro Pro Pro His His Asp Ile Tyr Ser Ile Glu Asp Leu Ala
210 215 220

cag ctg atc cac gac ctg aag aac gct aac cca cgc gca cga atc cac 783
Gln Leu Ile His Asp Leu Lys Asn Ala Asn Pro Arg Ala Arg Ile His
225 230 235

gtg aag cta gtg gca gaa caa ggc gtg ggc acc gtt gcc gca ggt gtg 831
Val Lys Leu Val Ala Glu Gln Gly Val Gly Thr Val Ala Ala Gly Val
240 245 250

tcc aaa gca cac gct gat gtg gtg ctt att tcc ggc cac gat ggc gga 879
Ser Lys Ala His Ala Asp Val Val Leu Ile Ser Gly His Asp Gly Gly
255 260 265 270

act ggc gca tct cct ttg acc tcc ctg aag cat gcc ggt ggt cca tgg 927

Thr Gly Ala Ser Pro Leu Thr Ser Leu Lys His Ala Gly Gly Pro Trp
275 280 285

gag ttg ggc ttg gct gaa acc cag caa acg ttg ctg ctc aac ggc ctg 975
Glu Leu Gly Leu Ala Glu Thr Gln Gln Thr Leu Leu Leu Asn Gly Leu
290 295 300

cgc gat cgt att cgc gtg cag tgc gat ggt cag ctg aaa act ggc cga
1023
Arg Asp Arg Ile Arg Val Gln Cys Asp Gly Gln Leu Lys Thr Gly Arg
305 310 315

gac gtg gtt atc gca gct ctt ctc ggt gcc gaa gaa ttc ggt ttt gcc
1071
Asp Val Val Ile Ala Ala Leu Leu Gly Ala Glu Glu Phe Gly Phe Ala
320 325 330

acc gca ccg ctg gtg gtt gaa ggc tgc atc atg atg cgc gtc tgc cac
1119
Thr Ala Pro Leu Val Val Glu Gly Cys Ile Met Met Arg Val Cys His
335 340 345 350

ctg gac acc tgc ccg gtg ggt atc gct acc cag aac ccg gat ttg cgt
1167
Leu Asp Thr Cys Pro Val Gly Ile Ala Thr Gln Asn Pro Asp Leu Arg
355 360 365

tcc aag ttc acc ggc aag gct gaa cac gtg gtc aac ttc ttc acc ttc
1215
Ser Lys Phe Thr Gly Lys Ala Glu His Val Val Asn Phe Phe Thr Phe
370 375 380

atc gcc cag gaa gtc cgt gag tac ttg gca cag ctt ggt ttc cgc tct
1263
Ile Ala Gln Glu Val Arg Glu Tyr Leu Ala Gln Leu Gly Phe Arg Ser
385 390 395

att gat gaa gcc gtc gga caa gcc cag gtg ctg cgc aag cgt tcc gga
1311
Ile Asp Glu Ala Val Gly Gln Ala Gln Val Leu Arg Lys Arg Ser Gly
400 405 410

atc cca gct gat tcc cgc gca gca cac ctg gat ttg agc cca att ttc
1359
Ile Pro Ala Asp Ser Arg Ala Ala His Leu Asp Leu Ser Pro Ile Phe
415 420 425 430

atc
1362
Ile

<210> 76
<211> 431
<212> PRT
<213> Corynebacterium glutamicum

<400> 76
Leu Pro Arg Pro Glu Glu His Ala His Arg Glu Leu Asp Leu Gly Gly
1 5 10 15

Glu Tyr Lys Trp Arg Arg Glu Gly Glu Tyr His Leu Phe Asn Pro Glu
20 25 30

Thr Ile Phe Lys Leu Gln His Ala Thr Arg Ser Gly Ser Tyr Glu Ile
35 40 45

Phe Lys Asp Tyr Thr Arg Lys Val Asp Asp Gln Ser Thr Arg Leu Gly
50 55 60

Thr Ile Arg Gly Leu Phe Glu Phe Ser Thr Asp Arg Lys Pro Ile Ser
65 70 75 80

Val Ser Glu Val Glu Pro Val Ser Glu Ile Val Lys Arg Phe Ser Thr
85 90 95

Gly Ala Met Ser Tyr Gly Ser Ile Ser Ala Glu Ala His Glu Val Leu
100 105 110

Ala Ile Ala Met Asn Arg Leu Gly Gly Met Ser Asn Ser Gly Glu Gly
115 120 125

Gly Glu Asp Ala Arg Arg Phe Asp Val Glu Pro Asn Gly Asp Trp Lys
130 135 140

Arg Ser Ala Ile Lys Gln Val Ala Ser Gly Arg Phe Gly Val Thr Ser
145 150 155 160

His Tyr Leu Asn Asn Cys Thr Asp Ile Gln Ile Lys Met Ala Gln Gly
165 170 175

Ala Lys Pro Gly Glu Gly Gly Gln Leu Pro Pro Asn Lys Val Tyr Pro
180 185 190

Trp Val Ala Glu Val Arg Ile Thr Thr Pro Gly Val Gly Leu Ile Ser
195 200 205

Pro Pro Pro His His Asp Ile Tyr Ser Ile Glu Asp Leu Ala Gln Leu
210 215 220

Ile His Asp Leu Lys Asn Ala Asn Pro Arg Ala Arg Ile His Val Lys
225 230 235 240

Leu Val Ala Glu Gln Gly Val Gly Thr Val Ala Ala Gly Val Ser Lys
245 250 255

Ala His Ala Asp Val Val Leu Ile Ser Gly His Asp Gly Gly Thr Gly
260 265 270

Ala Ser Pro Leu Thr Ser Leu Lys His Ala Gly Gly Pro Trp Glu Leu
275 280 285

Gly Leu Ala Glu Thr Gln Gln Thr Leu Leu Leu Asn Gly Leu Arg Asp
290 295 300

Arg Ile Arg Val Gln Cys Asp Gly Gln Leu Lys Thr Gly Arg Asp Val
305 310 315 320

Val Ile Ala Ala Leu Leu Gly Ala Glu Glu Phe Gly Phe Ala Thr Ala
325 330 335

```
Pro Leu Val Val Glu Gly Cys Ile Met Met Arg Val Cys His Leu Asp
            340                 345                 350

Thr Cys Pro Val Gly Ile Ala Thr Gln Asn Pro Asp Leu Arg Ser Lys
        355                 360                 365

Phe Thr Gly Lys Ala Glu His Val Val Asn Phe Phe Thr Phe Ile Ala
    370                 375                 380

Gln Glu Val Arg Glu Tyr Leu Ala Gln Leu Gly Phe Arg Ser Ile Asp
385                 390                 395                 400

Glu Ala Val Gly Gln Ala Gln Val Leu Arg Lys Arg Ser Gly Ile Pro
                405                 410                 415

Ala Asp Ser Arg Ala Ala His Leu Asp Leu Ser Pro Ile Phe Ile
            420                 425                 430


<210> 77
<211> 866
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(843)
<223> FRXA00367

<400> 77
cac agc cta gaa aaa gcc ctg gac aac gca ttt att gat aag gct tcg      48
His Ser Leu Glu Lys Ala Leu Asp Asn Ala Phe Ile Asp Lys Ala Ser
  1               5                  10                  15

gac acg atc acc cgt gcc gca gcg ggt gtg gaa acc agc att gtt att      96
Asp Thr Ile Thr Arg Ala Ala Ala Gly Val Glu Thr Ser Ile Val Ile
            20                  25                  30

gat agc tcc atc agc aac gtc aac cgt tca gtt ggc acg atg ctg ggt     144
Asp Ser Ser Ile Ser Asn Val Asn Arg Ser Val Gly Thr Met Leu Gly
        35                  40                  45

tct gca gtc agc cgc gtg gct ggt gcc caa ggt ttg cca gac ggc acc     192
Ser Ala Val Ser Arg Val Ala Gly Ala Gln Gly Leu Pro Asp Gly Thr
    50                  55                  60

atc acc ttg aat ctt caa ggc tgc gcc ggt aac tcc ttt ggc gcg ttc     240
Ile Thr Leu Asn Leu Gln Gly Cys Ala Gly Asn Ser Phe Gly Ala Phe
65                  70                  75                  80

atc cca cga ggc atc acc atc aac ctc acc ggc gat gcc aat gac ttt     288
Ile Pro Arg Gly Ile Thr Ile Asn Leu Thr Gly Asp Ala Asn Asp Phe
                85                  90                  95

gtg ggc aag gga tta tct ggc gga aag att gtg atc aag cct tcc gct     336
Val Gly Lys Gly Leu Ser Gly Gly Lys Ile Val Ile Lys Pro Ser Ala
            100                 105                 110

cag gct ccg aag cag ctg aag aac aat cca aat atc att gcc gga aac     384
Gln Ala Pro Lys Gln Leu Lys Asn Asn Pro Asn Ile Ile Ala Gly Asn
        115                 120                 125
```

gtg ctt gga tac ggc gca acc agt ggt gaa ttg ttc att cgt ggc cag 432
Val Leu Gly Tyr Gly Ala Thr Ser Gly Glu Leu Phe Ile Arg Gly Gln
130 135 140

gtc ggc gaa cgt ttc tgc gtc cgt aac tct ggc gcc acc gca gtg gtt 480
Val Gly Glu Arg Phe Cys Val Arg Asn Ser Gly Ala Thr Ala Val Val
145 150 155 160

gaa ggt atc gga aac cac ggt tgt gag tac atg act ggc ggc cga gtc 528
Glu Gly Ile Gly Asn His Gly Cys Glu Tyr Met Thr Gly Gly Arg Val
165 170 175

ctg gtt ttg ggc ccg gtt ggt gag aac ttt ggt gcc ggc atg tct ggt 576
Leu Val Leu Gly Pro Val Gly Glu Asn Phe Gly Ala Gly Met Ser Gly
180 185 190

ggc att gca tac ctg gct aat tcc ccg gac cta aac cag aag atc aat 624
Gly Ile Ala Tyr Leu Ala Asn Ser Pro Asp Leu Asn Gln Lys Ile Asn
195 200 205

ggc gaa ttg gtg gat gtt gtt cca ctg agc gct gac gat ctg acg tgg 672
Gly Glu Leu Val Asp Val Val Pro Leu Ser Ala Asp Asp Leu Thr Trp
210 215 220

gct gat gag ctc att gct cgc cac cgc gaa ctc acc gga tcc gag acc 720
Ala Asp Glu Leu Ile Ala Arg His Arg Glu Leu Thr Gly Ser Glu Thr
225 230 235 240

aag ctg cgt gca caa gat ttg gtg aaa atc atg ccg cgc gat ttc caa 768
Lys Leu Arg Ala Gln Asp Leu Val Lys Ile Met Pro Arg Asp Phe Gln
245 250 255

aaa gta ctc aac atc atc gaa acg gcc cac gct gag ggc caa gac cca 816
Lys Val Leu Asn Ile Ile Glu Thr Ala His Ala Glu Gly Gln Asp Pro
260 265 270

gca atc aag atc atg gag gca gtg agc taatggccga cccacaagga 863
Ala Ile Lys Ile Met Glu Ala Val Ser
275 280

ttc 866

<210> 78
<211> 281
<212> PRT
<213> Corynebacterium glutamicum

<400> 78
His Ser Leu Glu Lys Ala Leu Asp Asn Ala Phe Ile Asp Lys Ala Ser
1 5 10 15

Asp Thr Ile Thr Arg Ala Ala Ala Gly Val Glu Thr Ser Ile Val Ile
20 25 30

Asp Ser Ser Ile Ser Asn Val Asn Arg Ser Val Gly Thr Met Leu Gly
35 40 45

Ser Ala Val Ser Arg Val Ala Gly Ala Gln Gly Leu Pro Asp Gly Thr
50 55 60

Ile Thr Leu Asn Leu Gln Gly Cys Ala Gly Asn Ser Phe Gly Ala Phe
65 70 75 80

Ile Pro Arg Gly Ile Thr Ile Asn Leu Thr Gly Asp Ala Asn Asp Phe
85 90 95

Val Gly Lys Gly Leu Ser Gly Gly Lys Ile Val Ile Lys Pro Ser Ala
100 105 110

Gln Ala Pro Lys Gln Leu Lys Asn Asn Pro Asn Ile Ile Ala Gly Asn
115 120 125

Val Leu Gly Tyr Gly Ala Thr Ser Gly Glu Leu Phe Ile Arg Gly Gln
130 135 140

Val Gly Glu Arg Phe Cys Val Arg Asn Ser Gly Ala Thr Ala Val Val
145 150 155 160

Glu Gly Ile Gly Asn His Gly Cys Glu Tyr Met Thr Gly Gly Arg Val
165 170 175

Leu Val Leu Gly Pro Val Gly Glu Asn Phe Gly Ala Gly Met Ser Gly
180 185 190

Gly Ile Ala Tyr Leu Ala Asn Ser Pro Asp Leu Asn Gln Lys Ile Asn
195 200 205

Gly Glu Leu Val Asp Val Val Pro Leu Ser Ala Asp Asp Leu Thr Trp
210 215 220

Ala Asp Glu Leu Ile Ala Arg His Arg Glu Leu Thr Gly Ser Glu Thr
225 230 235 240

Lys Leu Arg Ala Gln Asp Leu Val Lys Ile Met Pro Arg Asp Phe Gln
245 250 255

Lys Val Leu Asn Ile Ile Glu Thr Ala His Ala Glu Gly Gln Asp Pro
260 265 270

Ala Ile Lys Ile Met Glu Ala Val Ser
275 280

<210> 79
<211> 1494
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1471)
<223> RXN00076

<400> 79
tctaggagtg ttaaacagcc tggacttgaa acacctttaa ctacttgatt ttcacaccct 60

tgtttccata aaagggctca cgaaaggcaa cttcaaacac atg aca act ccc ctg 115
Met Thr Thr Pro Leu
1 5

```
cgc gta gcc gtc atc gga gct ggc cct gct ggc att tac gca tcc gac     163
Arg Val Ala Val Ile Gly Ala Gly Pro Ala Gly Ile Tyr Ala Ser Asp
                10                  15                  20

ctc ctc atc cgc aat gaa gag cgc gaa gtg ttc gtt gac ctt ttc gag     211
Leu Leu Ile Arg Asn Glu Glu Arg Glu Val Phe Val Asp Leu Phe Glu
            25                  30                  35

caa atg cct gca ccg ttc gga ctc atc cgt tac ggc gtt gct cca gac     259
Gln Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr Gly Val Ala Pro Asp
        40                  45                  50

cac cca cgc atc aag ggc atc gtt aag tcc ctg cac aac gtg ttg gac     307
His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu His Asn Val Leu Asp
    55                  60                  65

aag cca cgc ctg cgc ctg ctc ggt aac att gaa atc ggc aaa gac atc     355
Lys Pro Arg Leu Arg Leu Leu Gly Asn Ile Glu Ile Gly Lys Asp Ile
70                  75                  80                  85

acc gtc gaa gaa ctc cgc gac tac tac gat gca gtc gtg ttc tcc acc     403
Thr Val Glu Glu Leu Arg Asp Tyr Tyr Asp Ala Val Val Phe Ser Thr
                90                  95                  100

ggc gca gtt gca gac cgc gac ctc aac atc ccc gga att gaa gca gaa     451
Gly Ala Val Ala Asp Arg Asp Leu Asn Ile Pro Gly Ile Glu Ala Glu
            105                 110                 115

ggc tcc ttc ggt gcc ggc gag ttc gtt ggc ttc tac gac ggc aac cca     499
Gly Ser Phe Gly Ala Gly Glu Phe Val Gly Phe Tyr Asp Gly Asn Pro
        120                 125                 130

cgc ttc gag cgc tcc tgg gat ctg tct gca cag tcc gtc gct gtt atc     547
Arg Phe Glu Arg Ser Trp Asp Leu Ser Ala Gln Ser Val Ala Val Ile
    135                 140                 145

ggc gtt ggt aac gtc ggc ctc gac gta gcc cgc atc ctg gct aag aca     595
Gly Val Gly Asn Val Gly Leu Asp Val Ala Arg Ile Leu Ala Lys Thr
150                 155                 160                 165

ggc gac gag ctc aaa gtc acc gaa att tcc gac aac gtc tac gac tcc     643
Gly Asp Glu Leu Lys Val Thr Glu Ile Ser Asp Asn Val Tyr Asp Ser
                170                 175                 180

ctc aaa gaa aac aag gcc act gaa gtg cac gtt ttc gga cgt cgt ggc     691
Leu Lys Glu Asn Lys Ala Thr Glu Val His Val Phe Gly Arg Arg Gly
            185                 190                 195

cca gca cag gtc aag ttc acc cca cag gaa ctc aaa gaa ctc gac cac     739
Pro Ala Gln Val Lys Phe Thr Pro Gln Glu Leu Lys Glu Leu Asp His
        200                 205                 210

tcc ccc acc atc aac gtg gtt gtt gat cca gaa gac atc gac tac gac     787
Ser Pro Thr Ile Asn Val Val Val Asp Pro Glu Asp Ile Asp Tyr Asp
    215                 220                 225

ggc gcc tct gaa gaa gcc cgc cgc gca tcc aag tcc cag gac ctg gtc     835
Gly Ala Ser Glu Glu Ala Arg Arg Ala Ser Lys Ser Gln Asp Leu Val
230                 235                 240                 245

tgc cag atc ctg gaa cag tac gca atc cgc gag cca aag gac gct ccg     883
```

Cys Gln Ile Leu Glu Gln Tyr Ala Ile Arg Glu Pro Lys Asp Ala Pro
250 255 260

cac acc ctg cag atc cac ctc ttt gaa aac cca gtt gag gtt ctt caa 931
His Thr Leu Gln Ile His Leu Phe Glu Asn Pro Val Glu Val Leu Gln
265 270 275

aag gac ggc aag gtt gtt ggc ctg cgc acc gaa cgc acc tca ctt gat 979
Lys Asp Gly Lys Val Val Gly Leu Arg Thr Glu Arg Thr Ser Leu Asp
280 285 290

ggc aac ggc ggc gta aac gga acc ggc gaa ttc aag gac tgg cca gtc
1027
Gly Asn Gly Gly Val Asn Gly Thr Gly Glu Phe Lys Asp Trp Pro Val
295 300 305

cag gct gtc tac cgc gca gtc ggc tac aag tcc gac ccc atc gac ggc
1075
Gln Ala Val Tyr Arg Ala Val Gly Tyr Lys Ser Asp Pro Ile Asp Gly
310 315 320 325

gtc cca ttc gat gag aac aag cac gtc atc cct aat gac ggc gga cat
1123
Val Pro Phe Asp Glu Asn Lys His Val Ile Pro Asn Asp Gly Gly His
330 335 340

gtc ctc acc gct cca ggc gca gaa cca gta cca ggc ctc tat gca acc
1171
Val Leu Thr Ala Pro Gly Ala Glu Pro Val Pro Gly Leu Tyr Ala Thr
345 350 355

ggc tgg atc aag cgt gga cca atc ggt cta atc ggc aac acc aag tcc
1219
Gly Trp Ile Lys Arg Gly Pro Ile Gly Leu Ile Gly Asn Thr Lys Ser
360 365 370

gac gcc aag gaa acc acc gac atc ctc atc aag gat gcc gtc gcc ggt
1267
Asp Ala Lys Glu Thr Thr Asp Ile Leu Ile Lys Asp Ala Val Ala Gly
375 380 385

gta ctt gaa gct cca aag cac cag ggc gaa gaa gcc atc atc gag ctt
1315
Val Leu Glu Ala Pro Lys His Gln Gly Glu Glu Ala Ile Ile Glu Leu
390 395 400 405

ctc gat tcc cgc aac atc cca ttc acc acc tgg gaa ggc tgg tac aaa
1363
Leu Asp Ser Arg Asn Ile Pro Phe Thr Thr Trp Glu Gly Trp Tyr Lys
410 415 420

ctc gac gca gca gag cgc gca ctc ggt gaa gcc gaa ggc cgc gag cgc
1411
Leu Asp Ala Ala Glu Arg Ala Leu Gly Glu Ala Glu Gly Arg Glu Arg
425 430 435

aag aag att gtt gat tgg gaa gaa atg gtc cgc cag gcc cgc gaa gct
1459
Lys Lys Ile Val Asp Trp Glu Glu Met Val Arg Gln Ala Arg Glu Ala
440 445 450

cca gca att gtc taaattgttt taacgcgtga agc
1494
Pro Ala Ile Val
455

<210> 80
<211> 457
<212> PRT
<213> Corynebacterium glutamicum

<400> 80
Met Thr Thr Pro Leu Arg Val Ala Val Ile Gly Ala Gly Pro Ala Gly
1 5 10 15

Ile Tyr Ala Ser Asp Leu Leu Ile Arg Asn Glu Glu Arg Glu Val Phe
20 25 30

Val Asp Leu Phe Glu Gln Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr
35 40 45

Gly Val Ala Pro Asp His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu
50 55 60

His Asn Val Leu Asp Lys Pro Arg Leu Arg Leu Leu Gly Asn Ile Glu
65 70 75 80

Ile Gly Lys Asp Ile Thr Val Glu Glu Leu Arg Asp Tyr Tyr Asp Ala
85 90 95

Val Val Phe Ser Thr Gly Ala Val Ala Asp Arg Asp Leu Asn Ile Pro
100 105 110

Gly Ile Glu Ala Glu Gly Ser Phe Gly Ala Gly Glu Phe Val Gly Phe
115 120 125

Tyr Asp Gly Asn Pro Arg Phe Glu Arg Ser Trp Asp Leu Ser Ala Gln
130 135 140

Ser Val Ala Val Ile Gly Val Gly Asn Val Gly Leu Asp Val Ala Arg
145 150 155 160

Ile Leu Ala Lys Thr Gly Asp Glu Leu Lys Val Thr Glu Ile Ser Asp
165 170 175

Asn Val Tyr Asp Ser Leu Lys Glu Asn Lys Ala Thr Glu Val His Val
180 185 190

Phe Gly Arg Arg Gly Pro Ala Gln Val Lys Phe Thr Pro Gln Glu Leu
195 200 205

Lys Glu Leu Asp His Ser Pro Thr Ile Asn Val Val Val Asp Pro Glu
210 215 220

Asp Ile Asp Tyr Asp Gly Ala Ser Glu Glu Ala Arg Arg Ala Ser Lys
225 230 235 240

Ser Gln Asp Leu Val Cys Gln Ile Leu Glu Gln Tyr Ala Ile Arg Glu
245 250 255

Pro Lys Asp Ala Pro His Thr Leu Gln Ile His Leu Phe Glu Asn Pro

260 265 270

Val Glu Val Leu Gln Lys Asp Gly Lys Val Val Gly Leu Arg Thr Glu
275 280 285

Arg Thr Ser Leu Asp Gly Asn Gly Gly Val Asn Gly Thr Gly Glu Phe
290 295 300

Lys Asp Trp Pro Val Gln Ala Val Tyr Arg Ala Val Gly Tyr Lys Ser
305 310 315 320

Asp Pro Ile Asp Gly Val Pro Phe Asp Glu Asn Lys His Val Ile Pro
325 330 335

Asn Asp Gly Gly His Val Leu Thr Ala Pro Gly Ala Glu Pro Val Pro
340 345 350

Gly Leu Tyr Ala Thr Gly Trp Ile Lys Arg Gly Pro Ile Gly Leu Ile
355 360 365

Gly Asn Thr Lys Ser Asp Ala Lys Glu Thr Thr Asp Ile Leu Ile Lys
370 375 380

Asp Ala Val Ala Gly Val Leu Glu Ala Pro Lys His Gln Gly Glu Glu
385 390 395 400

Ala Ile Ile Glu Leu Leu Asp Ser Arg Asn Ile Pro Phe Thr Thr Trp
405 410 415

Glu Gly Trp Tyr Lys Leu Asp Ala Ala Glu Arg Ala Leu Gly Glu Ala
420 425 430

Glu Gly Arg Glu Arg Lys Lys Ile Val Asp Trp Glu Glu Met Val Arg
435 440 445

Gln Ala Arg Glu Ala Pro Ala Ile Val
450 455

<210> 81
<211> 786
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(763)
<223> FRXA00075

<400> 81
tctaggagtg ttaaacagcc tggacttgaa acacctttaa ctacttgatt ttcacaccct 60

tgtttccata aaagggctca cgaaaggcaa cttcaaacac atg aca act ccc ctg 115
Met Thr Thr Pro Leu
1 5

cgc gta gcc gtc atc gga gct ggc cct gct ggc att tac gca tcc gac 163
Arg Val Ala Val Ile Gly Ala Gly Pro Ala Gly Ile Tyr Ala Ser Asp
10 15 20

ctc ctc atc cgc aat gaa gag cgc gaa gtg ttc gtt gac ctt ttc gag 211

Leu Leu Ile Arg Asn Glu Glu Arg Glu Val Phe Val Asp Leu Phe Glu
25 30 35

caa atg cct gca ccg ttc gga ctc atc cgt tac ggc gtt gct cca gac 259
Gln Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr Gly Val Ala Pro Asp
40 45 50

cac cca cgc atc aag ggc atc gtt aag tcc ctg cac aac gtg ttg gac 307
His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu His Asn Val Leu Asp
55 60 65

aag cca cgc ctg cgc ctg ctc ggt aac att gaa atc ggc aaa gac atc 355
Lys Pro Arg Leu Arg Leu Leu Gly Asn Ile Glu Ile Gly Lys Asp Ile
70 75 80 85

acc gtc gaa gaa ctc cgc gac tac tac gat gca gtc gtg ttc tcc acc 403
Thr Val Glu Glu Leu Arg Asp Tyr Tyr Asp Ala Val Val Phe Ser Thr
90 95 100

ggc gca gtt gca gac cgc gac ctc aac atc ccc gga att gaa gca gaa 451
Gly Ala Val Ala Asp Arg Asp Leu Asn Ile Pro Gly Ile Glu Ala Glu
105 110 115

ggc tcc ttc ggt gcc ggc gag ttc gtt ggc ttc tac gac ggc aac cca 499
Gly Ser Phe Gly Ala Gly Glu Phe Val Gly Phe Tyr Asp Gly Asn Pro
120 125 130

cgc ttc gag cgc tcc tgg gat ctg tct gca cag tcc gtc gct gtt atc 547
Arg Phe Glu Arg Ser Trp Asp Leu Ser Ala Gln Ser Val Ala Val Ile
135 140 145

ggc gtt ggt aac gtc ggc ctc gac gta gcc cgc atc ctg gct aag aca 595
Gly Val Gly Asn Val Gly Leu Asp Val Ala Arg Ile Leu Ala Lys Thr
150 155 160 165

ggc gac gag ctc aaa gtc acc gaa att tcc gac aac gtc tac gac tcc 643
Gly Asp Glu Leu Lys Val Thr Glu Ile Ser Asp Asn Val Tyr Asp Ser
170 175 180

ctc aaa gaa aac aag gyc wct gaa gtg cac gtt ttc gga cgt cgg tgg 691
Leu Lys Glu Asn Lys Xaa Xaa Glu Val His Val Phe Gly Arg Arg Trp
185 190 195

ccc agc aca ggt caa gtt cac ccc aca gga act maa aga act cgr cca 739
Pro Ser Thr Gly Gln Val His Pro Thr Gly Thr Xaa Arg Thr Xaa Pro
200 205 210

ctc ccc cac cat caa cgt ggt tgt tgatccagaa gacatcgact acg 786
Leu Pro His His Gln Arg Gly Cys
215 220

<210> 82
<211> 221
<212> PRT
<213> Corynebacterium glutamicum

<400> 82
Met Thr Thr Pro Leu Arg Val Ala Val Ile Gly Ala Gly Pro Ala Gly
1 5 10 15

Ile Tyr Ala Ser Asp Leu Leu Ile Arg Asn Glu Glu Arg Glu Val Phe
20 25 30

Val Asp Leu Phe Glu Gln Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr
35 40 45

Gly Val Ala Pro Asp His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu
50 55 60

His Asn Val Leu Asp Lys Pro Arg Leu Arg Leu Leu Gly Asn Ile Glu
65 70 75 80

Ile Gly Lys Asp Ile Thr Val Glu Glu Leu Arg Asp Tyr Tyr Asp Ala
85 90 95

Val Val Phe Ser Thr Gly Ala Val Ala Asp Arg Asp Leu Asn Ile Pro
100 105 110

Gly Ile Glu Ala Glu Gly Ser Phe Gly Ala Gly Glu Phe Val Gly Phe
115 120 125

Tyr Asp Gly Asn Pro Arg Phe Glu Arg Ser Trp Asp Leu Ser Ala Gln
130 135 140

Ser Val Ala Val Ile Gly Val Gly Asn Val Gly Leu Asp Val Ala Arg
145 150 155 160

Ile Leu Ala Lys Thr Gly Asp Glu Leu Lys Val Thr Glu Ile Ser Asp
165 170 175

Asn Val Tyr Asp Ser Leu Lys Glu Asn Lys Xaa Xaa Glu Val His Val
180 185 190

Phe Gly Arg Arg Trp Pro Ser Thr Gly Gln Val His Pro Thr Gly Thr
195 200 205

Xaa Arg Thr Xaa Pro Leu Pro His His Gln Arg Gly Cys
210 215 220

<210> 83
<211> 672
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(649)
<223> RXN00198

<400> 83
atgcaggatt agagcagcag caacggagcc agaatcagtc tcccaatttg atatccagcc 60

ccgcgctcct ttccagcgcg ccgattccac tccatggccg atg tac ccc aac ctc 115
Met Tyr Pro Asn Leu
1 5

ttc cgc acc gca acg gct cac gaa gaa ggc gaa tac atc atc act ggc 163
Phe Arg Thr Ala Thr Ala His Glu Glu Gly Glu Tyr Ile Ile Thr Gly
10 15 20

gat gaa tca gcc gat gaa atc gca gcc ctg ggc ctc gcc gaa cgt gcc 211
Asp Glu Ser Ala Asp Glu Ile Ala Ala Leu Gly Leu Ala Glu Arg Ala
25 30 35

gca ggc tcc acg ctt ggt gaa cgt aaa ttt gct gtc aac acc gtg gaa 259
Ala Gly Ser Thr Leu Gly Glu Arg Lys Phe Ala Val Asn Thr Val Glu
40 45 50

ttc cac ggc aac aac ggc cac gtc acc gga ctc acc ggc aac caa atc 307
Phe His Gly Asn Asn Gly His Val Thr Gly Leu Thr Gly Asn Gln Ile
55 60 65

cga gtt gtc aac ggc aaa cgt gaa cca atc gaa ggc acc gaa ttc ccc 355
Arg Val Val Asn Gly Lys Arg Glu Pro Ile Glu Gly Thr Glu Phe Pro
70 75 80 85

ttc gaa gca gac ctc gtt ctt gtt gca ctt ggc ttc acc ggc gca gaa 403
Phe Glu Ala Asp Leu Val Leu Val Ala Leu Gly Phe Thr Gly Ala Glu
90 95 100

caa ggc gga ttg gca cac gaa cta ggc gta ggt ttc gac gac cgg ggc 451
Gln Gly Gly Leu Ala His Glu Leu Gly Val Gly Phe Asp Asp Arg Gly
105 110 115

cgc atc ctc cgc gat tcc gaa tac cgc agc ccc acc aac tcc cgc gtt 499
Arg Ile Leu Arg Asp Ser Glu Tyr Arg Ser Pro Thr Asn Ser Arg Val
120 125 130

tac atc gca ggc gac aac ggc cgt ggc cag tcc ctg atc gtg tgg gca 547
Tyr Ile Ala Gly Asp Asn Gly Arg Gly Gln Ser Leu Ile Val Trp Ala
135 140 145

atc gcc gaa ggc cgc gca tgc gcc gca gct atc gac gcc gat ctc atg 595
Ile Ala Glu Gly Arg Ala Cys Ala Ala Ala Ile Asp Ala Asp Leu Met
150 155 160 165

ggt gaa act gca ctc cct gta gca gtt gca cca cag gac gtg ccg ctg 643
Gly Glu Thr Ala Leu Pro Val Ala Val Ala Pro Gln Asp Val Pro Leu
170 175 180

gct gtc tagcttgggt agaaaatgct aga 672
Ala Val

<210> 84
<211> 183
<212> PRT
<213> Corynebacterium glutamicum

<400> 84
Met Tyr Pro Asn Leu Phe Arg Thr Ala Thr Ala His Glu Glu Gly Glu
1 5 10 15

Tyr Ile Ile Thr Gly Asp Glu Ser Ala Asp Glu Ile Ala Ala Leu Gly
20 25 30

Leu Ala Glu Arg Ala Ala Gly Ser Thr Leu Gly Glu Arg Lys Phe Ala
35 40 45

Val Asn Thr Val Glu Phe His Gly Asn Asn Gly His Val Thr Gly Leu

```
        50                  55                  60

Thr Gly Asn Gln Ile Arg Val Val Asn Gly Lys Arg Glu Pro Ile Glu
65                  70                  75                  80

Gly Thr Glu Phe Pro Phe Glu Ala Asp Leu Val Leu Val Ala Leu Gly
                85                  90                  95

Phe Thr Gly Ala Glu Gln Gly Gly Leu Ala His Glu Leu Gly Val Gly
            100                 105                 110

Phe Asp Asp Arg Gly Arg Ile Leu Arg Asp Ser Glu Tyr Arg Ser Pro
        115                 120                 125

Thr Asn Ser Arg Val Tyr Ile Ala Gly Asp Asn Gly Arg Gly Gln Ser
    130                 135                 140

Leu Ile Val Trp Ala Ile Ala Glu Gly Arg Ala Cys Ala Ala Ala Ile
145                 150                 155                 160

Asp Ala Asp Leu Met Gly Glu Thr Ala Leu Pro Val Ala Val Ala Pro
                165                 170                 175

Gln Asp Val Pro Leu Ala Val
            180


<210> 85
<211> 305
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(282)
<223> FRXA00198

<400> 85
ctc gtt ctt gtt gca ctt ggc ttc acc ggc gca gaa caa ggc gga ttg      48
Leu Val Leu Val Ala Leu Gly Phe Thr Gly Ala Glu Gln Gly Gly Leu
1               5                   10                  15

gca cac gaa cta ggc gta ggt ttc gac gac cgg ggc cgc atc ctc cgc      96
Ala His Glu Leu Gly Val Gly Phe Asp Asp Arg Gly Arg Ile Leu Arg
            20                  25                  30

gat tcc gaa tac cgc agc ccc acc aac tcc cgc gtt tac atc gca ggc      144
Asp Ser Glu Tyr Arg Ser Pro Thr Asn Ser Arg Val Tyr Ile Ala Gly
        35                  40                  45

gac aac ggc cgt ggc cag tcc ctg atc gtg tgg gca atc gcc gaa ggc      192
Asp Asn Gly Arg Gly Gln Ser Leu Ile Val Trp Ala Ile Ala Glu Gly
    50                  55                  60

cgc gca tgc gcc gca gct atc gac gcc gat ctc atg ggt gaa act gca      240
Arg Ala Cys Ala Ala Ala Ile Asp Ala Asp Leu Met Gly Glu Thr Ala
65                  70                  75                  80

ctc cct gta gca gtt gca cca cag gac gtg ccg ctg gct gtc              282
Leu Pro Val Ala Val Ala Pro Gln Asp Val Pro Leu Ala Val
                85                  90
```

tagcttgggt agaaaatgct aga 305

<210> 86
<211> 94
<212> PRT
<213> Corynebacterium glutamicum

<400> 86
Leu Val Leu Val Ala Leu Gly Phe Thr Gly Ala Glu Gln Gly Gly Leu
1 5 10 15

Ala His Glu Leu Gly Val Gly Phe Asp Asp Arg Gly Arg Ile Leu Arg
20 25 30

Asp Ser Glu Tyr Arg Ser Pro Thr Asn Ser Arg Val Tyr Ile Ala Gly
35 40 45

Asp Asn Gly Arg Gly Gln Ser Leu Ile Val Trp Ala Ile Ala Glu Gly
50 55 60

Arg Ala Cys Ala Ala Ala Ile Asp Ala Asp Leu Met Gly Glu Thr Ala
65 70 75 80

Leu Pro Val Ala Val Ala Pro Gln Asp Val Pro Leu Ala Val
85 90

<210> 87
<211> 727
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(727)
<223> RXN00365

<400> 87
gaagcctacg atcgcttgca cgcgaccaac aatttccccg agttcaccgg ccgtttgtgc 60

cccgcaccct gcgaaggcgc ctgcgtgctc ggtatcaacg atg att ctg tca cca 115
Met Ile Leu Ser Pro
1 5

tca aaa acg ttt gag ctg gaa atc gtc gaa aaa gca ttc cgc gaa ggc 163
Ser Lys Thr Phe Glu Leu Glu Ile Val Glu Lys Ala Phe Arg Glu Gly
10 15 20

tgg gtg caa cca gta atc cca tcc atg tct acc ggg ctg tca gtc gcc 211
Trp Val Gln Pro Val Ile Pro Ser Met Ser Thr Gly Leu Ser Val Ala
25 30 35

gtc gtc ggt tcc ggc ccc gct ggc ctt gcc gcc gcg cag cag ctc acc 259
Val Val Gly Ser Gly Pro Ala Gly Leu Ala Ala Ala Gln Gln Leu Thr
40 45 50

cgc gca ggc cac agc gtt acc gtc ttt gaa cgc gac gac cgc ctc ggc 307
Arg Ala Gly His Ser Val Thr Val Phe Glu Arg Asp Asp Arg Leu Gly
55 60 65

ggc ctc atg cgc tac ggc gtg cca gaa tac aaa atg gag aac cgc tgg 355
Gly Leu Met Arg Tyr Gly Val Pro Glu Tyr Lys Met Glu Asn Arg Trp
70 75 80 85

atc gac cgc cgc atc gag caa atg gaa gca gag ggc aca act ttc cag 403
Ile Asp Arg Arg Ile Glu Gln Met Glu Ala Glu Gly Thr Thr Phe Gln
90 95 100

gta ggc acc tcg ccg cgc gcc gct gaa cta gcg ctt ttc gac gcg atc 451
Val Gly Thr Ser Pro Arg Ala Ala Glu Leu Ala Leu Phe Asp Ala Ile
105 110 115

ctc ctc gca acc ggc acc cca gtg gcc cgc gaa ctc tca gtt cca ggc 499
Leu Leu Ala Thr Gly Thr Pro Val Ala Arg Glu Leu Ser Val Pro Gly
120 125 130

cac gat ctc aac ggc atc cat gcg gca atg gat tac ctc acc gcc caa 547
His Asp Leu Asn Gly Ile His Ala Ala Met Asp Tyr Leu Thr Ala Gln
135 140 145

aac cgc atc aac gaa ggc gac ggt gaa gtc tct cca atc aac gcc aaa 595
Asn Arg Ile Asn Glu Gly Asp Gly Glu Val Ser Pro Ile Asn Ala Lys
150 155 160 165

ggc aag aaa gtt gtc atc atc ggt ggc ggc gac acc ggc acc gac tgc 643
Gly Lys Lys Val Val Ile Ile Gly Gly Gly Asp Thr Gly Thr Asp Cys
170 175 180

ttc ggc acc gca ctg cgc caa gga gca gaa tca gtc acc caa ttt gat 691
Phe Gly Thr Ala Leu Arg Gln Gly Ala Glu Ser Val Thr Gln Phe Asp
185 190 195

atc cgc ccc cgc gct cct ttc cag cgc gcc gat tcc 727
Ile Arg Pro Arg Ala Pro Phe Gln Arg Ala Asp Ser
200 205

<210> 88
<211> 209
<212> PRT
<213> Corynebacterium glutamicum

<400> 88
Met Ile Leu Ser Pro Ser Lys Thr Phe Glu Leu Glu Ile Val Glu Lys
1 5 10 15

Ala Phe Arg Glu Gly Trp Val Gln Pro Val Ile Pro Ser Met Ser Thr
20 25 30

Gly Leu Ser Val Ala Val Val Gly Ser Gly Pro Ala Gly Leu Ala Ala
35 40 45

Ala Gln Gln Leu Thr Arg Ala Gly His Ser Val Thr Val Phe Glu Arg
50 55 60

Asp Asp Arg Leu Gly Gly Leu Met Arg Tyr Gly Val Pro Glu Tyr Lys
65 70 75 80

Met Glu Asn Arg Trp Ile Asp Arg Arg Ile Glu Gln Met Glu Ala Glu
85 90 95

Gly Thr Thr Phe Gln Val Gly Thr Ser Pro Arg Ala Ala Glu Leu Ala
100 105 110

Leu Phe Asp Ala Ile Leu Leu Ala Thr Gly Thr Pro Val Ala Arg Glu
115 120 125

Leu Ser Val Pro Gly His Asp Leu Asn Gly Ile His Ala Ala Met Asp
130 135 140

Tyr Leu Thr Ala Gln Asn Arg Ile Asn Glu Gly Asp Gly Glu Val Ser
145 150 155 160

Pro Ile Asn Ala Lys Gly Lys Lys Val Val Ile Ile Gly Gly Gly Asp
165 170 175

Thr Gly Thr Asp Cys Phe Gly Thr Ala Leu Arg Gln Gly Ala Glu Ser
180 185 190

Val Thr Gln Phe Asp Ile Arg Pro Arg Ala Pro Phe Gln Arg Ala Asp
195 200 205

Ser

<210> 89
<211> 727
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(727)
<223> FRXA00365

<400> 89
gaagcctacg atcgcttgca cgcgaccaac aatttccccg agttcaccgg ccgtttgtgc 60

cccgcaccct gcgaaggcgc ctgcgtgctc ggtatcaacg atg att ctg tca cca 115
Met Ile Leu Ser Pro
1 5

tca aaa acg ttt gag ctg gaa atc gtc gaa aaa gca ttc cgc gaa ggc 163
Ser Lys Thr Phe Glu Leu Glu Ile Val Glu Lys Ala Phe Arg Glu Gly
10 15 20

tgg gtg caa cca gta atc cca tcc atg tct acc ggg ctg tca gtc gcc 211
Trp Val Gln Pro Val Ile Pro Ser Met Ser Thr Gly Leu Ser Val Ala
25 30 35

gtc gtc ggt tcc ggc ccc gct ggc ctt gcc gcc gcg cag cag ctc acc 259
Val Val Gly Ser Gly Pro Ala Gly Leu Ala Ala Ala Gln Gln Leu Thr
40 45 50

cgc gca ggc cac agc gtt acc gtc ttt gaa cgc gac gac cgc ctc ggc 307
Arg Ala Gly His Ser Val Thr Val Phe Glu Arg Asp Asp Arg Leu Gly
55 60 65

ggc ctc atg cgc tac ggc gtg cca gaa tac aaa atg gag aac cgc tgg 355
Gly Leu Met Arg Tyr Gly Val Pro Glu Tyr Lys Met Glu Asn Arg Trp

70 75 80 85

atc gac cgc cgc atc gag caa atg gaa gca gag ggc aca act ttc cag 403
Ile Asp Arg Arg Ile Glu Gln Met Glu Ala Glu Gly Thr Thr Phe Gln
90 95 100

gta ggc acc tcg ccg cgc gcc gct gaa cta gcg ctt ttc gac gcg atc 451
Val Gly Thr Ser Pro Arg Ala Ala Glu Leu Ala Leu Phe Asp Ala Ile
105 110 115

ctc ctc gca acc ggc acc cca gtg gcc cgc gaa ctc tca gtt cca ggc 499
Leu Leu Ala Thr Gly Thr Pro Val Ala Arg Glu Leu Ser Val Pro Gly
120 125 130

cac gat ctc aac ggc atc cat gcg gca atg gat tac ctc acc gcc caa 547
His Asp Leu Asn Gly Ile His Ala Ala Met Asp Tyr Leu Thr Ala Gln
135 140 145

aac cgc atc aac gaa ggc gac ggt gaa gtc tct cca atc aac gcc aaa 595
Asn Arg Ile Asn Glu Gly Asp Gly Glu Val Ser Pro Ile Asn Ala Lys
150 155 160 165

ggc aag aaa gtt gtc atc atc ggt ggc ggc gac acc ggc acc gac tgc 643
Gly Lys Lys Val Val Ile Ile Gly Gly Gly Asp Thr Gly Thr Asp Cys
170 175 180

ttc ggc acc gca ctg cgc caa gga gca gaa tca gtc acc caa ttt gat 691
Phe Gly Thr Ala Leu Arg Gln Gly Ala Glu Ser Val Thr Gln Phe Asp
185 190 195

atc cgc ccc cgc gct cct ttc cag cgc gcc gat tcc 727
Ile Arg Pro Arg Ala Pro Phe Gln Arg Ala Asp Ser
200 205

<210> 90
<211> 209
<212> PRT
<213> Corynebacterium glutamicum

<400> 90
Met Ile Leu Ser Pro Ser Lys Thr Phe Glu Leu Glu Ile Val Glu Lys
1 5 10 15

Ala Phe Arg Glu Gly Trp Val Gln Pro Val Ile Pro Ser Met Ser Thr
20 25 30

Gly Leu Ser Val Ala Val Val Gly Ser Gly Pro Ala Gly Leu Ala Ala
35 40 45

Ala Gln Gln Leu Thr Arg Ala Gly His Ser Val Thr Val Phe Glu Arg
50 55 60

Asp Asp Arg Leu Gly Gly Leu Met Arg Tyr Gly Val Pro Glu Tyr Lys
65 70 75 80

Met Glu Asn Arg Trp Ile Asp Arg Arg Ile Glu Gln Met Glu Ala Glu
85 90 95

Gly Thr Thr Phe Gln Val Gly Thr Ser Pro Arg Ala Ala Glu Leu Ala
100 105 110

```
Leu Phe Asp Ala Ile Leu Leu Ala Thr Gly Thr Pro Val Ala Arg Glu
        115                 120                 125

Leu Ser Val Pro Gly His Asp Leu Asn Gly Ile His Ala Ala Met Asp
    130                 135                 140

Tyr Leu Thr Ala Gln Asn Arg Ile Asn Glu Gly Asp Gly Glu Val Ser
145                 150                 155                 160

Pro Ile Asn Ala Lys Gly Lys Lys Val Val Ile Ile Gly Gly Gly Asp
                165                 170                 175

Thr Gly Thr Asp Cys Phe Gly Thr Ala Leu Arg Gln Gly Ala Glu Ser
            180                 185                 190

Val Thr Gln Phe Asp Ile Arg Pro Arg Ala Pro Phe Gln Arg Ala Asp
        195                 200                 205

Ser



&lt;210&gt; 91
&lt;211&gt; 480
&lt;212&gt; DNA
&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; (101)..(457)
&lt;223&gt; RXA00366

&lt;400&gt; 91
aaatcatgcc gcgcgatttc caaaaagtac tcaacatcat cgaaacggcc cacgctgagg 60

gccaagaccc agcaatcaag atcatggagg cagtgagcta atg gcc gac cca caa   115
                                           Met Ala Asp Pro Gln
                                           1               5

gga ttc atc aaa tac tcc cga cgc gag cct gca cac cgc ccg gtc ccg   163
Gly Phe Ile Lys Tyr Ser Arg Arg Glu Pro Ala His Arg Pro Val Pro
                10                  15                  20

ctg cgc ctc atg gac cac tcc gag gtc tac gaa aag gca ccg gca ggt   211
Leu Arg Leu Met Asp His Ser Glu Val Tyr Glu Lys Ala Pro Ala Gly
            25                  30                  35

cag atc gag gaa cag gct gcc cgc tgc atg gat tgc ggt gtc ccg ttc   259
Gln Ile Glu Glu Gln Ala Ala Arg Cys Met Asp Cys Gly Val Pro Phe
        40                  45                  50

tgc cac gaa ggc tgc cca ctg ggc aac atc atc cct gag tgg aat gat   307
Cys His Glu Gly Cys Pro Leu Gly Asn Ile Ile Pro Glu Trp Asn Asp
    55                  60                  65

ctg gta cgc caa ggt cgg tgg aag gaa gcc tac gat cgc ttg cac gcg   355
Leu Val Arg Gln Gly Arg Trp Lys Glu Ala Tyr Asp Arg Leu His Ala
70                  75                  80                  85

acc aac aat ttc ccc gag ttc acc ggc cgt ttg tgc ccc gca ccc tgc   403
```

Thr Asn Asn Phe Pro Glu Phe Thr Gly Arg Leu Cys Pro Ala Pro Cys
90 95 100

gaa ggc gcc tgc gtg ctc ggt atc aac gat gat tct gtc acc atc aaa 451
Glu Gly Ala Cys Val Leu Gly Ile Asn Asp Asp Ser Val Thr Ile Lys
105 110 115

aac gtt tgagctggaa atcgtcgaaa aag 480
Asn Val

<210> 92
<211> 119
<212> PRT
<213> Corynebacterium glutamicum

<400> 92
Met Ala Asp Pro Gln Gly Phe Ile Lys Tyr Ser Arg Arg Glu Pro Ala
1 5 10 15

His Arg Pro Val Pro Leu Arg Leu Met Asp His Ser Glu Val Tyr Glu
20 25 30

Lys Ala Pro Ala Gly Gln Ile Glu Glu Gln Ala Ala Arg Cys Met Asp
35 40 45

Cys Gly Val Pro Phe Cys His Glu Gly Cys Pro Leu Gly Asn Ile Ile
50 55 60

Pro Glu Trp Asn Asp Leu Val Arg Gln Gly Arg Trp Lys Glu Ala Tyr
65 70 75 80

Asp Arg Leu His Ala Thr Asn Asn Phe Pro Glu Phe Thr Gly Arg Leu
85 90 95

Cys Pro Ala Pro Cys Glu Gly Ala Cys Val Leu Gly Ile Asn Asp Asp
100 105 110

Ser Val Thr Ile Lys Asn Val
115

<210> 93
<211> 1464
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1441)
<223> RXA02072

<400> 93
tacatggtgc cctcaatggg aaccaccaac atcactaaat ggcccaggta cacactttaa 60

aatcgtgcgc gcatgcagcc gagatgggaa cgaggaaatc atg aca gtt gat gag 115
Met Thr Val Asp Glu
1 5

cag gtc tct aac tat tac gac atg ctt ctg aag cgc aat gct ggc gag 163

Gln Val Ser Asn Tyr Tyr Asp Met Leu Leu Lys Arg Asn Ala Gly Glu
10 15 20

cct gaa ttt cac cag gca gtg gca gag gtt ttg gaa tct ttg aag atc 211
Pro Glu Phe His Gln Ala Val Ala Glu Val Leu Glu Ser Leu Lys Ile
25 30 35

gtc ctg gaa aag gac cct cat tac gct gat tac ggt ctc atc cag cgc 259
Val Leu Glu Lys Asp Pro His Tyr Ala Asp Tyr Gly Leu Ile Gln Arg
40 45 50

ctg tgc gag cct gag cgt cag ctc atc ttc cgt gtg cct tgg gtt gat 307
Leu Cys Glu Pro Glu Arg Gln Leu Ile Phe Arg Val Pro Trp Val Asp
55 60 65

gac cag ggc cag gtc cac gtc aac cgt ggt ttc cgc gtg cag ttc aac 355
Asp Gln Gly Gln Val His Val Asn Arg Gly Phe Arg Val Gln Phe Asn
70 75 80 85

tct gca ctt gga cca tac aag ggc ggc ctg cgc ttc cac cca tct gta 403
Ser Ala Leu Gly Pro Tyr Lys Gly Gly Leu Arg Phe His Pro Ser Val
90 95 100

aac ctg ggc att gtg aag ttc ctg ggc ttt gag cag atc ttt aaa aac 451
Asn Leu Gly Ile Val Lys Phe Leu Gly Phe Glu Gln Ile Phe Lys Asn
105 110 115

tcc cta acc ggc ctg cca atc ggt ggt ggc aag ggt gga tcc gac ttc 499
Ser Leu Thr Gly Leu Pro Ile Gly Gly Gly Lys Gly Gly Ser Asp Phe
120 125 130

gac cct aag ggc aag tcc gat ctg gaa atc atg cgt ttc tgc cag tcc 547
Asp Pro Lys Gly Lys Ser Asp Leu Glu Ile Met Arg Phe Cys Gln Ser
135 140 145

ttc atg acc gag ctg cac cgc cac atc ggt gag tac cgc gac gtt cct 595
Phe Met Thr Glu Leu His Arg His Ile Gly Glu Tyr Arg Asp Val Pro
150 155 160 165

gca ggt aac atc gga gtt ggt ggc cac gag atc ggt tac ctg ttt ggc 643
Ala Gly Asn Ile Gly Val Gly Gly His Glu Ile Gly Tyr Leu Phe Gly
170 175 180

cac tac cgt cgc atg gct aac cag cac gag tcc ggc gtt ttg acc ggt 691
His Tyr Arg Arg Met Ala Asn Gln His Glu Ser Gly Val Leu Thr Gly
185 190 195

aag ggc ctg acc tgg ggt gga tcc ctg gtc cgc acc gag gca act ggc 739
Lys Gly Leu Thr Trp Gly Gly Ser Leu Val Arg Thr Glu Ala Thr Gly
200 205 210

tac ggc tgc gtt tac ttc gtg agt gaa atg atc aag gct aag ggc gag 787
Tyr Gly Cys Val Tyr Phe Val Ser Glu Met Ile Lys Ala Lys Gly Glu
215 220 225

agc atc agc ggc cag aag atc atc gtt tcc ggt tcc ggc aac gta gca 835
Ser Ile Ser Gly Gln Lys Ile Ile Val Ser Gly Ser Gly Asn Val Ala
230 235 240 245

acc tac gcg att gaa aag gct cag gaa ctc ggc gca acc gtt att ggt 883
Thr Tyr Ala Ile Glu Lys Ala Gln Glu Leu Gly Ala Thr Val Ile Gly

```
                250                 255                 260

ttc tcc gat tcc agc ggt tgg gtt cat acc cct aac ggc gtt gac gtg    931
Phe Ser Asp Ser Ser Gly Trp Val His Thr Pro Asn Gly Val Asp Val
            265                 270                 275

gct aag ctc cgc gaa atc aag gaa gtt cgt cgc gca cgc gta tcc gtg    979
Ala Lys Leu Arg Glu Ile Lys Glu Val Arg Arg Ala Arg Val Ser Val
        280                 285                 290

tac gcc gac gaa gtt gaa ggc gca acc tac cac acc gac ggt tcc atc
1027
Tyr Ala Asp Glu Val Glu Gly Ala Thr Tyr His Thr Asp Gly Ser Ile
    295                 300                 305

tgg gat ctc aag tgc gat atc gct ctt cct tgt gca act cag aac gag
1075
Trp Asp Leu Lys Cys Asp Ile Ala Leu Pro Cys Ala Thr Gln Asn Glu
310                 315                 320                 325

ctc aac ggc gag aac gct aag act ctt gca gac aac ggc tgc cgt ttc
1123
Leu Asn Gly Glu Asn Ala Lys Thr Leu Ala Asp Asn Gly Cys Arg Phe
                330                 335                 340

gtt gct gaa ggc gcg aac atg cct tcc acc cct gag gct gtt gag gtc
1171
Val Ala Glu Gly Ala Asn Met Pro Ser Thr Pro Glu Ala Val Glu Val
            345                 350                 355

ttc cgt gag cgc gac atc cgc ttc gga cca ggc aag gca gct aac gct
1219
Phe Arg Glu Arg Asp Ile Arg Phe Gly Pro Gly Lys Ala Ala Asn Ala
        360                 365                 370

ggt ggc gtt gca acc tcc gct ctg gag atg cag cag aac gct tcg cgc
1267
Gly Gly Val Ala Thr Ser Ala Leu Glu Met Gln Gln Asn Ala Ser Arg
    375                 380                 385

gat tcc tgg agc ttc gag tac acc gac gag cgc ctc cag gtg atc atg
1315
Asp Ser Trp Ser Phe Glu Tyr Thr Asp Glu Arg Leu Gln Val Ile Met
390                 395                 400                 405

aag aac atc ttc aag acc tgt gca gag acc gca gca gag tat gga cac
1363
Lys Asn Ile Phe Lys Thr Cys Ala Glu Thr Ala Ala Glu Tyr Gly His
                410                 415                 420

gag aac gat tac gtt gtc ggc gct aac att gct ggc ttc aag aag gta
1411
Glu Asn Asp Tyr Val Val Gly Ala Asn Ile Ala Gly Phe Lys Lys Val
            425                 430                 435

gct gac gcg atg ctg gca cag ggc gtc atc taagacccct gcgctttact
1461
Ala Asp Ala Met Leu Ala Gln Gly Val Ile
        440                 445
```

taa
1464

<210> 94
<211> 447
<212> PRT
<213> Corynebacterium glutamicum

<400> 94
Met Thr Val Asp Glu Gln Val Ser Asn Tyr Tyr Asp Met Leu Leu Lys
1 5 10 15

Arg Asn Ala Gly Glu Pro Glu Phe His Gln Ala Val Ala Glu Val Leu
20 25 30

Glu Ser Leu Lys Ile Val Leu Glu Lys Asp Pro His Tyr Ala Asp Tyr
35 40 45

Gly Leu Ile Gln Arg Leu Cys Glu Pro Glu Arg Gln Leu Ile Phe Arg
50 55 60

Val Pro Trp Val Asp Asp Gln Gly Gln Val His Val Asn Arg Gly Phe
65 70 75 80

Arg Val Gln Phe Asn Ser Ala Leu Gly Pro Tyr Lys Gly Gly Leu Arg
85 90 95

Phe His Pro Ser Val Asn Leu Gly Ile Val Lys Phe Leu Gly Phe Glu
100 105 110

Gln Ile Phe Lys Asn Ser Leu Thr Gly Leu Pro Ile Gly Gly Gly Lys
115 120 125

Gly Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Asp Leu Glu Ile Met
130 135 140

Arg Phe Cys Gln Ser Phe Met Thr Glu Leu His Arg His Ile Gly Glu
145 150 155 160

Tyr Arg Asp Val Pro Ala Gly Asn Ile Gly Val Gly Gly His Glu Ile
165 170 175

Gly Tyr Leu Phe Gly His Tyr Arg Arg Met Ala Asn Gln His Glu Ser
180 185 190

Gly Val Leu Thr Gly Lys Gly Leu Thr Trp Gly Gly Ser Leu Val Arg
195 200 205

Thr Glu Ala Thr Gly Tyr Gly Cys Val Tyr Phe Val Ser Glu Met Ile
210 215 220

Lys Ala Lys Gly Glu Ser Ile Ser Gly Gln Lys Ile Ile Val Ser Gly
225 230 235 240

Ser Gly Asn Val Ala Thr Tyr Ala Ile Glu Lys Ala Gln Glu Leu Gly
245 250 255

Ala Thr Val Ile Gly Phe Ser Asp Ser Ser Gly Trp Val His Thr Pro
260 265 270

```
Asn Gly Val Asp Val Ala Lys Leu Arg Glu Ile Lys Glu Val Arg Arg
        275                 280                 285

Ala Arg Val Ser Val Tyr Ala Asp Glu Val Glu Gly Ala Thr Tyr His
    290                 295                 300

Thr Asp Gly Ser Ile Trp Asp Leu Lys Cys Asp Ile Ala Leu Pro Cys
305                 310                 315                 320

Ala Thr Gln Asn Glu Leu Asn Gly Glu Asn Ala Lys Thr Leu Ala Asp
                325                 330                 335

Asn Gly Cys Arg Phe Val Ala Glu Gly Ala Asn Met Pro Ser Thr Pro
            340                 345                 350

Glu Ala Val Glu Val Phe Arg Glu Arg Asp Ile Arg Phe Gly Pro Gly
        355                 360                 365

Lys Ala Ala Asn Ala Gly Gly Val Ala Thr Ser Ala Leu Glu Met Gln
    370                 375                 380

Gln Asn Ala Ser Arg Asp Ser Trp Ser Phe Glu Tyr Thr Asp Glu Arg
385                 390                 395                 400

Leu Gln Val Ile Met Lys Asn Ile Phe Lys Thr Cys Ala Glu Thr Ala
                405                 410                 415

Ala Glu Tyr Gly His Glu Asn Asp Tyr Val Val Gly Ala Asn Ile Ala
            420                 425                 430

Gly Phe Lys Lys Val Ala Asp Ala Met Leu Ala Gln Gly Val Ile
        435                 440                 445


<210> 95
<211> 1461
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1438)
<223> RXA00323

<400> 95
cgcgacatcc ttgagtaact ctgagaaaaa ctaccccga tgggagtata aaagtggcaa 60

atgcgcagtc gatgtcccat cgctgcgtag attagttttc atg aac agc gaa cag   115
                                           Met Asn Ser Glu Gln
                                            1               5

gaa ttt gta ctc agc gcc att gaa gaa cgc gac att aag ttt gtg cgt   163
Glu Phe Val Leu Ser Ala Ile Glu Glu Arg Asp Ile Lys Phe Val Arg
                10                  15                  20

cta tgg ttc act gac att ctt ggc cac ttg aag tca gtg gtt gtg gct   211
Leu Trp Phe Thr Asp Ile Leu Gly His Leu Lys Ser Val Val Val Ala
            25                  30                  35

cct gca gaa cta gag tct gcg ttg gaa gaa ggc atc gga ttc gat ggc   259
Pro Ala Glu Leu Glu Ser Ala Leu Glu Glu Gly Ile Gly Phe Asp Gly
```

40 45 50

tca gcc att gag ggc tac gcg cgt atc tcg gaa gcg gac acc att gcc 307
Ser Ala Ile Glu Gly Tyr Ala Arg Ile Ser Glu Ala Asp Thr Ile Ala
55 60 65

cgc cca gat cca tcg aca ttc cag gtc ctc cca cta gaa gcg ggc atc 355
Arg Pro Asp Pro Ser Thr Phe Gln Val Leu Pro Leu Glu Ala Gly Ile
70 75 80 85

tca aaa ctg cag gca gca cgc ctg ttt tgc gat gtc acg atg cca gac 403
Ser Lys Leu Gln Ala Ala Arg Leu Phe Cys Asp Val Thr Met Pro Asp
90 95 100

gga cag cca tct ttt tct gac ccg cgc caa gtg ctg cgc agg cag gtc 451
Gly Gln Pro Ser Phe Ser Asp Pro Arg Gln Val Leu Arg Arg Gln Val
105 110 115

caa cta gct gca gat gaa ggc ttg acc tgc atg atc tca cca gag att 499
Gln Leu Ala Ala Asp Glu Gly Leu Thr Cys Met Ile Ser Pro Glu Ile
120 125 130

gag ttc tat ttg gtg caa agc ctt cgc acc aac gga ctg cca cct gtg 547
Glu Phe Tyr Leu Val Gln Ser Leu Arg Thr Asn Gly Leu Pro Pro Val
135 140 145

ccc act gac aac ggc gga tat ttc gac caa gcc aca ttc aat gag gcg 595
Pro Thr Asp Asn Gly Gly Tyr Phe Asp Gln Ala Thr Phe Asn Glu Ala
150 155 160 165

ccg aat ttc cgt cga aac gcg atg gta gcg ctg gag gaa ctc ggc atc 643
Pro Asn Phe Arg Arg Asn Ala Met Val Ala Leu Glu Glu Leu Gly Ile
170 175 180

cct gtc gag ttc tcc cac cat gaa act gca cct ggc cag caa gaa atc 691
Pro Val Glu Phe Ser His His Glu Thr Ala Pro Gly Gln Gln Glu Ile
185 190 195

gat tta cgc cat gcg gat gcg ctc acc atg gcc gac aac atc atg acc 739
Asp Leu Arg His Ala Asp Ala Leu Thr Met Ala Asp Asn Ile Met Thr
200 205 210

ttc cgc tac atc atg aaa cag gtg gca agg gac caa ggc gtc ggg gca 787
Phe Arg Tyr Ile Met Lys Gln Val Ala Arg Asp Gln Gly Val Gly Ala
215 220 225

tca ttt atg ccc aag cca ttc caa gaa cat gca ggc tcc gcc atg cac 835
Ser Phe Met Pro Lys Pro Phe Gln Glu His Ala Gly Ser Ala Met His
230 235 240 245

acg cac atg tcc tta ttt gag ggc gat acc aac gcg ttc cac gat cca 883
Thr His Met Ser Leu Phe Glu Gly Asp Thr Asn Ala Phe His Asp Pro
250 255 260

gac gat tct tac atg ctg tcc aaa acc gca aaa cag ttc atc gct gga 931
Asp Asp Ser Tyr Met Leu Ser Lys Thr Ala Lys Gln Phe Ile Ala Gly
265 270 275

atc ttg cat cac gct cca gaa ttc acc gct gtg acc aac cag tgg gtc 979
Ile Leu His His Ala Pro Glu Phe Thr Ala Val Thr Asn Gln Trp Val
280 285 290

aat tcc tac aaa cgc atc gtg tac gga aac gaa gct cca act gcg gca
1027
Asn Ser Tyr Lys Arg Ile Val Tyr Gly Asn Glu Ala Pro Thr Ala Ala
295 300 305

acc tgg ggt gta tct aat cgt tct gcg ctg gtt cgt gtt cct acc tac
1075
Thr Trp Gly Val Ser Asn Arg Ser Ala Leu Val Arg Val Pro Thr Tyr
310 315 320 325

cgt ttg aat aag gag gag tcg cgc cgg gtg gag gtg cgt ctt cct gat
1123
Arg Leu Asn Lys Glu Glu Ser Arg Arg Val Glu Val Arg Leu Pro Asp
330 335 340

acc gct tgt aac cca tat ttg gcg ttt tca gtg atg ctc ggc gct ggt
1171
Thr Ala Cys Asn Pro Tyr Leu Ala Phe Ser Val Met Leu Gly Ala Gly
345 350 355

ttg aaa ggc att aaa gaa ggt tat gag ctc gac gag cca gct gag gac
1219
Leu Lys Gly Ile Lys Glu Gly Tyr Glu Leu Asp Glu Pro Ala Glu Asp
360 365 370

gat atc tcc aac ttg agc ttc cgg gaa cgt cgc gcc atg ggc tac aac
1267
Asp Ile Ser Asn Leu Ser Phe Arg Glu Arg Arg Ala Met Gly Tyr Asn
375 380 385

gat ctg cca agc agc ctt gat cag gca ctg cgc caa atg gaa aag tca
1315
Asp Leu Pro Ser Ser Leu Asp Gln Ala Leu Arg Gln Met Glu Lys Ser
390 395 400 405

gag ctt gtt gct gac atc ctc ggt gag cac gtt ttt gag ttt ttc ttg
1363
Glu Leu Val Ala Asp Ile Leu Gly Glu His Val Phe Glu Phe Phe Leu
410 415 420

cgc aat aag tgg cgt gaa tgg cgt gac tac caa gag cag atc act ccg
1411
Arg Asn Lys Trp Arg Glu Trp Arg Asp Tyr Gln Glu Gln Ile Thr Pro
425 430 435

tgg gag ctc cga aac aat ctt gat tac tagacttttg cactccaatg
1458
Trp Glu Leu Arg Asn Asn Leu Asp Tyr
440 445

gaa
1461

<210> 96
<211> 446
<212> PRT
<213> Corynebacterium glutamicum

<400> 96

```
Met Asn Ser Glu Gln Glu Phe Val Leu Ser Ala Ile Glu Glu Arg Asp
 1               5                  10                  15

Ile Lys Phe Val Arg Leu Trp Phe Thr Asp Ile Leu Gly His Leu Lys
            20                  25                  30

Ser Val Val Val Ala Pro Ala Glu Leu Glu Ser Ala Leu Glu Glu Gly
        35                  40                  45

Ile Gly Phe Asp Gly Ser Ala Ile Glu Gly Tyr Ala Arg Ile Ser Glu
    50                  55                  60

Ala Asp Thr Ile Ala Arg Pro Asp Pro Ser Thr Phe Gln Val Leu Pro
65                  70                  75                  80

Leu Glu Ala Gly Ile Ser Lys Leu Gln Ala Ala Arg Leu Phe Cys Asp
                85                  90                  95

Val Thr Met Pro Asp Gly Gln Pro Ser Phe Ser Asp Pro Arg Gln Val
            100                 105                 110

Leu Arg Arg Gln Val Gln Leu Ala Ala Asp Glu Gly Leu Thr Cys Met
        115                 120                 125

Ile Ser Pro Glu Ile Glu Phe Tyr Leu Val Gln Ser Leu Arg Thr Asn
    130                 135                 140

Gly Leu Pro Pro Val Pro Thr Asp Asn Gly Gly Tyr Phe Asp Gln Ala
145                 150                 155                 160

Thr Phe Asn Glu Ala Pro Asn Phe Arg Arg Asn Ala Met Val Ala Leu
                165                 170                 175

Glu Glu Leu Gly Ile Pro Val Glu Phe Ser His His Glu Thr Ala Pro
            180                 185                 190

Gly Gln Gln Glu Ile Asp Leu Arg His Ala Asp Ala Leu Thr Met Ala
        195                 200                 205

Asp Asn Ile Met Thr Phe Arg Tyr Ile Met Lys Gln Val Ala Arg Asp
    210                 215                 220

Gln Gly Val Gly Ala Ser Phe Met Pro Lys Pro Phe Gln Glu His Ala
225                 230                 235                 240

Gly Ser Ala Met His Thr His Met Ser Leu Phe Glu Gly Asp Thr Asn
                245                 250                 255

Ala Phe His Asp Pro Asp Asp Ser Tyr Met Leu Ser Lys Thr Ala Lys
            260                 265                 270

Gln Phe Ile Ala Gly Ile Leu His His Ala Pro Glu Phe Thr Ala Val
        275                 280                 285

Thr Asn Gln Trp Val Asn Ser Tyr Lys Arg Ile Val Tyr Gly Asn Glu
    290                 295                 300

Ala Pro Thr Ala Ala Thr Trp Gly Val Ser Asn Arg Ser Ala Leu Val
305                 310                 315                 320

Arg Val Pro Thr Tyr Arg Leu Asn Lys Glu Glu Ser Arg Arg Val Glu
```

325 330 335

Val Arg Leu Pro Asp Thr Ala Cys Asn Pro Tyr Leu Ala Phe Ser Val
340 345 350

Met Leu Gly Ala Gly Leu Lys Gly Ile Lys Glu Gly Tyr Glu Leu Asp
355 360 365

Glu Pro Ala Glu Asp Asp Ile Ser Asn Leu Ser Phe Arg Glu Arg Arg
370 375 380

Ala Met Gly Tyr Asn Asp Leu Pro Ser Ser Leu Asp Gln Ala Leu Arg
385 390 395 400

Gln Met Glu Lys Ser Glu Leu Val Ala Asp Ile Leu Gly Glu His Val
405 410 415

Phe Glu Phe Phe Leu Arg Asn Lys Trp Arg Glu Trp Arg Asp Tyr Gln
420 425 430

Glu Gln Ile Thr Pro Trp Glu Leu Arg Asn Asn Leu Asp Tyr
435 440 445

<210> 97
<211> 1554
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1531)
<223> RXA00335

<400> 97
actacatttg cagccaagtc tactacttga tcttcaaagg tcagcaattg tgaacaaagc 60

tacaaataaa ccgttccgcc catgtcaatg aggagtcacc gtg gcg ttt gaa acc 115
Val Ala Phe Glu Thr
1 5

ccg gaa gaa att gtc aag ttc atc aag gat gaa aac gtc gag ttc gtt 163
Pro Glu Glu Ile Val Lys Phe Ile Lys Asp Glu Asn Val Glu Phe Val
10 15 20

gac gtt cga ttc acc gac ctt ccc ggc acc gag cag cac ttc agc atc 211
Asp Val Arg Phe Thr Asp Leu Pro Gly Thr Glu Gln His Phe Ser Ile
25 30 35

cca gct gcc agc ttc gat gca gat aca atc gaa gaa ggt ctc gca ttc 259
Pro Ala Ala Ser Phe Asp Ala Asp Thr Ile Glu Glu Gly Leu Ala Phe
40 45 50

gac gga tcc tcg atc cgt ggc ttc acc acg atc gac gaa tct gac atg 307
Asp Gly Ser Ser Ile Arg Gly Phe Thr Thr Ile Asp Glu Ser Asp Met
55 60 65

aat ctc ctg cca gac ctc gga acg gcc acc ctt gat cca ttc cgc aag 355
Asn Leu Leu Pro Asp Leu Gly Thr Ala Thr Leu Asp Pro Phe Arg Lys
70 75 80 85

gca aag acc ctg aac gtt aag ttc ttc gtt cac gat cct ttc acc cgc 403
Ala Lys Thr Leu Asn Val Lys Phe Phe Val His Asp Pro Phe Thr Arg
90 95 100

gag gca ttc tcc cgc gac cca cgc aac gtg gca cgc aag gca gag cag 451
Glu Ala Phe Ser Arg Asp Pro Arg Asn Val Ala Arg Lys Ala Glu Gln
105 110 115

tac ctg gca tcc acc ggc att gca gac acc tgc aac ttc ggc gcc gag 499
Tyr Leu Ala Ser Thr Gly Ile Ala Asp Thr Cys Asn Phe Gly Ala Glu
120 125 130

gct gag ttc tac ctc ttc gac tcc gtt cgc tac tcc acc gag atg aac 547
Ala Glu Phe Tyr Leu Phe Asp Ser Val Arg Tyr Ser Thr Glu Met Asn
135 140 145

tcc ggc ttc tac gaa gta gat acc gaa gaa ggc tgg tgg aac cgt ggc 595
Ser Gly Phe Tyr Glu Val Asp Thr Glu Glu Gly Trp Trp Asn Arg Gly
150 155 160 165

aag gaa acc aac ctc gac ggc acc cca aac ctg ggc gca aag aac cgc 643
Lys Glu Thr Asn Leu Asp Gly Thr Pro Asn Leu Gly Ala Lys Asn Arg
170 175 180

gtc aag ggt ggc tac ttc cca gta gca cca tac gac caa acc gtt gac 691
Val Lys Gly Gly Tyr Phe Pro Val Ala Pro Tyr Asp Gln Thr Val Asp
185 190 195

gtg cgc gat gac atg gtt cgc aac ctc gca gct tcc ggc ttc gct ctt 739
Val Arg Asp Asp Met Val Arg Asn Leu Ala Ala Ser Gly Phe Ala Leu
200 205 210

gag cgt ttc cac cac gaa gtc ggt ggc gga cag cag gaa atc aac tac 787
Glu Arg Phe His His Glu Val Gly Gly Gly Gln Gln Glu Ile Asn Tyr
215 220 225

cgc ttc aac acc atg ctc cac gcg gca gat gat atc cag acc ttc aag 835
Arg Phe Asn Thr Met Leu His Ala Ala Asp Asp Ile Gln Thr Phe Lys
230 235 240 245

tac atc atc aag aac acc gct cgc ctc cac ggc aag gct gca acc ttc 883
Tyr Ile Ile Lys Asn Thr Ala Arg Leu His Gly Lys Ala Ala Thr Phe
250 255 260

atg cct aag cca ctg gct ggc gac aac ggt tcc ggc atg cac gct cac 931
Met Pro Lys Pro Leu Ala Gly Asp Asn Gly Ser Gly Met His Ala His
265 270 275

cag tcc ctc tgg aag gac ggc aag cca ctc ttc cac gat gag tcc ggc 979
Gln Ser Leu Trp Lys Asp Gly Lys Pro Leu Phe His Asp Glu Ser Gly
280 285 290

tac gca ggc ctg tcc gac atc gcc cgc tac tac atc ggc ggc atc ctg
1027
Tyr Ala Gly Leu Ser Asp Ile Ala Arg Tyr Tyr Ile Gly Gly Ile Leu
295 300 305

cac cac gca ggc gct gtt ctg gcg ttc acc aac gca acc ctg aac tcc
1075
His His Ala Gly Ala Val Leu Ala Phe Thr Asn Ala Thr Leu Asn Ser
310 315 320 325

tac cac cgt ctg gtt cca ggc ttc gag gct cca atc aac ctg gtg tac
1123
Tyr His Arg Leu Val Pro Gly Phe Glu Ala Pro Ile Asn Leu Val Tyr
330 335 340

tca cag cgc aac cgt tcc gct gct gtc cgt atc cca atc acc gga tcc
1171
Ser Gln Arg Asn Arg Ser Ala Ala Val Arg Ile Pro Ile Thr Gly Ser
345 350 355

aac ccg aag gca aag cgc atc gaa ttc cgc gct cca gac cca tca ggc
1219
Asn Pro Lys Ala Lys Arg Ile Glu Phe Arg Ala Pro Asp Pro Ser Gly
360 365 370

aac cca tac ctg ggc ttt gca gcg atg atg atg gcc ggc ctc gac ggc
1267
Asn Pro Tyr Leu Gly Phe Ala Ala Met Met Met Ala Gly Leu Asp Gly
375 380 385

atc aag aac cgc atc gag cca cac gct cca gtg gac aag gac ctc tac
1315
Ile Lys Asn Arg Ile Glu Pro His Ala Pro Val Asp Lys Asp Leu Tyr
390 395 400 405

gaa cta cca cca gag gaa gct gca tcc att cca cag gca cca acc tcc
1363
Glu Leu Pro Pro Glu Glu Ala Ala Ser Ile Pro Gln Ala Pro Thr Ser
410 415 420

ctg gaa gca tcc ctg aag gca ctg cag gaa gac acc gac ttc ctc acc
1411
Leu Glu Ala Ser Leu Lys Ala Leu Gln Glu Asp Thr Asp Phe Leu Thr
425 430 435

gag tct gac gtc ttc acc gag gat ctc atc gag gcg tac atc cag tac
1459
Glu Ser Asp Val Phe Thr Glu Asp Leu Ile Glu Ala Tyr Ile Gln Tyr
440 445 450

aag tac gac aac gag atc tcc cca gtt cgc ctg cgc cca acc ccg cag
1507
Lys Tyr Asp Asn Glu Ile Ser Pro Val Arg Leu Arg Pro Thr Pro Gln
455 460 465

gaa ttc gaa ttg tac ttc gac tgc taattcactt agctagccga tag
1554
Glu Phe Glu Leu Tyr Phe Asp Cys
470 475

<210> 98
<211> 477
<212> PRT
<213> Corynebacterium glutamicum

<400> 98
Val Ala Phe Glu Thr Pro Glu Glu Ile Val Lys Phe Ile Lys Asp Glu
1 5 10 15

Asn Val Glu Phe Val Asp Val Arg Phe Thr Asp Leu Pro Gly Thr Glu
20 25 30

Gln His Phe Ser Ile Pro Ala Ala Ser Phe Asp Ala Asp Thr Ile Glu
35 40 45

Glu Gly Leu Ala Phe Asp Gly Ser Ser Ile Arg Gly Phe Thr Thr Ile
50 55 60

Asp Glu Ser Asp Met Asn Leu Leu Pro Asp Leu Gly Thr Ala Thr Leu
65 70 75 80

Asp Pro Phe Arg Lys Ala Lys Thr Leu Asn Val Lys Phe Phe Val His
85 90 95

Asp Pro Phe Thr Arg Glu Ala Phe Ser Arg Asp Pro Arg Asn Val Ala
100 105 110

Arg Lys Ala Glu Gln Tyr Leu Ala Ser Thr Gly Ile Ala Asp Thr Cys
115 120 125

Asn Phe Gly Ala Glu Ala Glu Phe Tyr Leu Phe Asp Ser Val Arg Tyr
130 135 140

Ser Thr Glu Met Asn Ser Gly Phe Tyr Glu Val Asp Thr Glu Glu Gly
145 150 155 160

Trp Trp Asn Arg Gly Lys Glu Thr Asn Leu Asp Gly Thr Pro Asn Leu
165 170 175

Gly Ala Lys Asn Arg Val Lys Gly Gly Tyr Phe Pro Val Ala Pro Tyr
180 185 190

Asp Gln Thr Val Asp Val Arg Asp Asp Met Val Arg Asn Leu Ala Ala
195 200 205

Ser Gly Phe Ala Leu Glu Arg Phe His His Glu Val Gly Gly Gly Gln
210 215 220

Gln Glu Ile Asn Tyr Arg Phe Asn Thr Met Leu His Ala Ala Asp Asp
225 230 235 240

Ile Gln Thr Phe Lys Tyr Ile Ile Lys Asn Thr Ala Arg Leu His Gly
245 250 255

Lys Ala Ala Thr Phe Met Pro Lys Pro Leu Ala Gly Asp Asn Gly Ser
260 265 270

Gly Met His Ala His Gln Ser Leu Trp Lys Asp Gly Lys Pro Leu Phe
275 280 285

His Asp Glu Ser Gly Tyr Ala Gly Leu Ser Asp Ile Ala Arg Tyr Tyr
290 295 300

Ile Gly Gly Ile Leu His His Ala Gly Ala Val Leu Ala Phe Thr Asn
305 310 315 320

Ala Thr Leu Asn Ser Tyr His Arg Leu Val Pro Gly Phe Glu Ala Pro
325 330 335

Ile Asn Leu Val Tyr Ser Gln Arg Asn Arg Ser Ala Ala Val Arg Ile

340 345 350

Pro Ile Thr Gly Ser Asn Pro Lys Ala Lys Arg Ile Glu Phe Arg Ala
355 360 365

Pro Asp Pro Ser Gly Asn Pro Tyr Leu Gly Phe Ala Ala Met Met Met
370 375 380

Ala Gly Leu Asp Gly Ile Lys Asn Arg Ile Glu Pro His Ala Pro Val
385 390 395 400

Asp Lys Asp Leu Tyr Glu Leu Pro Pro Glu Glu Ala Ala Ser Ile Pro
405 410 415

Gln Ala Pro Thr Ser Leu Glu Ala Ser Leu Lys Ala Leu Gln Glu Asp
420 425 430

Thr Asp Phe Leu Thr Glu Ser Asp Val Phe Thr Glu Asp Leu Ile Glu
435 440 445

Ala Tyr Ile Gln Tyr Lys Tyr Asp Asn Glu Ile Ser Pro Val Arg Leu
450 455 460

Arg Pro Thr Pro Gln Glu Phe Glu Leu Tyr Phe Asp Cys
465 470 475

<210> 99
<211> 3258
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(3235)
<223> RXA00324

<400> 99
tccgtgggag ctccgaaaca atcttgatta ctagactttt gcactccaat ggaaacccta 60

cggcgaccca attgcgaccc gatgaaggag gggagaagct atg tca gga ccg tta 115
Met Ser Gly Pro Leu
1 5

aga agt gaa cgt aaa gtc gtt ggc ttt gtc aga gac cca ctg cca aaa 163
Arg Ser Glu Arg Lys Val Val Gly Phe Val Arg Asp Pro Leu Pro Lys
10 15 20

gtt ggt tct tta tcg ctg aaa tct gag cat gcc caa gca gat cta gag 211
Val Gly Ser Leu Ser Leu Lys Ser Glu His Ala Gln Ala Asp Leu Glu
25 30 35

cat ttg ggt tgg cgc aat gtt gag tct ttg gat ttg ttg tgg ggc ttg 259
His Leu Gly Trp Arg Asn Val Glu Ser Leu Asp Leu Leu Trp Gly Leu
40 45 50

tca ggt gca ggc gat ccc gat gtc gcg ctg aac ctt ctt att cgg ctg 307
Ser Gly Ala Gly Asp Pro Asp Val Ala Leu Asn Leu Leu Ile Arg Leu
55 60 65

tat cag gca ctt gaa gca atc ggc gag gat gct cga aac gag ctt gat 355

Tyr Gln Ala Leu Glu Ala Ile Gly Glu Asp Ala Arg Asn Glu Leu Asp
70 75 80 85

caa gag att cgc cag gat gaa aaa cta cga gtc cgc ctt ttt gca ttg 403
Gln Glu Ile Arg Gln Asp Glu Lys Leu Arg Val Arg Leu Phe Ala Leu
90 95 100

ttg ggt ggt tcc tcg gct gtc ggt gat cac ttg gtc gcc aat cct ttg 451
Leu Gly Gly Ser Ser Ala Val Gly Asp His Leu Val Ala Asn Pro Leu
105 110 115

cag tgg aaa ctc tta aaa ctt gat gcg cca tcg agg gaa gag atg ttt 499
Gln Trp Lys Leu Leu Lys Leu Asp Ala Pro Ser Arg Glu Glu Met Phe
120 125 130

cag gcg ctg ctg gaa tct gtg aaa gct cag cct gct gtg ctt gag gtt 547
Gln Ala Leu Leu Glu Ser Val Lys Ala Gln Pro Ala Val Leu Glu Val
135 140 145

gag gat ttc agc gat gca cac aac att gcc cga gac gat ttg agc acg 595
Glu Asp Phe Ser Asp Ala His Asn Ile Ala Arg Asp Asp Leu Ser Thr
150 155 160 165

cct ggt ttt tac acg gct agt gtt acc ggg cct gaa gca gag cga gtc 643
Pro Gly Phe Tyr Thr Ala Ser Val Thr Gly Pro Glu Ala Glu Arg Val
170 175 180

ttg aaa tgg act tat cgc acg ttg ctg acc cgg att gct gcg cat gat 691
Leu Lys Trp Thr Tyr Arg Thr Leu Leu Thr Arg Ile Ala Ala His Asp
185 190 195

tta gcg ggt acc tat ccc acc gac atg cgg aga aaa ggt ggc gat cct 739
Leu Ala Gly Thr Tyr Pro Thr Asp Met Arg Arg Lys Gly Gly Asp Pro
200 205 210

gtt ccg ttt agc aca gtg acc atg cag ctc agc gac cta gct gat gct 787
Val Pro Phe Ser Thr Val Thr Met Gln Leu Ser Asp Leu Ala Asp Ala
215 220 225

gct ttg act gct gct tta gct gtg gca att gcc aat gtt tat ggt gaa 835
Ala Leu Thr Ala Ala Leu Ala Val Ala Ile Ala Asn Val Tyr Gly Glu
230 235 240 245

aag ccg gtt gat tca gct tta tct gtc atc gcg atg ggc aaa tgt ggc 883
Lys Pro Val Asp Ser Ala Leu Ser Val Ile Ala Met Gly Lys Cys Gly
250 255 260

gcg cag gaa ttg aac tac att tca gat gtg gac gtg gtg ttt gtt gca 931
Ala Gln Glu Leu Asn Tyr Ile Ser Asp Val Asp Val Val Phe Val Ala
265 270 275

gag ccg gca aac tct aaa tca aca cgc acc gca gca gag ctc att cgc 979
Glu Pro Ala Asn Ser Lys Ser Thr Arg Thr Ala Ala Glu Leu Ile Arg
280 285 290

atc ggt agc aac tcg ttc ttt gag gtg gat gca gca ctt cgc cca gaa
1027
Ile Gly Ser Asn Ser Phe Phe Glu Val Asp Ala Ala Leu Arg Pro Glu
295 300 305

ggt aaa agt ggc gct ctt gtg cgc tct ttg gat tcc cat atg gcg tat
1075
Gly Lys Ser Gly Ala Leu Val Arg Ser Leu Asp Ser His Met Ala Tyr
310 315 320 325

tac aag cgc tgg gcg gaa acc tgg gag ttt cag gca ctg ctg aaa gct
1123
Tyr Lys Arg Trp Ala Glu Thr Trp Glu Phe Gln Ala Leu Leu Lys Ala
330 335 340

cgt ccc atg acg ggt gat att aac ctt ggg cag tcc tat gtg gat gct
1171
Arg Pro Met Thr Gly Asp Ile Asn Leu Gly Gln Ser Tyr Val Asp Ala
345 350 355

ctt tca ccg ttg att tgg acg gct agc cag cgg gaa tca ttt gtc aca
1219
Leu Ser Pro Leu Ile Trp Thr Ala Ser Gln Arg Glu Ser Phe Val Thr
360 365 370

gat gtc caa gct atg cgc cgt cga gtg ttg gac aat gtt ccg gaa gac
1267
Asp Val Gln Ala Met Arg Arg Arg Val Leu Asp Asn Val Pro Glu Asp
375 380 385

ttg cgt gat cgt gag ctg aag ctt ggt cgc ggt ggt ttg agg gat gtg
1315
Leu Arg Asp Arg Glu Leu Lys Leu Gly Arg Gly Gly Leu Arg Asp Val
390 395 400 405

gag ttt gct gtc cag ctc ctt cag atg gtg cat ggt cgc att gat gag
1363
Glu Phe Ala Val Gln Leu Leu Gln Met Val His Gly Arg Ile Asp Glu
410 415 420

acg ttg cgg gtt cgg tca acg gta aat gct ttg cat gtg ttg gtt gat
1411
Thr Leu Arg Val Arg Ser Thr Val Asn Ala Leu His Val Leu Val Asp
425 430 435

cag gga tat gtg ggt cgt gaa gac ggg cat aat ctc att gag tcg tat
1459
Gln Gly Tyr Val Gly Arg Glu Asp Gly His Asn Leu Ile Glu Ser Tyr
440 445 450

gag ttt ttg cgt ctg ttg gag cat cgc ctt caa ttg gag cgg atc aag
1507
Glu Phe Leu Arg Leu Leu Glu His Arg Leu Gln Leu Glu Arg Ile Lys
455 460 465

cgc act cac ttg tta ccg aaa cct gat gac cga atg aat atg cgc tgg
1555
Arg Thr His Leu Leu Pro Lys Pro Asp Asp Arg Met Asn Met Arg Trp
470 475 480 485

ttg gcg cgc gct tct ggg ttt act ggt tcg atg gag caa agt tcg gcc
1603
Leu Ala Arg Ala Ser Gly Phe Thr Gly Ser Met Glu Gln Ser Ser Ala
490 495 500

aaa gct atg gaa cgg cat ttg cgt aag gtt cgt ttg cag att cag tcg
1651
Lys Ala Met Glu Arg His Leu Arg Lys Val Arg Leu Gln Ile Gln Ser
505 510 515

ttg cat agt cag ctg ttt tat cgg cca ctg ctg aac tct gtg gtc aac
1699
Leu His Ser Gln Leu Phe Tyr Arg Pro Leu Leu Asn Ser Val Val Asn
520 525 530

ttg agc gcg gat gcc atc agg ttg tct ccg gat gct gca aag cta caa
1747
Leu Ser Ala Asp Ala Ile Arg Leu Ser Pro Asp Ala Ala Lys Leu Gln
535 540 545

ttg gcg gca ttg gga tac ctg cat cca tca cgt gct tat gaa cac ctg
1795
Leu Ala Ala Leu Gly Tyr Leu His Pro Ser Arg Ala Tyr Glu His Leu
550 555 560 565

act gct ctt gca tca gga gct agc cgt aaa gcc aag att cag gcg atg
1843
Thr Ala Leu Ala Ser Gly Ala Ser Arg Lys Ala Lys Ile Gln Ala Met
570 575 580

ttg ctg ccc acg ttg atg gag tgg ctg tct caa aca gct gaa cca gat
1891
Leu Leu Pro Thr Leu Met Glu Trp Leu Ser Gln Thr Ala Glu Pro Asp
585 590 595

gcg gga ttg ctg aat tac cgc aag ctt tct gat gct tcc tat gat cgc
1939
Ala Gly Leu Leu Asn Tyr Arg Lys Leu Ser Asp Ala Ser Tyr Asp Arg
600 605 610

agc tgg ttt ttg cgc atg ctg cgt gat gag ggc gta gtg ggg cag cgg
1987
Ser Trp Phe Leu Arg Met Leu Arg Asp Glu Gly Val Val Gly Gln Arg
615 620 625

ttg atg cgt att ttg gga aat tct ccc tat att tct gaa ctg att atc
2035
Leu Met Arg Ile Leu Gly Asn Ser Pro Tyr Ile Ser Glu Leu Ile Ile
630 635 640 645

tcc act ccg gac ttt atg aaa cag ctg ggt gat gcg gcg tct ggt cct
2083
Ser Thr Pro Asp Phe Met Lys Gln Leu Gly Asp Ala Ala Ser Gly Pro
650 655 660

aaa ttg ctt gct act gca ccg act cag gtt gtg aaa gca atc aag gca
2131
Lys Leu Leu Ala Thr Ala Pro Thr Gln Val Val Lys Ala Ile Lys Ala
665 670 675

acg gtg tcg cgt cat gag tca cct gat cgg gcg atc cag gct gca cga
2179
Thr Val Ser Arg His Glu Ser Pro Asp Arg Ala Ile Gln Ala Ala Arg
680 685 690

tcg ctg agg agg cag gag ctg gca cgc att gcc tct gct gat ttg ctc
2227
Ser Leu Arg Arg Gln Glu Leu Ala Arg Ile Ala Ser Ala Asp Leu Leu
695 700 705

aac atg ctc act gtt cag gaa gta tgc caa agc ttg tca cta gtc tgg
2275
Asn Met Leu Thr Val Gln Glu Val Cys Gln Ser Leu Ser Leu Val Trp
710 715 720 725

gat gcg gtg ttg gat gct gcc ttg gat gcg gaa atc cgt gct gca ctt
2323
Asp Ala Val Leu Asp Ala Ala Leu Asp Ala Glu Ile Arg Ala Ala Leu
730 735 740

aac gat cca cag aaa cca gat cag cct ctg gcc aat att tct gtg atc
2371
Asn Asp Pro Gln Lys Pro Asp Gln Pro Leu Ala Asn Ile Ser Val Ile
745 750 755

ggc atg ggc cgt ttg ggt gga gca gaa ctt gga tac ggt tct gat gcc
2419
Gly Met Gly Arg Leu Gly Gly Ala Glu Leu Gly Tyr Gly Ser Asp Ala
760 765 770

gat gtg atg ttt gta tgc gag ccg gta gcc ggt gtg gaa gag cat gag
2467
Asp Val Met Phe Val Cys Glu Pro Val Ala Gly Val Glu Glu His Glu
775 780 785

gcc gtc aca tgg tct att gct atc tgt gat tcc atg cgg tcg agg ctt
2515
Ala Val Thr Trp Ser Ile Ala Ile Cys Asp Ser Met Arg Ser Arg Leu
790 795 800 805

gcg cag cct tcc ggt gat cca cct ttg gag gtg gat ctg ggg ctg cgt
2563
Ala Gln Pro Ser Gly Asp Pro Pro Leu Glu Val Asp Leu Gly Leu Arg
810 815 820

cct gaa ggg aga tct ggt gcg att gtg cgc acc gtt gat tcc tat gtg
2611
Pro Glu Gly Arg Ser Gly Ala Ile Val Arg Thr Val Asp Ser Tyr Val
825 830 835

aag tac tac gaa aag tgg ggt gaa act tgg gag att cag gcg ctg ctg
2659
Lys Tyr Tyr Glu Lys Trp Gly Glu Thr Trp Glu Ile Gln Ala Leu Leu
840 845 850

agg gct gcg tgg gtt gct ggt gat cgt gag ctg ggt att aag ttc ttg
2707
Arg Ala Ala Trp Val Ala Gly Asp Arg Glu Leu Gly Ile Lys Phe Leu
855 860 865

gag tcg att gat cgt ttc cgc tac cca gtt gac ggg gca acg cag gcg
2755
Glu Ser Ile Asp Arg Phe Arg Tyr Pro Val Asp Gly Ala Thr Gln Ala
870 875 880 885

cag ctt cgt gaa gtt cgt cga att aag gcg agg gtg gat aat gag agg
2803
Gln Leu Arg Glu Val Arg Arg Ile Lys Ala Arg Val Asp Asn Glu Arg
890 895 900

ctt ccg cgc ggg gct gat cga aat acc cat acc aag ctg ggt cgg gga
2851
Leu Pro Arg Gly Ala Asp Arg Asn Thr His Thr Lys Leu Gly Arg Gly
905 910 915

gcg tta act gac atc gag tgg act gtg cag ttg ttg acc atg atg cat
2899
Ala Leu Thr Asp Ile Glu Trp Thr Val Gln Leu Leu Thr Met Met His
920 925 930

gct cat gag att ccg gag ctg cac aat acg tcg acg ttg gaa gtt ctt
2947
Ala His Glu Ile Pro Glu Leu His Asn Thr Ser Thr Leu Glu Val Leu
935 940 945

gaa gtg ctg gaa aag cat cag att att aac cct gtg cag gtg cag acg
2995
Glu Val Leu Glu Lys His Gln Ile Ile Asn Pro Val Gln Val Gln Thr
950 955 960 965

ctt cgg gaa gcg tgg ctg acg gca acg gct gct agg aat gcg ctt gtg
3043
Leu Arg Glu Ala Trp Leu Thr Ala Thr Ala Ala Arg Asn Ala Leu Val
970 975 980

ctg gtc agg ggt aag aga tta gat cag tta cct act cct ggt ccg cac
3091
Leu Val Arg Gly Lys Arg Leu Asp Gln Leu Pro Thr Pro Gly Pro His
985 990 995

ctt gcg cag gtg gct ggt gcg tct ggt tgg gat cca aat gag tac cag
3139
Leu Ala Gln Val Ala Gly Ala Ser Gly Trp Asp Pro Asn Glu Tyr Gln
1000 1005 1010

gag tat ttg gaa aac tat ctg aaa gtg acc agg aag agt cgt cag gtt
3187
Glu Tyr Leu Glu Asn Tyr Leu Lys Val Thr Arg Lys Ser Arg Gln Val
1015 1020 1025

gtt gat gaa gtc ttc tgg ggt gtg gac tct atg gag caa cgt gag ttt
3235
Val Asp Glu Val Phe Trp Gly Val Asp Ser Met Glu Gln Arg Glu Phe
1030 1035 1040 1045

taggtaggtg gtgggagccc caa
3258

<210> 100
<211> 1045
<212> PRT
<213> Corynebacterium glutamicum

<400> 100
Met Ser Gly Pro Leu Arg Ser Glu Arg Lys Val Val Gly Phe Val Arg

1 5 10 15

Asp Pro Leu Pro Lys Val Gly Ser Leu Ser Leu Lys Ser Glu His Ala
20 25 30

Gln Ala Asp Leu Glu His Leu Gly Trp Arg Asn Val Glu Ser Leu Asp
35 40 45

Leu Leu Trp Gly Leu Ser Gly Ala Gly Asp Pro Asp Val Ala Leu Asn
50 55 60

Leu Leu Ile Arg Leu Tyr Gln Ala Leu Glu Ala Ile Gly Glu Asp Ala
65 70 75 80

Arg Asn Glu Leu Asp Gln Glu Ile Arg Gln Asp Glu Lys Leu Arg Val
85 90 95

Arg Leu Phe Ala Leu Leu Gly Gly Ser Ser Ala Val Gly Asp His Leu
100 105 110

Val Ala Asn Pro Leu Gln Trp Lys Leu Leu Lys Leu Asp Ala Pro Ser
115 120 125

Arg Glu Glu Met Phe Gln Ala Leu Leu Glu Ser Val Lys Ala Gln Pro
130 135 140

Ala Val Leu Glu Val Glu Asp Phe Ser Asp Ala His Asn Ile Ala Arg
145 150 155 160

Asp Asp Leu Ser Thr Pro Gly Phe Tyr Thr Ala Ser Val Thr Gly Pro
165 170 175

Glu Ala Glu Arg Val Leu Lys Trp Thr Tyr Arg Thr Leu Leu Thr Arg
180 185 190

Ile Ala Ala His Asp Leu Ala Gly Thr Tyr Pro Thr Asp Met Arg Arg
195 200 205

Lys Gly Gly Asp Pro Val Pro Phe Ser Thr Val Thr Met Gln Leu Ser
210 215 220

Asp Leu Ala Asp Ala Ala Leu Thr Ala Ala Leu Ala Val Ala Ile Ala
225 230 235 240

Asn Val Tyr Gly Glu Lys Pro Val Asp Ser Ala Leu Ser Val Ile Ala
245 250 255

Met Gly Lys Cys Gly Ala Gln Glu Leu Asn Tyr Ile Ser Asp Val Asp
260 265 270

Val Val Phe Val Ala Glu Pro Ala Asn Ser Lys Ser Thr Arg Thr Ala
275 280 285

Ala Glu Leu Ile Arg Ile Gly Ser Asn Ser Phe Phe Glu Val Asp Ala
290 295 300

Ala Leu Arg Pro Glu Gly Lys Ser Gly Ala Leu Val Arg Ser Leu Asp
305 310 315 320

Ser His Met Ala Tyr Tyr Lys Arg Trp Ala Glu Thr Trp Glu Phe Gln
325 330 335

Ala Leu Leu Lys Ala Arg Pro Met Thr Gly Asp Ile Asn Leu Gly Gln
340 345 350

Ser Tyr Val Asp Ala Leu Ser Pro Leu Ile Trp Thr Ala Ser Gln Arg
355 360 365

Glu Ser Phe Val Thr Asp Val Gln Ala Met Arg Arg Arg Val Leu Asp
370 375 380

Asn Val Pro Glu Asp Leu Arg Asp Arg Glu Leu Lys Leu Gly Arg Gly
385 390 395 400

Gly Leu Arg Asp Val Glu Phe Ala Val Gln Leu Leu Gln Met Val His
405 410 415

Gly Arg Ile Asp Glu Thr Leu Arg Val Arg Ser Thr Val Asn Ala Leu
420 425 430

His Val Leu Val Asp Gln Gly Tyr Val Gly Arg Glu Asp Gly His Asn
435 440 445

Leu Ile Glu Ser Tyr Glu Phe Leu Arg Leu Leu Glu His Arg Leu Gln
450 455 460

Leu Glu Arg Ile Lys Arg Thr His Leu Leu Pro Lys Pro Asp Asp Arg
465 470 475 480

Met Asn Met Arg Trp Leu Ala Arg Ala Ser Gly Phe Thr Gly Ser Met
485 490 495

Glu Gln Ser Ser Ala Lys Ala Met Glu Arg His Leu Arg Lys Val Arg
500 505 510

Leu Gln Ile Gln Ser Leu His Ser Gln Leu Phe Tyr Arg Pro Leu Leu
515 520 525

Asn Ser Val Val Asn Leu Ser Ala Asp Ala Ile Arg Leu Ser Pro Asp
530 535 540

Ala Ala Lys Leu Gln Leu Ala Ala Leu Gly Tyr Leu His Pro Ser Arg
545 550 555 560

Ala Tyr Glu His Leu Thr Ala Leu Ala Ser Gly Ala Ser Arg Lys Ala
565 570 575

Lys Ile Gln Ala Met Leu Leu Pro Thr Leu Met Glu Trp Leu Ser Gln
580 585 590

Thr Ala Glu Pro Asp Ala Gly Leu Leu Asn Tyr Arg Lys Leu Ser Asp
595 600 605

Ala Ser Tyr Asp Arg Ser Trp Phe Leu Arg Met Leu Arg Asp Glu Gly
610 615 620

Val Val Gly Gln Arg Leu Met Arg Ile Leu Gly Asn Ser Pro Tyr Ile
625 630 635 640

Ser Glu Leu Ile Ile Ser Thr Pro Asp Phe Met Lys Gln Leu Gly Asp
645 650 655

Ala Ala Ser Gly Pro Lys Leu Leu Ala Thr Ala Pro Thr Gln Val Val
660 665 670

Lys Ala Ile Lys Ala Thr Val Ser Arg His Glu Ser Pro Asp Arg Ala
675 680 685

Ile Gln Ala Ala Arg Ser Leu Arg Arg Gln Glu Leu Ala Arg Ile Ala
690 695 700

Ser Ala Asp Leu Leu Asn Met Leu Thr Val Gln Glu Val Cys Gln Ser
705 710 715 720

Leu Ser Leu Val Trp Asp Ala Val Leu Asp Ala Ala Leu Asp Ala Glu
725 730 735

Ile Arg Ala Ala Leu Asn Asp Pro Gln Lys Pro Asp Gln Pro Leu Ala
740 745 750

Asn Ile Ser Val Ile Gly Met Gly Arg Leu Gly Gly Ala Glu Leu Gly
755 760 765

Tyr Gly Ser Asp Ala Asp Val Met Phe Val Cys Glu Pro Val Ala Gly
770 775 780

Val Glu Glu His Glu Ala Val Thr Trp Ser Ile Ala Ile Cys Asp Ser
785 790 795 800

Met Arg Ser Arg Leu Ala Gln Pro Ser Gly Asp Pro Pro Leu Glu Val
805 810 815

Asp Leu Gly Leu Arg Pro Glu Gly Arg Ser Gly Ala Ile Val Arg Thr
820 825 830

Val Asp Ser Tyr Val Lys Tyr Tyr Glu Lys Trp Gly Glu Thr Trp Glu
835 840 845

Ile Gln Ala Leu Leu Arg Ala Ala Trp Val Ala Gly Asp Arg Glu Leu
850 855 860

Gly Ile Lys Phe Leu Glu Ser Ile Asp Arg Phe Arg Tyr Pro Val Asp
865 870 875 880

Gly Ala Thr Gln Ala Gln Leu Arg Glu Val Arg Arg Ile Lys Ala Arg
885 890 895

Val Asp Asn Glu Arg Leu Pro Arg Gly Ala Asp Arg Asn Thr His Thr
900 905 910

Lys Leu Gly Arg Gly Ala Leu Thr Asp Ile Glu Trp Thr Val Gln Leu
915 920 925

Leu Thr Met Met His Ala His Glu Ile Pro Glu Leu His Asn Thr Ser
930 935 940

Thr Leu Glu Val Leu Glu Val Leu Glu Lys His Gln Ile Ile Asn Pro
945 950 955 960

Val Gln Val Gln Thr Leu Arg Glu Ala Trp Leu Thr Ala Thr Ala Ala
965 970 975

Arg Asn Ala Leu Val Leu Val Arg Gly Lys Arg Leu Asp Gln Leu Pro

980 985 990

Thr Pro Gly Pro His Leu Ala Gln Val Ala Gly Ala Ser Gly Trp Asp
995 1000 1005

Pro Asn Glu Tyr Gln Glu Tyr Leu Glu Asn Tyr Leu Lys Val Thr Arg
1010 1015 1020

Lys Ser Arg Gln Val Val Asp Glu Val Phe Trp Gly Val Asp Ser Met
1025 1030 1035 1040

Glu Gln Arg Glu Phe
1045

<210> 101
<211> 861
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(861)
<223> RXN03176

<400> 101
gag ttg gcc gat tac atc ccg gaa cta aaa tct gcg gac cca aac ccg 48
Glu Leu Ala Asp Tyr Ile Pro Glu Leu Lys Ser Ala Asp Pro Asn Pro
1 5 10 15

ctg gca gta gcc ctg tgc acc gtt aac gga cac atc tac agc gca ggc 96
Leu Ala Val Ala Leu Cys Thr Val Asn Gly His Ile Tyr Ser Ala Gly
20 25 30

gat gac gac atc gaa ttc acc atg caa agt att tcc aag cca ttt gcc 144
Asp Asp Asp Ile Glu Phe Thr Met Gln Ser Ile Ser Lys Pro Phe Ala
35 40 45

tac gca ctc gca ctc caa gaa tgc ggc ttt gat gag gtc tct gca tcc 192
Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser
50 55 60

gtg gcc ttg gag ccc tcc ggt gag gcc ttc aac gaa ctt tcc ctc gac 240
Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp
65 70 75 80

ggc gaa aac cgc ccc atg aac ccc atg atc aac gcc ggc gcg atc gcc 288
Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala
85 90 95

atc aac cag ctg atc aac ggc tcc gat tcc acc gtg gaa gac cgc gtg 336
Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val
100 105 110

gaa aaa atc cga cac tac ttc tct gaa ctt gct gga cgc gaa ctc acc 384
Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr
115 120 125

atc gac cgc gtg ctt gcc gaa tcc gaa ctc gcc ggc gcc gac cgc aac 432
Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn
130 135 140

ctc tcc atc gcc cac atg ctg cgc aat tac ggc gtc atc gaa gac gaa 480
Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu
145 150 155 160

gcc cac gac gcc gtc ctc agc tac acg ctg caa tgc gcc atc aaa gta 528
Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val
165 170 175

acc acg cgc gac ctc gca gtc atg acc gcc acg ctc gcc gcc ggc ggc 576
Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly
180 185 190

aca cac cca att acc ggc aag aag ctt ctc gac gcc cgc gtc tgc cgc 624
Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg
195 200 205

ctc acc ctc tcc gtc atg gct tca gca ggc atg tac gac gag gca ggg 672
Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly
210 215 220

cag tgg ctc tcc acc gta ggc atc ccc gcg aaa tca gga gtc gcc ggc 720
Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly
225 230 235 240

gga ctc atc ggc att ctg cca ggt cag ctg ggc atc gcc aca ttt tcc 768
Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser
245 250 255

cca cgc ctg aac ccc aaa ggc aac agc gtg cgc ggc gta aaa ata ttc 816
Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe
260 265 270

aaa cag ctt tcc gac gac atg ggc ctc cac ctc atg tcc acc gag 861
Lys Gln Leu Ser Asp Asp Met Gly Leu His Leu Met Ser Thr Glu
275 280 285

<210> 102
<211> 287
<212> PRT
<213> Corynebacterium glutamicum

<400> 102
Glu Leu Ala Asp Tyr Ile Pro Glu Leu Lys Ser Ala Asp Pro Asn Pro
1 5 10 15

Leu Ala Val Ala Leu Cys Thr Val Asn Gly His Ile Tyr Ser Ala Gly
20 25 30

Asp Asp Asp Ile Glu Phe Thr Met Gln Ser Ile Ser Lys Pro Phe Ala
35 40 45

Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser
50 55 60

Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp
65 70 75 80

Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala
85 90 95

Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val
100 105 110

Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr
115 120 125

Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn
130 135 140

Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu
145 150 155 160

Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val
165 170 175

Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly
180 185 190

Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg
195 200 205

Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly
210 215 220

Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly
225 230 235 240

Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser
245 250 255

Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe
260 265 270

Lys Gln Leu Ser Asp Asp Met Gly Leu His Leu Met Ser Thr Glu
275 280 285

<210> 103
<211> 861
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(861)
<223> FRXA02879

<400> 103
gag ttg gcc gat tac atc ccg gaa cta aaa tct gcg gac cca aac ccg 48
Glu Leu Ala Asp Tyr Ile Pro Glu Leu Lys Ser Ala Asp Pro Asn Pro
1 5 10 15

ctg gca gta gcc ctg tgc acc gtt aac gga cac atc tac agc gca ggc 96
Leu Ala Val Ala Leu Cys Thr Val Asn Gly His Ile Tyr Ser Ala Gly
20 25 30

gat gac gac atc gaa ttc acc atg caa agt att tcc aag cca ttt gcc 144
Asp Asp Asp Ile Glu Phe Thr Met Gln Ser Ile Ser Lys Pro Phe Ala
35 40 45

```
tac gca ctc gca ctc caa gaa tgc ggc ttt gat gag gtc tct gca tcc     192
Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser
     50                  55                  60

gtg gcc ttg gag ccc tcc ggt gag gcc ttc aac gaa ctt tcc ctc gac     240
Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp
 65                  70                  75                  80

ggc gaa aac cgc ccc atg aac ccc atg atc aac gcc ggc gcg atc gcc     288
Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala
                 85                  90                  95

atc aac cag ctg atc aac ggc tcc gat tcc acc gtg gaa gac cgc gtg     336
Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val
            100                 105                 110

gaa aaa atc cga cac tac ttc tct gaa ctt gct gga cgc gaa ctc acc     384
Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr
        115                 120                 125

atc gac cgc gtg ctt gcc gaa tcc gaa ctc gcc ggc gcc gac cgc aac     432
Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn
    130                 135                 140

ctc tcc atc gcc cac atg ctg cgc aat tac ggc gtc atc gaa gac gaa     480
Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu
145                 150                 155                 160

gcc cac gac gcc gtc ctc agc tac acg ctg caa tgc gcc atc aaa gta     528
Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val
                165                 170                 175

acc acg cgc gac ctc gca gtc atg acc gcc acg ctc gcc gcc ggc ggc     576
Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly
            180                 185                 190

aca cac cca att acc ggc aag aag ctt ctc gac gcc cgc gtc tgc cgc     624
Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg
        195                 200                 205

ctc acc ctc tcc gtc atg gct tca gca ggc atg tac gac gag gca ggg     672
Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly
    210                 215                 220

cag tgg ctc tcc acc gta ggc atc ccc gcg aaa tca gga gtc gcc ggc     720
Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly
225                 230                 235                 240

gga ctc atc ggc att ctg cca ggt cag ctg ggc atc gcc aca ttt tcc     768
Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser
                245                 250                 255

cca cgc ctg aac ccc aaa ggc aac agc gtg cgc ggc gta aaa ata ttc     816
Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe
            260                 265                 270

aaa cag ctt tcc gac gac atg ggc ctc cac ctc atg tcc acc gag         861
Lys Gln Leu Ser Asp Asp Met Gly Leu His Leu Met Ser Thr Glu
        275                 280                 285
```

<210> 104
<211> 287
<212> PRT
<213> Corynebacterium glutamicum

<400> 104
Glu Leu Ala Asp Tyr Ile Pro Glu Leu Lys Ser Ala Asp Pro Asn Pro
1 5 10 15

Leu Ala Val Ala Leu Cys Thr Val Asn Gly His Ile Tyr Ser Ala Gly
20 25 30

Asp Asp Asp Ile Glu Phe Thr Met Gln Ser Ile Ser Lys Pro Phe Ala
35 40 45

Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser
50 55 60

Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp
65 70 75 80

Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala
85 90 95

Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val
100 105 110

Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr
115 120 125

Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn
130 135 140

Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu
145 150 155 160

Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val
165 170 175

Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly
180 185 190

Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg
195 200 205

Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly
210 215 220

Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly
225 230 235 240

Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser
245 250 255

Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe
260 265 270

Lys Gln Leu Ser Asp Asp Met Gly Leu His Leu Met Ser Thr Glu
275 280 285

<210> 105
<211> 1155
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1132)
<223> RXA00278

<400> 105
```
ggccacggag ttggtgtccg tcatggtgat gattctgtct gtcgtttctg tgttggcttt 60

gtgggtcggc atccgccccc gtttgcagga gtacttataa atg cac gct ttt cga   115
                                           Met His Ala Phe Arg
                                           1               5

cgc ccc cct cca ctc acc acg cga gtc ggc gct gca ttg ctg gcc gca   163
Arg Pro Pro Pro Leu Thr Thr Arg Val Gly Ala Ala Leu Leu Ala Ala
                10                  15                  20

acg ctg ctt gct tcc tgc act cca aca cct gtg gaa ccg gca gaa acc   211
Thr Leu Leu Ala Ser Cys Thr Pro Thr Pro Val Glu Pro Ala Glu Thr
            25                  30                  35

ttg act gct ttg gat ccc gat gcc ggt cca cca ctg cca ccg gat tct   259
Leu Thr Ala Leu Asp Pro Asp Ala Gly Pro Pro Leu Pro Pro Asp Ser
        40                  45                  50

tcg att gaa gct ccc ggt gaa aaa gag ccc att gtg gaa gta ata gag   307
Ser Ile Glu Ala Pro Gly Glu Lys Glu Pro Ile Val Glu Val Ile Glu
    55                  60                  65

aat tgg cca ggt tct tta cgc ccg gat gat ctg acc cct gag gag cgg   355
Asn Trp Pro Gly Ser Leu Arg Pro Asp Asp Leu Thr Pro Glu Glu Arg
70                  75                  80                  85

gta cct ggc atc gtc aac cgg ggt cgc atc att gtg ggt gtg gat caa   403
Val Pro Gly Ile Val Asn Arg Gly Arg Ile Ile Val Gly Val Asp Gln
                90                  95                  100

tcg caa aac ttg ctc agt ttc cgt gat ccg gtg act ggt gag ctg cgc   451
Ser Gln Asn Leu Leu Ser Phe Arg Asp Pro Val Thr Gly Glu Leu Arg
            105                 110                 115

ggt ttt gaa gtg gaa tta gcg agg gaa att tcc cgc gac att ttc ggt   499
Gly Phe Glu Val Glu Leu Ala Arg Glu Ile Ser Arg Asp Ile Phe Gly
        120                 125                 130

gac ccc aat aag gtg gat ttc cga ttc gtc ggc tcg tcc gac cgt ctg   547
Asp Pro Asn Lys Val Asp Phe Arg Phe Val Gly Ser Ser Asp Arg Leu
    135                 140                 145

cgt tcc ctt gac caa ggt gat gta gat att gtg att cgt tcc gtc acg   595
Arg Ser Leu Asp Gln Gly Asp Val Asp Ile Val Ile Arg Ser Val Thr
150                 155                 160                 165

atc acc gac gaa cgc gcc aaa ttg gtg gaa ttt tcc aca ccg tac ctg   643
Ile Thr Asp Glu Arg Ala Lys Leu Val Glu Phe Ser Thr Pro Tyr Leu
                170                 175                 180
```

```
cgc acc caa acc cgc atg ttg acc atg gaa tct tca gga atc acg tcc    691
Arg Thr Gln Thr Arg Met Leu Thr Met Glu Ser Ser Gly Ile Thr Ser
            185                 190                 195

atc gca gat cta ccc ggc cac acc att tgt gtc acc gat ggc tcc act    739
Ile Ala Asp Leu Pro Gly His Thr Ile Cys Val Thr Asp Gly Ser Thr
        200                 205                 210

tca ttg cag cga gcc cgc acc att gcg ccg gag gcc tca atc tta aaa    787
Ser Leu Gln Arg Ala Arg Thr Ile Ala Pro Glu Ala Ser Ile Leu Lys
    215                 220                 225

act cgc aat tgg tcc gat tgt ctc atg gcg ttg cag cag cat cag gct    835
Thr Arg Asn Trp Ser Asp Cys Leu Met Ala Leu Gln Gln His Gln Ala
230                 235                 240                 245

cag gtc att ttg ggc gat gat gtc att ttg tcc ggc atc gca gca cag    883
Gln Val Ile Leu Gly Asp Asp Val Ile Leu Ser Gly Ile Ala Ala Gln
                250                 255                 260

gat ccc tac acc gag att ctt gat acc tcc ctc gat tcc cat tcc tat    931
Asp Pro Tyr Thr Glu Ile Leu Asp Thr Ser Leu Asp Ser His Ser Tyr
            265                 270                 275

gga gtg gca gcg gca tcg acc act gct gaa aca gac tct tcg ggg ttg    979
Gly Val Ala Ala Ala Ser Thr Thr Ala Glu Thr Asp Ser Ser Gly Leu
        280                 285                 290

att cgg cag gta aac tac aca att gaa cgg atc cgc aca gac cgc atg
1027
Ile Arg Gln Val Asn Tyr Thr Ile Glu Arg Ile Arg Thr Asp Arg Met
    295                 300                 305

tgg tgg aca atg ttc gac gat tgg ttc gga cct tat ctc tgg tcc tac
1075
Trp Trp Thr Met Phe Asp Asp Trp Phe Gly Pro Tyr Leu Trp Ser Tyr
310                 315                 320                 325

ggt cca cca cag ctg cag tac atg cca gag gaa gaa ggg aca gaa aac
1123
Gly Pro Pro Gln Leu Gln Tyr Met Pro Glu Glu Glu Gly Thr Glu Asn
                330                 335                 340

gat gaa gga taatgaagat ttcgatccag att
1155
Asp Glu Gly
```

```
&lt;210&gt; 106
&lt;211&gt; 344
&lt;212&gt; PRT
&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 106
Met His Ala Phe Arg Arg Pro Pro Pro Leu Thr Thr Arg Val Gly Ala
  1               5                  10                  15

Ala Leu Leu Ala Ala Thr Leu Leu Ala Ser Cys Thr Pro Thr Pro Val
             20                  25                  30
```

Glu Pro Ala Glu Thr Leu Thr Ala Leu Asp Pro Asp Ala Gly Pro Pro
35 40 45

Leu Pro Pro Asp Ser Ser Ile Glu Ala Pro Gly Glu Lys Glu Pro Ile
50 55 60

Val Glu Val Ile Glu Asn Trp Pro Gly Ser Leu Arg Pro Asp Asp Leu
65 70 75 80

Thr Pro Glu Glu Arg Val Pro Gly Ile Val Asn Arg Gly Arg Ile Ile
85 90 95

Val Gly Val Asp Gln Ser Gln Asn Leu Leu Ser Phe Arg Asp Pro Val
100 105 110

Thr Gly Glu Leu Arg Gly Phe Glu Val Glu Leu Ala Arg Glu Ile Ser
115 120 125

Arg Asp Ile Phe Gly Asp Pro Asn Lys Val Asp Phe Arg Phe Val Gly
130 135 140

Ser Ser Asp Arg Leu Arg Ser Leu Asp Gln Gly Asp Val Asp Ile Val
145 150 155 160

Ile Arg Ser Val Thr Ile Thr Asp Glu Arg Ala Lys Leu Val Glu Phe
165 170 175

Ser Thr Pro Tyr Leu Arg Thr Gln Thr Arg Met Leu Thr Met Glu Ser
180 185 190

Ser Gly Ile Thr Ser Ile Ala Asp Leu Pro Gly His Thr Ile Cys Val
195 200 205

Thr Asp Gly Ser Thr Ser Leu Gln Arg Ala Arg Thr Ile Ala Pro Glu
210 215 220

Ala Ser Ile Leu Lys Thr Arg Asn Trp Ser Asp Cys Leu Met Ala Leu
225 230 235 240

Gln Gln His Gln Ala Gln Val Ile Leu Gly Asp Asp Val Ile Leu Ser
245 250 255

Gly Ile Ala Ala Gln Asp Pro Tyr Thr Glu Ile Leu Asp Thr Ser Leu
260 265 270

Asp Ser His Ser Tyr Gly Val Ala Ala Ala Ser Thr Thr Ala Glu Thr
275 280 285

Asp Ser Ser Gly Leu Ile Arg Gln Val Asn Tyr Thr Ile Glu Arg Ile
290 295 300

Arg Thr Asp Arg Met Trp Trp Thr Met Phe Asp Asp Trp Phe Gly Pro
305 310 315 320

Tyr Leu Trp Ser Tyr Gly Pro Pro Gln Leu Gln Tyr Met Pro Glu Glu
325 330 335

Glu Gly Thr Glu Asn Asp Glu Gly
340

<210> 107
<211> 1035
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1012)
<223> RXA00727

<400> 107
ttattgcacc atggcaggta gtattttgcc catgattgag agtttcaccc gattgcgaat 60

ttcgcagaca ccgcctctga aacggctact gcatagcact ttg cgt ttc ccc aaa 115
Leu Arg Phe Pro Lys
1 5

atc ccc aag cgc gct gta gcg gcg acc gtc ggc atc gtg gca acc tca 163
Ile Pro Lys Arg Ala Val Ala Ala Thr Val Gly Ile Val Ala Thr Ser
10 15 20

ttc acc ttg gct tct tgt gtc acc aat gag gag cag ggc aac cca gat 211
Phe Thr Leu Ala Ser Cys Val Thr Asn Glu Glu Gln Gly Asn Pro Asp
25 30 35

ggc tgg gag cag atc gtt cca gat cct gta ccg gag att cag gcg atg 259
Gly Trp Glu Gln Ile Val Pro Asp Pro Val Pro Glu Ile Gln Ala Met
40 45 50

gtt ccc gaa gct ctg gct cag cgc ggt gtg ctc acc gcc ggt gcc aac 307
Val Pro Glu Ala Leu Ala Gln Arg Gly Val Leu Thr Ala Gly Ala Asn
55 60 65

cca cct ttc cca ccg ttt gag ttt aaa gat tcc gat ggt cag att atc 355
Pro Pro Phe Pro Pro Phe Glu Phe Lys Asp Ser Asp Gly Gln Ile Ile
70 75 80 85

ggt gtg gaa atg gac ctc gtg cgt gca atg gcg ggg gtg atg ggc ttg 403
Gly Val Glu Met Asp Leu Val Arg Ala Met Ala Gly Val Met Gly Leu
90 95 100

gag ttc agc cct cag gag cag gat ttc tcc ctc atc ctt cca tcg gtt 451
Glu Phe Ser Pro Gln Glu Gln Asp Phe Ser Leu Ile Leu Pro Ser Val
105 110 115

caa gct ggc acc ctt gat atc gga gcc tct ggc ttc act gac aac gag 499
Gln Ala Gly Thr Leu Asp Ile Gly Ala Ser Gly Phe Thr Asp Asn Glu
120 125 130

gaa cgc cgc gag aac ttt gat ttc atc gat ttc ctc ttc gca ggt gtg 547
Glu Arg Arg Glu Asn Phe Asp Phe Ile Asp Phe Leu Phe Ala Gly Val
135 140 145

cag tgg gcg cag gca act gat cgt gaa acc cca atc gat ccg gaa aac 595
Gln Trp Ala Gln Ala Thr Asp Arg Glu Thr Pro Ile Asp Pro Glu Asn
150 155 160 165

gcc tgt ggt ctc acc gtt gct gta cag cgc aca acc gtg gca gag acc 643
Ala Cys Gly Leu Thr Val Ala Val Gln Arg Thr Thr Val Ala Glu Thr
170 175 180

gac gat gtc cgt cct cgc tca gct caa tgt gaa gcc gaa ggc aaa gag 691
Asp Asp Val Arg Pro Arg Ser Ala Gln Cys Glu Ala Glu Gly Lys Glu
185 190 195

ccg atc acc att ttg tct tat gaa acc gca gat act gca gct acc gca 739
Pro Ile Thr Ile Leu Ser Tyr Glu Thr Ala Asp Thr Ala Ala Thr Ala
200 205 210

ttg atc ctg gga cgc gca gac gca ctt gct gcg gac tcc cct gtt tca 787
Leu Ile Leu Gly Arg Ala Asp Ala Leu Ala Ala Asp Ser Pro Val Ser
215 220 225

gct tgg gct gca gag cgc tcc gaa ggc cgc atc gaa gtt gtg ggc gat 835
Ala Trp Ala Ala Glu Arg Ser Glu Gly Arg Ile Glu Val Val Gly Asp
230 235 240 245

atg tac ttg gct gcg cca ttt ggt ttc gca ttc ccg ttg gaa tct gac 883
Met Tyr Leu Ala Ala Pro Phe Gly Phe Ala Phe Pro Leu Glu Ser Asp
250 255 260

ctc acc cca gca gca gct gcg gcg ttc caa cac ttg att gac acc ggc 931
Leu Thr Pro Ala Ala Ala Ala Ala Phe Gln His Leu Ile Asp Thr Gly
265 270 275

gat tac cag cgc atc atg gcg caa tgg ggc att gaa gaa ggc ctt ctt 979
Asp Tyr Gln Arg Ile Met Ala Gln Trp Gly Ile Glu Glu Gly Leu Leu
280 285 290

gat gag gcc ctg atc aac gaa cag cca ctc aac tagagccttc cagcaactaa
1032
Asp Glu Ala Leu Ile Asn Glu Gln Pro Leu Asn
295 300

aaa
1035

<210> 108
<211> 304
<212> PRT
<213> Corynebacterium glutamicum

<400> 108
Leu Arg Phe Pro Lys Ile Pro Lys Arg Ala Val Ala Ala Thr Val Gly
1 5 10 15

Ile Val Ala Thr Ser Phe Thr Leu Ala Ser Cys Val Thr Asn Glu Glu
20 25 30

Gln Gly Asn Pro Asp Gly Trp Glu Gln Ile Val Pro Asp Pro Val Pro
35 40 45

Glu Ile Gln Ala Met Val Pro Glu Ala Leu Ala Gln Arg Gly Val Leu
50 55 60

Thr Ala Gly Ala Asn Pro Pro Phe Pro Pro Phe Glu Phe Lys Asp Ser
65 70 75 80

Asp Gly Gln Ile Ile Gly Val Glu Met Asp Leu Val Arg Ala Met Ala
85 90 95

```
Gly Val Met Gly Leu Glu Phe Ser Pro Gln Glu Gln Asp Phe Ser Leu
            100                 105                 110

Ile Leu Pro Ser Val Gln Ala Gly Thr Leu Asp Ile Gly Ala Ser Gly
        115                 120                 125

Phe Thr Asp Asn Glu Glu Arg Arg Glu Asn Phe Asp Phe Ile Asp Phe
    130                 135                 140

Leu Phe Ala Gly Val Gln Trp Ala Gln Ala Thr Asp Arg Glu Thr Pro
145                 150                 155                 160

Ile Asp Pro Glu Asn Ala Cys Gly Leu Thr Val Ala Val Gln Arg Thr
                165                 170                 175

Thr Val Ala Glu Thr Asp Asp Val Arg Pro Arg Ser Ala Gln Cys Glu
            180                 185                 190

Ala Glu Gly Lys Glu Pro Ile Thr Ile Leu Ser Tyr Glu Thr Ala Asp
        195                 200                 205

Thr Ala Ala Thr Ala Leu Ile Leu Gly Arg Ala Asp Ala Leu Ala Ala
    210                 215                 220

Asp Ser Pro Val Ser Ala Trp Ala Ala Glu Arg Ser Glu Gly Arg Ile
225                 230                 235                 240

Glu Val Val Gly Asp Met Tyr Leu Ala Ala Pro Phe Gly Phe Ala Phe
                245                 250                 255

Pro Leu Glu Ser Asp Leu Thr Pro Ala Ala Ala Ala Ala Phe Gln His
            260                 265                 270

Leu Ile Asp Thr Gly Asp Tyr Gln Arg Ile Met Ala Gln Trp Gly Ile
        275                 280                 285

Glu Glu Gly Leu Leu Asp Glu Ala Leu Ile Asn Glu Gln Pro Leu Asn
    290                 295                 300


<210> 109
<211> 1962
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1939)
<223> RXA02139

<400> 109
tcaggaggat ttttcaatca tgtgcggcct tcttggcata ttgactgcaa atgggaacgc 60

tgaagcattc gttcctgcac tcgagcgggc cttgccatgc atg cgc cac cgt ggt   115
                                            Met Arg His Arg Gly
                                             1               5

cct gac gat gcc ggc act tgg cat gac gcc gat gca gcg ttt gga ttc   163
```

```
Pro Asp Asp Ala Gly Thr Trp His Asp Ala Asp Ala Ala Phe Gly Phe
                10                  15                  20

aac cgc ctc tcc atc att gat att gca cac tcc cac caa cca ctg cgt     211
Asn Arg Leu Ser Ile Ile Asp Ile Ala His Ser His Gln Pro Leu Arg
            25                  30                  35

tgg gga cct gcg gat gaa ccc gac cgc tac gca atg act ttc aac ggt     259
Trp Gly Pro Ala Asp Glu Pro Asp Arg Tyr Ala Met Thr Phe Asn Gly
        40                  45                  50

gag atc tac aac tac gtt gag ctg cgt aaa gag ctc tcg gat ttg gga     307
Glu Ile Tyr Asn Tyr Val Glu Leu Arg Lys Glu Leu Ser Asp Leu Gly
    55                  60                  65

tat gcc ttt aat act tct ggc gat ggc gag cca att gtt gtc ggt ttc     355
Tyr Ala Phe Asn Thr Ser Gly Asp Gly Glu Pro Ile Val Val Gly Phe
70                  75                  80                  85

cac cac tgg ggc gag tcc gtg gtc gag cat ctc cgc gga atg ttc ggc     403
His His Trp Gly Glu Ser Val Val Glu His Leu Arg Gly Met Phe Gly
                90                  95                  100

att gcc att tgg gat aca aag gaa aag tcg ctt ttc ctt gcg cgt gat     451
Ile Ala Ile Trp Asp Thr Lys Glu Lys Ser Leu Phe Leu Ala Arg Asp
            105                 110                 115

cag ttc ggc att aag cca ctg ttc tac gca acc acc gag cat ggc acc     499
Gln Phe Gly Ile Lys Pro Leu Phe Tyr Ala Thr Thr Glu His Gly Thr
        120                 125                 130

gtg ttc tcc tca gag aag aag acc atc ttg gag atg gcc gag gag atg     547
Val Phe Ser Ser Glu Lys Lys Thr Ile Leu Glu Met Ala Glu Glu Met
    135                 140                 145

aat cta gat ctg ggc ctt gat aag cgc acc att gag cac tac gtg gac     595
Asn Leu Asp Leu Gly Leu Asp Lys Arg Thr Ile Glu His Tyr Val Asp
150                 155                 160                 165

ttg cag tac gtg ccc gag cca gat acc ctt cac gcg cag att tcc cgc     643
Leu Gln Tyr Val Pro Glu Pro Asp Thr Leu His Ala Gln Ile Ser Arg
                170                 175                 180

ttg gag tca ggc tgc acc gca aca gtt cgt ccg ggc ggc aag ctg gaa     691
Leu Glu Ser Gly Cys Thr Ala Thr Val Arg Pro Gly Gly Lys Leu Glu
            185                 190                 195

cag aag cgt tac ttc aag cct cag ttc cca gta cag aag gtc gta aag     739
Gln Lys Arg Tyr Phe Lys Pro Gln Phe Pro Val Gln Lys Val Val Lys
        200                 205                 210

ggt aag gag cag gac ctc ttc gat cgc att gcc cag gtg ttg gag gat     787
Gly Lys Glu Gln Asp Leu Phe Asp Arg Ile Ala Gln Val Leu Glu Asp
    215                 220                 225

agc gtc gaa aag cat atg cgt gcc gac gtg acc gta ggc tcg ttc ctt     835
Ser Val Glu Lys His Met Arg Ala Asp Val Thr Val Gly Ser Phe Leu
230                 235                 240                 245

ttc ggc ggc att gac tca acc gca att gcg gcg ctt gca aag cgc cac     883
Phe Gly Gly Ile Asp Ser Thr Ala Ile Ala Ala Leu Ala Lys Arg His
```

```
                250                 255                 260

aac cct gac ctg ctc acc ttc acc acc ggt ttc gag cgt gaa ggc tac     931
Asn Pro Asp Leu Leu Thr Phe Thr Thr Gly Phe Glu Arg Glu Gly Tyr
            265                 270                 275

tcg gag gtc gat gtg gct gcg gag tcc gcc gct gcg att ggc gct gag     979
Ser Glu Val Asp Val Ala Ala Glu Ser Ala Ala Ala Ile Gly Ala Glu
        280                 285                 290

cac atc gtg aag att gtc tcg cct gag gaa tac gcc aac gcg att cct
1027
His Ile Val Lys Ile Val Ser Pro Glu Glu Tyr Ala Asn Ala Ile Pro
    295                 300                 305

aag atc atg tgg tac ttg gat gat cct gta gct gac cca tca ttg gtc
1075
Lys Ile Met Trp Tyr Leu Asp Asp Pro Val Ala Asp Pro Ser Leu Val
310                 315                 320                 325

ccg ctg tac ttc gtg gca gcg gaa gca cgt aag cac gtc aag gtt gtg
1123
Pro Leu Tyr Phe Val Ala Ala Glu Ala Arg Lys His Val Lys Val Val
                330                 335                 340

ctg tct ggc gag ggc gca gat gag ctg ttc ggt gga tac acc att tac
1171
Leu Ser Gly Glu Gly Ala Asp Glu Leu Phe Gly Gly Tyr Thr Ile Tyr
            345                 350                 355

aag gag ccg cta tcg ctt gct cca ttt gag aag atc cct tcc cca cta
1219
Lys Glu Pro Leu Ser Leu Ala Pro Phe Glu Lys Ile Pro Ser Pro Leu
        360                 365                 370

cgt aaa ggc ctg gga aag ctc agc aag gtt ctg cca gac ggc atg aag
1267
Arg Lys Gly Leu Gly Lys Leu Ser Lys Val Leu Pro Asp Gly Met Lys
    375                 380                 385

ggc aag tcc ctt ctt gag cgt ggc tcc atg acc atg gaa gag cgc tac
1315
Gly Lys Ser Leu Leu Glu Arg Gly Ser Met Thr Met Glu Glu Arg Tyr
390                 395                 400                 405

tac ggc aac gct cgc tcc ttc aat ttc gag cag atg caa cgc gtt att
1363
Tyr Gly Asn Ala Arg Ser Phe Asn Phe Glu Gln Met Gln Arg Val Ile
                410                 415                 420

cca tgg gca aag cgc gaa tgg gac cac cgc gaa gtc act gcg ccg atc
1411
Pro Trp Ala Lys Arg Glu Trp Asp His Arg Glu Val Thr Ala Pro Ile
            425                 430                 435

tac gca cag tcc cgc aac ttt gat cca gta gcc cgc atg caa cac ctg
1459
Tyr Ala Gln Ser Arg Asn Phe Asp Pro Val Ala Arg Met Gln His Leu
        440                 445                 450
```

gat ctg ttc acc tgg atg cgc ggc gac atc ctg gtc aag gct gac aag
1507
Asp Leu Phe Thr Trp Met Arg Gly Asp Ile Leu Val Lys Ala Asp Lys
455 460 465

atc aac atg gcg aac tcc ctt gag ctg cga gtt cca ttc ttg gat aag
1555
Ile Asn Met Ala Asn Ser Leu Glu Leu Arg Val Pro Phe Leu Asp Lys
470 475 480 485

gaa gtt ttc aag gtt gca gag acc att cct tac gac ctg aag att gcc
1603
Glu Val Phe Lys Val Ala Glu Thr Ile Pro Tyr Asp Leu Lys Ile Ala
490 495 500

aac ggt acc acc aag tac gcg ctg cgc agg gca ctc gag cag att gtt
1651
Asn Gly Thr Thr Lys Tyr Ala Leu Arg Arg Ala Leu Glu Gln Ile Val
505 510 515

ccg cct cac gtt ttg cac cgc aag aag ctg ggc ttc cct gtt ccc atg
1699
Pro Pro His Val Leu His Arg Lys Lys Leu Gly Phe Pro Val Pro Met
520 525 530

cgc cac tgg ctt gcc ggc gat gag ctg ttc ggt tgg gcg cag gac acc
1747
Arg His Trp Leu Ala Gly Asp Glu Leu Phe Gly Trp Ala Gln Asp Thr
535 540 545

atc aag gaa tcc ggt act gaa gat atc ttc aac aag cag gct gtg ctg
1795
Ile Lys Glu Ser Gly Thr Glu Asp Ile Phe Asn Lys Gln Ala Val Leu
550 555 560 565

gat atg ctg aac gag cac cgc gat ggc gtg tca gat cat tcc cgt cga
1843
Asp Met Leu Asn Glu His Arg Asp Gly Val Ser Asp His Ser Arg Arg
570 575 580

ctg tgg act gtt ctg tca ttt atg gtg tgg cac ggc att ttt gtg gaa
1891
Leu Trp Thr Val Leu Ser Phe Met Val Trp His Gly Ile Phe Val Glu
585 590 595

aac cgc att gat cca cag att gag gac cgc tcc tac cca gtc gag ctt
1939
Asn Arg Ile Asp Pro Gln Ile Glu Asp Arg Ser Tyr Pro Val Glu Leu
600 605 610

taagtcttaa agcctaaacc ccc
1962

<210> 110
<211> 613
<212> PRT
<213> Corynebacterium glutamicum

<400> 110
Met Arg His Arg Gly Pro Asp Asp Ala Gly Thr Trp His Asp Ala Asp

1 5 10 15

Ala Ala Phe Gly Phe Asn Arg Leu Ser Ile Ile Asp Ile Ala His Ser
20 25 30

His Gln Pro Leu Arg Trp Gly Pro Ala Asp Glu Pro Asp Arg Tyr Ala
35 40 45

Met Thr Phe Asn Gly Glu Ile Tyr Asn Tyr Val Glu Leu Arg Lys Glu
50 55 60

Leu Ser Asp Leu Gly Tyr Ala Phe Asn Thr Ser Gly Asp Gly Glu Pro
65 70 75 80

Ile Val Val Gly Phe His His Trp Gly Glu Ser Val Val Glu His Leu
85 90 95

Arg Gly Met Phe Gly Ile Ala Ile Trp Asp Thr Lys Glu Lys Ser Leu
100 105 110

Phe Leu Ala Arg Asp Gln Phe Gly Ile Lys Pro Leu Phe Tyr Ala Thr
115 120 125

Thr Glu His Gly Thr Val Phe Ser Ser Glu Lys Lys Thr Ile Leu Glu
130 135 140

Met Ala Glu Glu Met Asn Leu Asp Leu Gly Leu Asp Lys Arg Thr Ile
145 150 155 160

Glu His Tyr Val Asp Leu Gln Tyr Val Pro Glu Pro Asp Thr Leu His
165 170 175

Ala Gln Ile Ser Arg Leu Glu Ser Gly Cys Thr Ala Thr Val Arg Pro
180 185 190

Gly Gly Lys Leu Glu Gln Lys Arg Tyr Phe Lys Pro Gln Phe Pro Val
195 200 205

Gln Lys Val Val Lys Gly Lys Glu Gln Asp Leu Phe Asp Arg Ile Ala
210 215 220

Gln Val Leu Glu Asp Ser Val Glu Lys His Met Arg Ala Asp Val Thr
225 230 235 240

Val Gly Ser Phe Leu Phe Gly Gly Ile Asp Ser Thr Ala Ile Ala Ala
245 250 255

Leu Ala Lys Arg His Asn Pro Asp Leu Leu Thr Phe Thr Thr Gly Phe
260 265 270

Glu Arg Glu Gly Tyr Ser Glu Val Asp Val Ala Ala Glu Ser Ala Ala
275 280 285

Ala Ile Gly Ala Glu His Ile Val Lys Ile Val Ser Pro Glu Glu Tyr
290 295 300

Ala Asn Ala Ile Pro Lys Ile Met Trp Tyr Leu Asp Asp Pro Val Ala
305 310 315 320

Asp Pro Ser Leu Val Pro Leu Tyr Phe Val Ala Ala Glu Ala Arg Lys
325 330 335

His Val Lys Val Val Leu Ser Gly Glu Gly Ala Asp Glu Leu Phe Gly
340 345 350

Gly Tyr Thr Ile Tyr Lys Glu Pro Leu Ser Leu Ala Pro Phe Glu Lys
355 360 365

Ile Pro Ser Pro Leu Arg Lys Gly Leu Gly Lys Leu Ser Lys Val Leu
370 375 380

Pro Asp Gly Met Lys Gly Lys Ser Leu Leu Glu Arg Gly Ser Met Thr
385 390 395 400

Met Glu Glu Arg Tyr Tyr Gly Asn Ala Arg Ser Phe Asn Phe Glu Gln
405 410 415

Met Gln Arg Val Ile Pro Trp Ala Lys Arg Glu Trp Asp His Arg Glu
420 425 430

Val Thr Ala Pro Ile Tyr Ala Gln Ser Arg Asn Phe Asp Pro Val Ala
435 440 445

Arg Met Gln His Leu Asp Leu Phe Thr Trp Met Arg Gly Asp Ile Leu
450 455 460

Val Lys Ala Asp Lys Ile Asn Met Ala Asn Ser Leu Glu Leu Arg Val
465 470 475 480

Pro Phe Leu Asp Lys Glu Val Phe Lys Val Ala Glu Thr Ile Pro Tyr
485 490 495

Asp Leu Lys Ile Ala Asn Gly Thr Thr Lys Tyr Ala Leu Arg Arg Ala
500 505 510

Leu Glu Gln Ile Val Pro Pro His Val Leu His Arg Lys Lys Leu Gly
515 520 525

Phe Pro Val Pro Met Arg His Trp Leu Ala Gly Asp Glu Leu Phe Gly
530 535 540

Trp Ala Gln Asp Thr Ile Lys Glu Ser Gly Thr Glu Asp Ile Phe Asn
545 550 555 560

Lys Gln Ala Val Leu Asp Met Leu Asn Glu His Arg Asp Gly Val Ser
565 570 575

Asp His Ser Arg Arg Leu Trp Thr Val Leu Ser Phe Met Val Trp His
580 585 590

Gly Ile Phe Val Glu Asn Arg Ile Asp Pro Gln Ile Glu Asp Arg Ser
595 600 605

Tyr Pro Val Glu Leu
610

<210> 111
<211> 1284
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1261)
<223> RXN00116

<400> 111

```
cgcggcacgc acgctggggg caagcgtcga caagcacaaa ctttttgctt aattgaatcc 60

tttgcgcacc aatcaatggg ggatcaaata tagtagctgc atg agt aat gac ttc   115
                                            Met Ser Asn Asp Phe
                                            1               5

gtc gtt tct agg ctt aga ccc ttt ggt gaa acg att ttt gca acc atg   163
Val Val Ser Arg Leu Arg Pro Phe Gly Glu Thr Ile Phe Ala Thr Met
            10                  15                  20

acc cag cga gct gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt   211
Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe
        25                  30                  35

cct gat gag gat ggt cct cgt cgg atg tta gag atc gcg tcg gag cag   259
Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln
    40                  45                  50

att ctc ggg gga aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg   307
Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser
55                  60                  65

ttg agg gca gct gtg gct cgt gat cat ttg gag agg ttt gat ctg gag   355
Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu
70                  75                  80                  85

tac aac cct gat tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg   403
Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala
                90                  95                  100

att acg gcg act gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc   451
Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile
            105                 110                 115

gtt ttg gaa ccg tat tac gat gcg tat gcg gcg gct att gcg ttg gcg   499
Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala
        120                 125                 130

ggg gcg acg cgg gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg   547
Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp
    135                 140                 145

gat gtg gat gtc gat aag ttg cat gcg gcg gtg act aag aag acg cgg   595
Asp Val Asp Val Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg
150                 155                 160                 165

atg att atc gtt aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct   643
Met Ile Ile Val Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser
                170                 175                 180

aag aag gcg ttg aag cag ttg gcg ggt gtt gct cgt gcg tat gac ttg   691
Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala Arg Ala Tyr Asp Leu
            185                 190                 195

ttg gtg ttg tca gat gag gtg tat gag cat ctt gtt ttt gat gat cag   739
```

```
Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu Val Phe Asp Asp Gln
        200                 205                 210

aag cat gtg agt gtc gcg aag ctg ccc ggt atg tgg gat cgc acg gtg    787
Lys His Val Ser Val Ala Lys Leu Pro Gly Met Trp Asp Arg Thr Val
    215                 220                 225

acg gtg tcg tcg gcg gcg aaa acg ttc aat gtg act ggt tgg aag acg    835
Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val Thr Gly Trp Lys Thr
230                 235                 240                 245

ggg tgg gcg ttg gca ccg gag ccg ttg ttg gag gcg gtg ttg aag gcg    883
Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu Ala Val Leu Lys Ala
                250                 255                 260

aag cag ttt atg tct tat gtg ggg gct aca cct ttt cag ccg gct gtg    931
Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro Phe Gln Pro Ala Val
            265                 270                 275

gcg cat gcg att gaa cat gag cag aag tgg gtg tca aag atg tct aag    979
Ala His Ala Ile Glu His Glu Gln Lys Trp Val Ser Lys Met Ser Lys
        280                 285                 290

ggg ctt gag ctc aag cgg gat att ttg cgt act gcg tta gat aag gcg
1027
Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr Ala Leu Asp Lys Ala
    295                 300                 305

ggg ctg aag act cat gac agt atg ggc acg tat ttc atc gtt gcg gat
1075
Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr Phe Ile Val Ala Asp
310                 315                 320                 325

att ggg gat cgt gat ggt gcg gag ttc tgt ttt gag ttg att gag aag
1123
Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe Glu Leu Ile Glu Lys
                330                 335                 340

gtt ggg gtg gcg gcg att ccg gtg cag gcg ttt gtg gat cat ccg aag
1171
Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe Val Asp His Pro Lys
            345                 350                 355

aag tgg tcg tcg aag gtt cgt ttt gcg ttt tgc aaa aaa gaa gag acg
1219
Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys Lys Lys Glu Glu Thr
        360                 365                 370

ctc cgc gaa gct gcg gag cgt ctc aag ggg att aag aaa cta
1261
Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile Lys Lys Leu
    375                 380                 385

tagtttgaac aggttgttgg ggg
1284


<210> 112
<211> 387
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 112

Met Ser Asn Asp Phe Val Val Ser Arg Leu Arg Pro Phe Gly Glu Thr
1 5 10 15

Ile Phe Ala Thr Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn
20 25 30

Leu Gly Gln Gly Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu
35 40 45

Ile Ala Ser Glu Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly
50 55 60

Arg Gly Asp Ala Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu
65 70 75 80

Arg Phe Asp Leu Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val
85 90 95

Gly Ala Thr Glu Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro
100 105 110

Gly Asp Glu Val Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala
115 120 125

Ala Ile Ala Leu Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu
130 135 140

Val Glu Asn Ser Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val
145 150 155 160

Thr Lys Lys Thr Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr
165 170 175

Gly Ser Val Phe Ser Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala
180 185 190

Arg Ala Tyr Asp Leu Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu
195 200 205

Val Phe Asp Asp Gln Lys His Val Ser Val Ala Lys Leu Pro Gly Met
210 215 220

Trp Asp Arg Thr Val Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val
225 230 235 240

Thr Gly Trp Lys Thr Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu
245 250 255

Ala Val Leu Lys Ala Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro
260 265 270

Phe Gln Pro Ala Val Ala His Ala Ile Glu His Glu Gln Lys Trp Val
275 280 285

Ser Lys Met Ser Lys Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr
290 295 300

Ala Leu Asp Lys Ala Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr
305 310 315 320

Phe Ile Val Ala Asp Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe
325 330 335

Glu Leu Ile Glu Lys Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe
340 345 350

Val Asp His Pro Lys Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys
355 360 365

Lys Lys Glu Glu Thr Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile
370 375 380

Lys Lys Leu
385

<210> 113
<211> 607
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(607)
<223> FRXA00116

<400> 113
tttgcgcacc aatcaatggg ggatcaaata tagtagctgc atgagtaatg acttcgtcgt 60

ttctaggctt agaccctttg gtgaaacgat ttttgcaacc atg acc cag cga gct 115
Met Thr Gln Arg Ala
1 5

gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt cct gat gag gat 163
Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe Pro Asp Glu Asp
10 15 20

ggt cct cgt cgg atg tta gag atc gcg tcg gag cag att ctc ggg gga 211
Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln Ile Leu Gly Gly
25 30 35

aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg ttg agg gca gct 259
Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser Leu Arg Ala Ala
40 45 50

gtg gct cgt gat cat ttg gag agg ttt gat ctg gag tac aac cct gat 307
Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu Tyr Asn Pro Asp
55 60 65

tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg att acg gcg act 355
Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala Ile Thr Ala Thr
70 75 80 85

gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc gtt ttg gaa ccg 403
Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile Val Leu Glu Pro
90 95 100

tat tac gat gcg tat gcg gcg gct att gcg ttg gcg ggg gcg acg cgg 451
Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala Gly Ala Thr Arg
105 110 115

```
gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg gat gtg gat gtc    499
Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp Asp Val Asp Val
        120                 125                 130

gat aag ttg cat gcg gcg gtg act aag aag acg cgg atg att atc gtt    547
Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg Met Ile Ile Val
    135                 140                 145

aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct aag aag gcg ttg    595
Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser Lys Lys Ala Leu
150                 155                 160                 165

aag cag ttg gcg                                                    607
Lys Gln Leu Ala


&lt;210&gt; 114
&lt;211&gt; 169
&lt;212&gt; PRT
&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 114
Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly
  1               5                  10                  15

Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu
             20                  25                  30

Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala
         35                  40                  45

Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu
     50                  55                  60

Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu
 65                  70                  75                  80

Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val
                 85                  90                  95

Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu
            100                 105                 110

Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser
        115                 120                 125

Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr
    130                 135                 140

Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe
145                 150                 155                 160

Ser Lys Lys Ala Leu Lys Gln Leu Ala
                165


&lt;210&gt; 115
&lt;211&gt; 1230
&lt;212&gt; DNA
```

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1207)
<223> RXN00618

<400> 115
gctgcattag agggtcgtat ctcgatctaa aagcagtacg cagataggct tgtctcttat 60

gaagccaagc actagaagca atgttcagcc gtttcgcgtc atg cag atg ttg gac 115
Met Gln Met Leu Asp
1 5

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163
Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys
10 15 20

gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211
Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala
25 30 35

gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259
Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly
40 45 50

gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307
Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr
55 60 65

gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355
Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser
70 75 80 85

ggt gga ttc gtg gca tcg ttt atc gcc acc ttg gat cac ggg gat tat 403
Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu Asp His Gly Asp Tyr
90 95 100

gtg gca atg cct acc ccg ggg tac ccg gca tat cgc aat att ctg gaa 451
Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr Arg Asn Ile Leu Glu
105 110 115

tct ttg ggg gcg aag gtt ctg aac ctg cgc tgt act gca gag act cgt 499
Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys Thr Ala Glu Thr Arg
120 125 130

ttc cag cca acc gct caa atg ttg gag gaa ctg cca cac aag ccg aag 547
Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu Pro His Lys Pro Lys
135 140 145

gct gtt att gtc acc agc cca gga aac cca acg ggc acc atc att gat 595
Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr Gly Thr Ile Ile Asp
150 155 160 165

ccg gaa gag cta gag cgc atc gcc aag tgg tgc gat gac aat gat gct 643
Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys Asp Asp Asn Asp Ala
170 175 180

gtt ctt atc tct gat gag gac tac cac ggc atg agc ttt ggt cgt ccg 691
Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met Ser Phe Gly Arg Pro
185 190 195

ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt acc 739
Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly Thr
200 205 210

ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc atc 787
Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile Ile
215 220 225

gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct ctt 835
Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser Leu
230 235 240 245

tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc ttc 883
Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala Phe
250 255 260

act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat cgc 931
Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr Arg
265 270 275

gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt ggc 979
Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu Gly
280 285 290

act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt tct
1027
Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val Ser
295 300 305

gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat gaa
1075
Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp Glu
310 315 320 325

gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa ggc
1123
Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu Gly
330 335 340

cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc att
1171
His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr Ile
345 350 355

gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac
1217
Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys
360 365

taggttagtt tcg
1230

<210> 116
<211> 369
<212> PRT
<213> Corynebacterium glutamicum

<400> 116
Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp

```
1               5                   10                  15

Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala
            20                  25                  30

Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr
        35                  40                  45

Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp
    50                  55                  60

His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val
65                  70                  75                  80

Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu
                85                  90                  95

Asp His Gly Asp Tyr Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr
            100                 105                 110

Arg Asn Ile Leu Glu Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys
        115                 120                 125

Thr Ala Glu Thr Arg Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu
    130                 135                 140

Pro His Lys Pro Lys Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr
145                 150                 155                 160

Gly Thr Ile Ile Asp Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys
                165                 170                 175

Asp Asp Asn Asp Ala Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met
            180                 185                 190

Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala
        195                 200                 205

Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg
    210                 215                 220

Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn
225                 230                 235                 240

Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala
                245                 250                 255

Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His
            260                 265                 270

Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro
        275                 280                 285

Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu
    290                 295                 300

Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu
305                 310                 315                 320

Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe
                325                 330                 335
```

Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser
340 345 350

Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys
355 360 365

Lys

<210> 117
<211> 657
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(634)
<223> FRXA00618

<400> 117
cccaacgggc accatcattg atccggaaga gctagagcgc atcgccaagt ggtgcgatga 60

caatgatgct gttcttatct ctgatgagga ctaccacggc atg agc ttt ggt cgt 115
Met Ser Phe Gly Arg
1 5

ccg ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt 163
Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly
10 15 20

acc ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc 211
Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile
25 30 35

atc gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct 259
Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser
40 45 50

ctt tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc 307
Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala
55 60 65

ttc act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat 355
Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr
70 75 80 85

cgc gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt 403
Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu
90 95 100

ggc act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt 451
Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val
105 110 115

tct gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat 499
Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp
120 125 130

gaa gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa 547

Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu
135 140 145

ggc cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc 595
Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr
150 155 160 165

att gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac 644
Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys
170 175

taggttagtt tcg 657

<210> 118
<211> 178
<212> PRT
<213> Corynebacterium glutamicum

<400> 118
Met Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn
1 5 10 15

Ala Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp
20 25 30

Arg Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu
35 40 45

Asn Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala
50 55 60

Ala Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala
65 70 75 80

His Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu
85 90 95

Pro Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr
100 105 110

Leu Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala
115 120 125

Leu Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp
130 135 140

Phe Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala
145 150 155 160

Ser Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile
165 170 175

Lys Lys

<210> 119
<211> 385
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(385)
<223> FRXA00627

<400> 119
gctgcattag agggtcgtat ctcgatctaa aagcagtacg cagataggct tgtctcttat 60

gaagccaagc actagaagca atgttcagcc gtttcgcgtc atg cag atg ttg gac 115
Met Gln Met Leu Asp
1 5

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163
Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys
10 15 20

gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211
Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala
25 30 35

gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259
Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly
40 45 50

gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307
Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr
55 60 65

gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355
Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser
70 75 80 85

ggt gga ttc gtg gca tcg ttt atc gcc acc 385
Gly Gly Phe Val Ala Ser Phe Ile Ala Thr
90 95

<210> 120
<211> 95
<212> PRT
<213> Corynebacterium glutamicum

<400> 120
Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp
1 5 10 15

Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala
20 25 30

Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr
35 40 45

Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp
50 55 60

His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val
65 70 75 80

Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr
85 90 95

<210> 121
<211> 1434
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1411)
<223> RXA02550

<400> 121
gatcttaggc agccgtggga ttacaccctt ttagagctag aacagtaaaa attcacccaa 60

tagctttcaa ctacgcacac aaagtggcaa cattgagcgg gtg act aca gac aag 115
Val Thr Thr Asp Lys
1 5

cgc aaa acc tct aag acc acc gac acc gcc aac aag gct gtg ggc gcg 163
Arg Lys Thr Ser Lys Thr Thr Asp Thr Ala Asn Lys Ala Val Gly Ala
10 15 20

gat cag gca gcg cgt ccc act cgg cga aca act cgc cgc atc ttc gat 211
Asp Gln Ala Ala Arg Pro Thr Arg Arg Thr Thr Arg Arg Ile Phe Asp
25 30 35

cag tcg gag aag atg aag gac gtg ctg tac gag atc cgt ggc ccg gtg 259
Gln Ser Glu Lys Met Lys Asp Val Leu Tyr Glu Ile Arg Gly Pro Val
40 45 50

gcc gcg gag gcg gaa cgc atg gag ctt gat ggg cat aac atc tta aag 307
Ala Ala Glu Ala Glu Arg Met Glu Leu Asp Gly His Asn Ile Leu Lys
55 60 65

ctc aac acg gga aat cca gcc gtg ttc gga ttc gat gcc ccc gac gtg 355
Leu Asn Thr Gly Asn Pro Ala Val Phe Gly Phe Asp Ala Pro Asp Val
70 75 80 85

att atg cgt gac atg atc gcc aac ctt cca act tcc caa ggg tat tcc 403
Ile Met Arg Asp Met Ile Ala Asn Leu Pro Thr Ser Gln Gly Tyr Ser
90 95 100

acc tcc aaa ggc att att ccg gcc cgg cga gca gtg gtc acc cgc tac 451
Thr Ser Lys Gly Ile Ile Pro Ala Arg Arg Ala Val Val Thr Arg Tyr
105 110 115

gaa gtt gtg ccc gga ttc ccc cac ttc gat gtt gat gat gtg ttc tta 499
Glu Val Val Pro Gly Phe Pro His Phe Asp Val Asp Asp Val Phe Leu
120 125 130

ggc aac ggt gtc tca gaa cta atc acc atg acc acc caa gca ctc ctc 547
Gly Asn Gly Val Ser Glu Leu Ile Thr Met Thr Thr Gln Ala Leu Leu
135 140 145

aac gac ggc gat gaa gtt ctt atc ccc gca ccg gac tac cca ctg tgg 595
Asn Asp Gly Asp Glu Val Leu Ile Pro Ala Pro Asp Tyr Pro Leu Trp
150 155 160 165

act gcc gca acc tcc ctg gct ggt ggt aag cct gtg cac tac ctc tgt 643
Thr Ala Ala Thr Ser Leu Ala Gly Gly Lys Pro Val His Tyr Leu Cys

170 175 180

gat gag gaa gat gac tgg aac cca tcc atc gaa gac atc aag tcc aaa 691
Asp Glu Glu Asp Asp Trp Asn Pro Ser Ile Glu Asp Ile Lys Ser Lys
185 190 195

atc tca gag aaa acc aaa gct att gtg gtg atc aac ccc aac aac ccc 739
Ile Ser Glu Lys Thr Lys Ala Ile Val Val Ile Asn Pro Asn Asn Pro
200 205 210

acg gga gct gtc tac ccg cgc cgg gtg ttg gaa caa atc gtc gag att 787
Thr Gly Ala Val Tyr Pro Arg Arg Val Leu Glu Gln Ile Val Glu Ile
215 220 225

gca cgc gag cat gac ctg ctg att ttg gcc gat gaa atc tac gac cgc 835
Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp Glu Ile Tyr Asp Arg
230 235 240 245

att ctc tac gat gat gcc gag cac atc agc ctg gca acc ctt gca cca 883
Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu Ala Thr Leu Ala Pro
250 255 260

gat ctc ctt tgc atc aca tac aac ggt cta tcc aag gca tac cgc gtc 931
Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser Lys Ala Tyr Arg Val
265 270 275

gca gga tac cga gct ggc tgg atg gta ttg act gga cca aag caa tac 979
Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr Gly Pro Lys Gln Tyr
280 285 290

gca cgt gga ttt att gag ggc ctc gaa ctc ctc gca ggc act cga ctc
1027
Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu Ala Gly Thr Arg Leu
295 300 305

tgc cca aat gtc cca gct cag cac gct att cag gta gct ctg ggt gga
1075
Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln Val Ala Leu Gly Gly
310 315 320 325

cgc cag tcc atc tac gac ctc act ggc gaa cac ggc cga ctc ctg gaa
1123
Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His Gly Arg Leu Leu Glu
330 335 340

cag cgc aac atg gca tgg acg aaa ctc aac gaa atc cca ggt gtc agc
1171
Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu Ile Pro Gly Val Ser
345 350 355

tgt gtg aaa cca atg gga gct cta tac gcg ttc ccc aag ctc gac ccc
1219
Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe Pro Lys Leu Asp Pro
360 365 370

aac gtg tac gaa atc cac gac gac acc caa ctc atg ctg gat ctt ctc
1267
Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu Met Leu Asp Leu Leu
375 380 385

cgt gcc gag aaa atc ctc atg gtt cag ggc act ggc ttc aac tgg cca
1315
Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr Gly Phe Asn Trp Pro
390 395 400 405

cat cac gat cac ttc cga gtg gtc acc ctg cca tgg gca tcc cag ttg
1363
His His Asp His Phe Arg Val Val Thr Leu Pro Trp Ala Ser Gln Leu
410 415 420

gaa aac gca att gag cgc ctg ggt aac ttc ctg tcc act tac aag cag
1411
Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu Ser Thr Tyr Lys Gln
425 430 435

tagtagttgt taggattcac cac
1434

<210> 122
<211> 437
<212> PRT
<213> Corynebacterium glutamicum

<400> 122
Val Thr Thr Asp Lys Arg Lys Thr Ser Lys Thr Thr Asp Thr Ala Asn
1 5 10 15

Lys Ala Val Gly Ala Asp Gln Ala Ala Arg Pro Thr Arg Arg Thr Thr
20 25 30

Arg Arg Ile Phe Asp Gln Ser Glu Lys Met Lys Asp Val Leu Tyr Glu
35 40 45

Ile Arg Gly Pro Val Ala Ala Glu Ala Glu Arg Met Glu Leu Asp Gly
50 55 60

His Asn Ile Leu Lys Leu Asn Thr Gly Asn Pro Ala Val Phe Gly Phe
65 70 75 80

Asp Ala Pro Asp Val Ile Met Arg Asp Met Ile Ala Asn Leu Pro Thr
85 90 95

Ser Gln Gly Tyr Ser Thr Ser Lys Gly Ile Ile Pro Ala Arg Arg Ala
100 105 110

Val Val Thr Arg Tyr Glu Val Val Pro Gly Phe Pro His Phe Asp Val
115 120 125

Asp Asp Val Phe Leu Gly Asn Gly Val Ser Glu Leu Ile Thr Met Thr
130 135 140

Thr Gln Ala Leu Leu Asn Asp Gly Asp Glu Val Leu Ile Pro Ala Pro
145 150 155 160

Asp Tyr Pro Leu Trp Thr Ala Ala Thr Ser Leu Ala Gly Gly Lys Pro
165 170 175

Val His Tyr Leu Cys Asp Glu Glu Asp Asp Trp Asn Pro Ser Ile Glu
180 185 190

Asp Ile Lys Ser Lys Ile Ser Glu Lys Thr Lys Ala Ile Val Val Ile
195 200 205

Asn Pro Asn Asn Pro Thr Gly Ala Val Tyr Pro Arg Arg Val Leu Glu
210 215 220

Gln Ile Val Glu Ile Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp
225 230 235 240

Glu Ile Tyr Asp Arg Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu
245 250 255

Ala Thr Leu Ala Pro Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser
260 265 270

Lys Ala Tyr Arg Val Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr
275 280 285

Gly Pro Lys Gln Tyr Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu
290 295 300

Ala Gly Thr Arg Leu Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln
305 310 315 320

Val Ala Leu Gly Gly Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His
325 330 335

Gly Arg Leu Leu Glu Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu
340 345 350

Ile Pro Gly Val Ser Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe
355 360 365

Pro Lys Leu Asp Pro Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu
370 375 380

Met Leu Asp Leu Leu Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr
385 390 395 400

Gly Phe Asn Trp Pro His His Asp His Phe Arg Val Val Thr Leu Pro
405 410 415

Trp Ala Ser Gln Leu Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu
420 425 430

Ser Thr Tyr Lys Gln
435

<210> 123
<211> 1701
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1678)
<223> RXA02193

<400> 123
cccccgaaaa tgtagtgggt agttccacac tgcctcttac aagtacgtag gataatccac 60

```
agcaccattg tgatttcctt caacttgtga gaggcagtac atg tct aag acg agc    115
                                            Met Ser Lys Thr Ser
                                             1               5

aac aag tct tca gca gac tca aag aat gac gca aaa gcc gaa gac att    163
Asn Lys Ser Ser Ala Asp Ser Lys Asn Asp Ala Lys Ala Glu Asp Ile
                 10                  15                  20

gtg aac ggc gag aac caa atc gcc acg aat gag tcg cag tct tca gac    211
Val Asn Gly Glu Asn Gln Ile Ala Thr Asn Glu Ser Gln Ser Ser Asp
             25                  30                  35

agc gct gca gtt tcg gaa cgt gtc gtc gaa cca aaa acc acg gtt cag    259
Ser Ala Ala Val Ser Glu Arg Val Val Glu Pro Lys Thr Thr Val Gln
         40                  45                  50

aaa aag ttc cga atc gaa tcg gat ctg ctt ggt gaa ctt cag atc cca    307
Lys Lys Phe Arg Ile Glu Ser Asp Leu Leu Gly Glu Leu Gln Ile Pro
     55                  60                  65

tcc cac gca tat tac ggg gtg cac acc ctt cgt gcg gtg gac aac ttc    355
Ser His Ala Tyr Tyr Gly Val His Thr Leu Arg Ala Val Asp Asn Phe
 70                  75                  80                  85

caa atc tca cga acc acc atc aac cac gtc cca gat ttc att cgc ggc    403
Gln Ile Ser Arg Thr Thr Ile Asn His Val Pro Asp Phe Ile Arg Gly
                 90                  95                 100

atg gtc cag gtg aaa aag gcc gca gct tta gca aac cgc cga ctg cac    451
Met Val Gln Val Lys Lys Ala Ala Ala Leu Ala Asn Arg Arg Leu His
            105                 110                 115

aca ctt cca gca caa aaa gca gaa gca att gtc tgg gct tgt gat cag    499
Thr Leu Pro Ala Gln Lys Ala Glu Ala Ile Val Trp Ala Cys Asp Gln
        120                 125                 130

atc ctc att gag gaa cgc tgt atg gat cag ttc ccc atc gat gtg ttc    547
Ile Leu Ile Glu Glu Arg Cys Met Asp Gln Phe Pro Ile Asp Val Phe
    135                 140                 145

cag ggt ggc gca ggt acc tca ctg aac atg aac acc aac gag gtt gtt    595
Gln Gly Gly Ala Gly Thr Ser Leu Asn Met Asn Thr Asn Glu Val Val
150                 155                 160                 165

gcc aac ctt gca ctt gag ttc tta ggc cat gaa aag ggc gag tac cac    643
Ala Asn Leu Ala Leu Glu Phe Leu Gly His Glu Lys Gly Glu Tyr His
                170                 175                 180

atc ctg cac ccc atg gat gat gtg aac atg tcc cag tcc acc aac gat    691
Ile Leu His Pro Met Asp Asp Val Asn Met Ser Gln Ser Thr Asn Asp
            185                 190                 195

tcc tac cca act ggt ttc cgc ctg ggc att tac gct gga ctg cag acc    739
Ser Tyr Pro Thr Gly Phe Arg Leu Gly Ile Tyr Ala Gly Leu Gln Thr
        200                 205                 210

ctc atc gct gaa att gat gag ctt cag gtt gcg ttc cgc cac aag ggc    787
Leu Ile Ala Glu Ile Asp Glu Leu Gln Val Ala Phe Arg His Lys Gly
    215                 220                 225
```

```
aat gag ttt gtc gac atc atc aag atg ggc cgc acc cag ttg cag gat      835
Asn Glu Phe Val Asp Ile Ile Lys Met Gly Arg Thr Gln Leu Gln Asp
230                 235                 240                 245

gct gtt ccc atg agc ttg ggc gaa gag ttc cga gca ttc gcg cac aac      883
Ala Val Pro Met Ser Leu Gly Glu Glu Phe Arg Ala Phe Ala His Asn
                250                 255                 260

ctc gca gaa gag cag acc gtg ctg cgt gaa gct gcc aac cgt ctc ctc      931
Leu Ala Glu Glu Gln Thr Val Leu Arg Glu Ala Ala Asn Arg Leu Leu
            265                 270                 275

gag gtc aat ctt ggt gca acc gca atc ggt act ggt gtg aac act cca      979
Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr Gly Val Asn Thr Pro
        280                 285                 290

gca ggc tac cgc cac cag gtt gtc gct gct ctg tct gag gtc acc gga
1027
Ala Gly Tyr Arg His Gln Val Val Ala Ala Leu Ser Glu Val Thr Gly
    295                 300                 305

ctg gaa cta aag tcc gca cgt gat ctc atc gag gct acc tct gac acc
1075
Leu Glu Leu Lys Ser Ala Arg Asp Leu Ile Glu Ala Thr Ser Asp Thr
310                 315                 320                 325

ggt gca tat gtt cat gcg cac tcc gca atc aag cgt gca gcc atg aaa
1123
Gly Ala Tyr Val His Ala His Ser Ala Ile Lys Arg Ala Ala Met Lys
                330                 335                 340

ctg tcc aag atc tgt aac gat cta cgt ctg ctg tct tct ggt cct cgt
1171
Leu Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro Arg
            345                 350                 355

gct ggc ttg aac gaa atc aac ctg cca cca cgc cag gct ggt tcc tcc
1219
Ala Gly Leu Asn Glu Ile Asn Leu Pro Pro Arg Gln Ala Gly Ser Ser
        360                 365                 370

atc atg cca gcc aag gtc aac cca gtg atc cca gaa gtg gtc aac cag
1267
Ile Met Pro Ala Lys Val Asn Pro Val Ile Pro Glu Val Val Asn Gln
    375                 380                 385

gtc tgc ttc aag gtc ttc ggt aac gat ctc acc gtc acc atg gct gcg
1315
Val Cys Phe Lys Val Phe Gly Asn Asp Leu Thr Val Thr Met Ala Ala
390                 395                 400                 405

gaa gct ggc cag ttg cag ctc aac gtc atg gag cca gtc att ggc gaa
1363
Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu Pro Val Ile Gly Glu
                410                 415                 420

tcc ctc ttc cag tca ctg cgc atc ctg ggc aat gca gcc aag act ttg
1411
Ser Leu Phe Gln Ser Leu Arg Ile Leu Gly Asn Ala Ala Lys Thr Leu
            425                 430                 435
```

cgt gag aag tgc gtc gta gga atc acc gcc aac gct gat gtt tgc cgt
1459
Arg Glu Lys Cys Val Val Gly Ile Thr Ala Asn Ala Asp Val Cys Arg
440 445 450

gct tac gtt gat aac tcc atc ggg att atc act tac ctg aac cca ttc
1507
Ala Tyr Val Asp Asn Ser Ile Gly Ile Ile Thr Tyr Leu Asn Pro Phe
455 460 465

ctg ggc cac gac att gga gat cag atc ggt aag gaa gca gcc gaa act
1555
Leu Gly His Asp Ile Gly Asp Gln Ile Gly Lys Glu Ala Ala Glu Thr
470 475 480 485

ggt cga cca gtg cgt gaa ctc atc ctg gaa aag aag ctc atg gat gaa
1603
Gly Arg Pro Val Arg Glu Leu Ile Leu Glu Lys Lys Leu Met Asp Glu
490 495 500

aag acg ctc gag gca gtc ctg tcc aag gag aac ctc atg cac cca atg
1651
Lys Thr Leu Glu Ala Val Leu Ser Lys Glu Asn Leu Met His Pro Met
505 510 515

ttc cgc gga agg ctc tac ttg gag aac taatccaaga tctcgtctga
1698
Phe Arg Gly Arg Leu Tyr Leu Glu Asn
520 525

tac
1701

<210> 124
<211> 526
<212> PRT
<213> Corynebacterium glutamicum

<400> 124
Met Ser Lys Thr Ser Asn Lys Ser Ser Ala Asp Ser Lys Asn Asp Ala
1 5 10 15

Lys Ala Glu Asp Ile Val Asn Gly Glu Asn Gln Ile Ala Thr Asn Glu
20 25 30

Ser Gln Ser Ser Asp Ser Ala Ala Val Ser Glu Arg Val Val Glu Pro
35 40 45

Lys Thr Thr Val Gln Lys Lys Phe Arg Ile Glu Ser Asp Leu Leu Gly
50 55 60

Glu Leu Gln Ile Pro Ser His Ala Tyr Tyr Gly Val His Thr Leu Arg
65 70 75 80

Ala Val Asp Asn Phe Gln Ile Ser Arg Thr Thr Ile Asn His Val Pro
85 90 95

Asp Phe Ile Arg Gly Met Val Gln Val Lys Lys Ala Ala Ala Leu Ala
100 105 110

Asn Arg Arg Leu His Thr Leu Pro Ala Gln Lys Ala Glu Ala Ile Val
115 120 125

Trp Ala Cys Asp Gln Ile Leu Ile Glu Glu Arg Cys Met Asp Gln Phe
130 135 140

Pro Ile Asp Val Phe Gln Gly Gly Ala Gly Thr Ser Leu Asn Met Asn
145 150 155 160

Thr Asn Glu Val Val Ala Asn Leu Ala Leu Glu Phe Leu Gly His Glu
165 170 175

Lys Gly Glu Tyr His Ile Leu His Pro Met Asp Asp Val Asn Met Ser
180 185 190

Gln Ser Thr Asn Asp Ser Tyr Pro Thr Gly Phe Arg Leu Gly Ile Tyr
195 200 205

Ala Gly Leu Gln Thr Leu Ile Ala Glu Ile Asp Glu Leu Gln Val Ala
210 215 220

Phe Arg His Lys Gly Asn Glu Phe Val Asp Ile Ile Lys Met Gly Arg
225 230 235 240

Thr Gln Leu Gln Asp Ala Val Pro Met Ser Leu Gly Glu Glu Phe Arg
245 250 255

Ala Phe Ala His Asn Leu Ala Glu Glu Gln Thr Val Leu Arg Glu Ala
260 265 270

Ala Asn Arg Leu Leu Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr
275 280 285

Gly Val Asn Thr Pro Ala Gly Tyr Arg His Gln Val Val Ala Ala Leu
290 295 300

Ser Glu Val Thr Gly Leu Glu Leu Lys Ser Ala Arg Asp Leu Ile Glu
305 310 315 320

Ala Thr Ser Asp Thr Gly Ala Tyr Val His Ala His Ser Ala Ile Lys
325 330 335

Arg Ala Ala Met Lys Leu Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu
340 345 350

Ser Ser Gly Pro Arg Ala Gly Leu Asn Glu Ile Asn Leu Pro Pro Arg
355 360 365

Gln Ala Gly Ser Ser Ile Met Pro Ala Lys Val Asn Pro Val Ile Pro
370 375 380

Glu Val Val Asn Gln Val Cys Phe Lys Val Phe Gly Asn Asp Leu Thr
385 390 395 400

Val Thr Met Ala Ala Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu
405 410 415

Pro Val Ile Gly Glu Ser Leu Phe Gln Ser Leu Arg Ile Leu Gly Asn
420 425 430

Ala Ala Lys Thr Leu Arg Glu Lys Cys Val Val Gly Ile Thr Ala Asn

435 440 445

Ala Asp Val Cys Arg Ala Tyr Val Asp Asn Ser Ile Gly Ile Ile Thr
450 455 460

Tyr Leu Asn Pro Phe Leu Gly His Asp Ile Gly Asp Gln Ile Gly Lys
465 470 475 480

Glu Ala Ala Glu Thr Gly Arg Pro Val Arg Glu Leu Ile Leu Glu Lys
485 490 495

Lys Leu Met Asp Glu Lys Thr Leu Glu Ala Val Leu Ser Lys Glu Asn
500 505 510

Leu Met His Pro Met Phe Arg Gly Arg Leu Tyr Leu Glu Asn
515 520 525

<210> 125
<211> 1098
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1075)
<223> RXA02432

<400> 125
cacgtgattc atttgtgacc aacaaccgaa actgagccag aagactgtca atcccctgct 60

gtgcacataa caactgcagc tagttgatac gctagagcgc atg tcg aag cag cac 115
Met Ser Lys Gln His
1 5

tcc aca cca tta aac aat gat gaa gaa cac act tcc gct cct caa aag 163
Ser Thr Pro Leu Asn Asn Asp Glu Glu His Thr Ser Ala Pro Gln Lys
10 15 20

gtt gcg gta atc acc acg ggc gga acc atc gcc tgt act tcc gac gca 211
Val Ala Val Ile Thr Thr Gly Gly Thr Ile Ala Cys Thr Ser Asp Ala
25 30 35

aat ggg cat ctg ctt ccc acc gtc agc ggt gca gac ctg ctt gcg cca 259
Asn Gly His Leu Leu Pro Thr Val Ser Gly Ala Asp Leu Leu Ala Pro
40 45 50

atc gca cca cgg ttc aat gga gcg cag atc gct ttc gaa atc cac gaa 307
Ile Ala Pro Arg Phe Asn Gly Ala Gln Ile Ala Phe Glu Ile His Glu
55 60 65

atc aac cgc ctt gat tcc tcc tcc atg acg ttt gag gat ctc gat tcc 355
Ile Asn Arg Leu Asp Ser Ser Ser Met Thr Phe Glu Asp Leu Asp Ser
70 75 80 85

atc atc gcc acg gtt cat aag gtg ttg gag gat ccg gat gtt gtt ggc 403
Ile Ile Ala Thr Val His Lys Val Leu Glu Asp Pro Asp Val Val Gly
90 95 100

gta gta gtt acc cac ggc acc gat tcc atg gaa gag tcc gcc atc gcc 451
Val Val Val Thr His Gly Thr Asp Ser Met Glu Glu Ser Ala Ile Ala

105 110 115

gta gac acc ttc ctt gat gat ccc cgc cca gtc att ttc acc ggc gcc 499
Val Asp Thr Phe Leu Asp Asp Pro Arg Pro Val Ile Phe Thr Gly Ala
120 125 130

caa aaa ccc ttc gat cat ccc gaa gcc gac ggc cca aac aac ctt ttc 547
Gln Lys Pro Phe Asp His Pro Glu Ala Asp Gly Pro Asn Asn Leu Phe
135 140 145

gaa gcc tgc ctc atc gca tcc gac ccc tcc gct cgc gga att ggt gca 595
Glu Ala Cys Leu Ile Ala Ser Asp Pro Ser Ala Arg Gly Ile Gly Ala
150 155 160 165

ctc att gtc ttc ggt cac gcc gtc atc cct gct cgc ggc tgc gtt aaa 643
Leu Ile Val Phe Gly His Ala Val Ile Pro Ala Arg Gly Cys Val Lys
170 175 180

tgg cac acc tct gat gag ctg gcg ttt gca acc aac ggc cct gaa gaa 691
Trp His Thr Ser Asp Glu Leu Ala Phe Ala Thr Asn Gly Pro Glu Glu
185 190 195

cca gag cgc ccc gat gcg ctg ccc gta gct aaa ttg gcg gat gtc tct 739
Pro Glu Arg Pro Asp Ala Leu Pro Val Ala Lys Leu Ala Asp Val Ser
200 205 210

gtc gaa atc atc ccc gca tac cct ggt gcc acc ggc gca atg gtg gaa 787
Val Glu Ile Ile Pro Ala Tyr Pro Gly Ala Thr Gly Ala Met Val Glu
215 220 225

gct gcc atc gct gcc ggt gct caa gga ctt gta gtg gaa gca atg gga 835
Ala Ala Ile Ala Ala Gly Ala Gln Gly Leu Val Val Glu Ala Met Gly
230 235 240 245

tca ggc aat gtt ggt tcc cgc atg ggt gat gcc cta ggt aaa gca ctt 883
Ser Gly Asn Val Gly Ser Arg Met Gly Asp Ala Leu Gly Lys Ala Leu
250 255 260

gac gct gga att ccc gtg gtg atg agc act agg gtt cct cgt ggt gaa 931
Asp Ala Gly Ile Pro Val Val Met Ser Thr Arg Val Pro Arg Gly Glu
265 270 275

gta tcc gga gtg tat ggc ggt gca ggt gga ggt gcg act ttg gct gcg 979
Val Ser Gly Val Tyr Gly Gly Ala Gly Gly Gly Ala Thr Leu Ala Ala
280 285 290

aag ggc gct gtg gga tct cgc tac ttc aga gct ggt cag gca cgt att
1027
Lys Gly Ala Val Gly Ser Arg Tyr Phe Arg Ala Gly Gln Ala Arg Ile
295 300 305

ttg ctc gcg att gcc att gcg acg ggc gca cat ccg gtg acg ctt tac
1075
Leu Leu Ala Ile Ala Ile Ala Thr Gly Ala His Pro Val Thr Leu Tyr
310 315 320 325

taatttcgcc cttggtcttg cat
1098

<210> 126

<211> 325
<212> PRT
<213> Corynebacterium glutamicum

<400> 126
Met Ser Lys Gln His Ser Thr Pro Leu Asn Asn Asp Glu Glu His Thr
1 5 10 15

Ser Ala Pro Gln Lys Val Ala Val Ile Thr Thr Gly Gly Thr Ile Ala
20 25 30

Cys Thr Ser Asp Ala Asn Gly His Leu Leu Pro Thr Val Ser Gly Ala
35 40 45

Asp Leu Leu Ala Pro Ile Ala Pro Arg Phe Asn Gly Ala Gln Ile Ala
50 55 60

Phe Glu Ile His Glu Ile Asn Arg Leu Asp Ser Ser Ser Met Thr Phe
65 70 75 80

Glu Asp Leu Asp Ser Ile Ile Ala Thr Val His Lys Val Leu Glu Asp
85 90 95

Pro Asp Val Val Gly Val Val Val Thr His Gly Thr Asp Ser Met Glu
100 105 110

Glu Ser Ala Ile Ala Val Asp Thr Phe Leu Asp Asp Pro Arg Pro Val
115 120 125

Ile Phe Thr Gly Ala Gln Lys Pro Phe Asp His Pro Glu Ala Asp Gly
130 135 140

Pro Asn Asn Leu Phe Glu Ala Cys Leu Ile Ala Ser Asp Pro Ser Ala
145 150 155 160

Arg Gly Ile Gly Ala Leu Ile Val Phe Gly His Ala Val Ile Pro Ala
165 170 175

Arg Gly Cys Val Lys Trp His Thr Ser Asp Glu Leu Ala Phe Ala Thr
180 185 190

Asn Gly Pro Glu Glu Pro Glu Arg Pro Asp Ala Leu Pro Val Ala Lys
195 200 205

Leu Ala Asp Val Ser Val Glu Ile Ile Pro Ala Tyr Pro Gly Ala Thr
210 215 220

Gly Ala Met Val Glu Ala Ala Ile Ala Ala Gly Ala Gln Gly Leu Val
225 230 235 240

Val Glu Ala Met Gly Ser Gly Asn Val Gly Ser Arg Met Gly Asp Ala
245 250 255

Leu Gly Lys Ala Leu Asp Ala Gly Ile Pro Val Val Met Ser Thr Arg
260 265 270

Val Pro Arg Gly Glu Val Ser Gly Val Tyr Gly Gly Ala Gly Gly Gly
275 280 285

Ala Thr Leu Ala Ala Lys Gly Ala Val Gly Ser Arg Tyr Phe Arg Ala
290 295 300

```
Gly Gln Ala Arg Ile Leu Leu Ala Ile Ala Ile Ala Thr Gly Ala His
305                 310                 315                 320

Pro Val Thr Leu Tyr
                325


<210> 127
<211> 775
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(775)
<223> RXN03003

<400> 127
tcgatgatct gggctcccca ggtggtgcgg ctaagcttgg accacaagat tttgatcacc 60

caatgatcgc tgcgctgccg cctcaggcat aatctaacgc atg acc tct cgc acc    115
                                           Met Thr Ser Arg Thr
                                           1               5

ccg ctt gtt tct gtt ctt cct gat ttt ccg tgg gat tcg ctc gct tcc    163
Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp Asp Ser Leu Ala Ser
                10                  15                  20

gca aaa gcc aaa gct gcg tct cac ccg gat ggg atc gtg aat ctt tct    211
Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly Ile Val Asn Leu Ser
            25                  30                  35

gtt ggc act ccg gtt gat ccg gtc gcg ccc agc att cag atc gcg ttg    259
Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser Ile Gln Ile Ala Leu
        40                  45                  50

gca gaa gca gcg ggg ttt tcg ggt tac cct caa acc atc ggc acc ccg    307
Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln Thr Ile Gly Thr Pro
    55                  60                  65

gaa ctc cgc gca gcc atc agg ggc gcg ctt gag cgg cgc tac aac atg    355
Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu Arg Arg Tyr Asn Met
70                  75                  80                  85

aca aag ctt gtc gac gcc tcc ctc ctc ccc gtc gtg ggt acc aag gag    403
Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val Val Gly Thr Lys Glu
                90                  95                  100

gca att gcc ctt ctt cca ttc gcg ttg ggt att tcc ggc acc gtt gtc    451
Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile Ser Gly Thr Val Val
            105                 110                 115

atc cca gag att gcg tac cca acc tac gaa gtc gct gtc gtg gcc gca    499
Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val Ala Val Val Ala Ala
        120                 125                 130

gga tgc acc gtg ttg cgt tct gat tcg ctg ttt aag ctc ggc ccg cag    547
Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe Lys Leu Gly Pro Gln
    135                 140                 145
```

```
atc ccg tcg atg atg ttt atc aac tca cca tcc aac ccc aca ggc aag     595
Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser Asn Pro Thr Gly Lys
150                 155                 160                 165

gtt ctg ggc atc cca cac ttg cgc aag gtt gtg aag tgg gcg cag gaa     643
Val Leu Gly Ile Pro His Leu Arg Lys Val Val Lys Trp Ala Gln Glu
                170                 175                 180

aac aac gtg atc ctc gca gct gat gaa tgc tac ttg ggt ctt ggc tgg     691
Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr Leu Gly Leu Gly Trp
            185                 190                 195

gac gat gaa aac cca ccg atc tca att ttg gat cca cgt gtc tgc gat     739
Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp Pro Arg Val Cys Asp
        200                 205                 210

ggc gac cac acc aac ttg atc gcc att cac tcg ctg                     775
Gly Asp His Thr Asn Leu Ile Ala Ile His Ser Leu
    215                 220                 225


<210> 128
<211> 225
<212> PRT
<213> Corynebacterium glutamicum

<400> 128
Met Thr Ser Arg Thr Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp
 1               5                  10                  15

Asp Ser Leu Ala Ser Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly
            20                  25                  30

Ile Val Asn Leu Ser Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser
        35                  40                  45

Ile Gln Ile Ala Leu Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln
    50                  55                  60

Thr Ile Gly Thr Pro Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu
65                  70                  75                  80

Arg Arg Tyr Asn Met Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val
                85                  90                  95

Val Gly Thr Lys Glu Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile
            100                 105                 110

Ser Gly Thr Val Val Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val
        115                 120                 125

Ala Val Val Ala Ala Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe
    130                 135                 140

Lys Leu Gly Pro Gln Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser
145                 150                 155                 160

Asn Pro Thr Gly Lys Val Leu Gly Ile Pro His Leu Arg Lys Val Val
                165                 170                 175

Lys Trp Ala Gln Glu Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr
```

180 185 190

Leu Gly Leu Gly Trp Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp
195 200 205

Pro Arg Val Cys Asp Gly Asp His Thr Asn Leu Ile Ala Ile His Ser
210 215 220

Leu
225

<210> 129
<211> 1206
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1183)
<223> RXN00508

<400> 129
agccacgtgt ttaaggatag ttgaaagcgt ggggcaatac tggcactaac cccggcacca 60

atcgtatttc tgtccgcggt tggtggcaca atagttcaac atg aac ttg ctg acc 115
Met Asn Leu Leu Thr
1 5

acc aaa att gac ctg gat gcc atc gcc cat aac acg agg gtg ctt aaa 163
Thr Lys Ile Asp Leu Asp Ala Ile Ala His Asn Thr Arg Val Leu Lys
10 15 20

caa atg gcg ggt ccg gcg aag ctg atg gcg gtg gtg aag gcg aat gca 211
Gln Met Ala Gly Pro Ala Lys Leu Met Ala Val Val Lys Ala Asn Ala
25 30 35

tat aac cat ggc gta gag aag gtc gct ccg gtt att gct gct cat ggt 259
Tyr Asn His Gly Val Glu Lys Val Ala Pro Val Ile Ala Ala His Gly
40 45 50

gcg gat gcg ttt ggt gtg gca act ctt gcg gag gct atg cag ttg cgt 307
Ala Asp Ala Phe Gly Val Ala Thr Leu Ala Glu Ala Met Gln Leu Arg
55 60 65

gat atc ggc atc agc caa gag gtt ttg tgt tgg att tgg aca ccg gag 355
Asp Ile Gly Ile Ser Gln Glu Val Leu Cys Trp Ile Trp Thr Pro Glu
70 75 80 85

cag gat ttc cgc gcc gcc att gat cgc aat att gat ttg gct gtt att 403
Gln Asp Phe Arg Ala Ala Ile Asp Arg Asn Ile Asp Leu Ala Val Ile
90 95 100

tct ccc gcg cat gcc aaa gcc ttg atc gaa act gat gcg gag cat att 451
Ser Pro Ala His Ala Lys Ala Leu Ile Glu Thr Asp Ala Glu His Ile
105 110 115

cgg gtg tcc atc aag att gat tct ggg ttg cat cgt tcg ggt gtg gat 499
Arg Val Ser Ile Lys Ile Asp Ser Gly Leu His Arg Ser Gly Val Asp
120 125 130

gag cag gag tgg gag ggc gtg ttc agc gcg ttg gct gct gcc ccg cac 547
Glu Gln Glu Trp Glu Gly Val Phe Ser Ala Leu Ala Ala Ala Pro His
135 140 145

att gag gtc acg ggc atg ttc acg cac ttg gcg tgc gcg gat gag cca 595
Ile Glu Val Thr Gly Met Phe Thr His Leu Ala Cys Ala Asp Glu Pro
150 155 160 165

gag aat ccg gaa act gat cgc caa att att gct ttt cga cgc gcc ctt 643
Glu Asn Pro Glu Thr Asp Arg Gln Ile Ile Ala Phe Arg Arg Ala Leu
170 175 180

gcg ctc gcc cgc aag cac ggg ctt gag tgc ccg gtc aac cac gta tgc 691
Ala Leu Ala Arg Lys His Gly Leu Glu Cys Pro Val Asn His Val Cys
185 190 195

aac tca cct gca ttc ttg act cga tct gat tta cac atg gag atg gtc 739
Asn Ser Pro Ala Phe Leu Thr Arg Ser Asp Leu His Met Glu Met Val
200 205 210

cga ccg ggt ttg gcc ttt tat ggg ttg gaa ccc gtg gcg gga ctg gag 787
Arg Pro Gly Leu Ala Phe Tyr Gly Leu Glu Pro Val Ala Gly Leu Glu
215 220 225

cat ggt ttg aag ccg gcg atg acg tgg gag gcg aag gtg agc gtc gta 835
His Gly Leu Lys Pro Ala Met Thr Trp Glu Ala Lys Val Ser Val Val
230 235 240 245

aag caa att gaa gct gga caa ggc act tcc tat ggc ctg acc tgg cgc 883
Lys Gln Ile Glu Ala Gly Gln Gly Thr Ser Tyr Gly Leu Thr Trp Arg
250 255 260

gct gag gat cgc ggc ttt gtg gct gtg gtg cct gcg ggc tat gcc gat 931
Ala Glu Asp Arg Gly Phe Val Ala Val Val Pro Ala Gly Tyr Ala Asp
265 270 275

ggc atg ccg cgg cat gcc cag ggg aaa ttc tcc gtc acg att gat ggc 979
Gly Met Pro Arg His Ala Gln Gly Lys Phe Ser Val Thr Ile Asp Gly
280 285 290

ctg gac tat ccg cag gtt ggg cgc gta tgc atg gat cag ttc gtt att
1027
Leu Asp Tyr Pro Gln Val Gly Arg Val Cys Met Asp Gln Phe Val Ile
295 300 305

tct ttg ggc gac aat cca cac ggc gtg gaa gct ggg gcg aag gcc gtg
1075
Ser Leu Gly Asp Asn Pro His Gly Val Glu Ala Gly Ala Lys Ala Val
310 315 320 325

ata ttc ggt gag aat ggg cat gac gca act gat ttt gcg gag cgt tta
1123
Ile Phe Gly Glu Asn Gly His Asp Ala Thr Asp Phe Ala Glu Arg Leu
330 335 340

gac acc att aac tat gag gta gtg tgc cga cca acc ggc cga act gtc
1171
Asp Thr Ile Asn Tyr Glu Val Val Cys Arg Pro Thr Gly Arg Thr Val
345 350 355

cgc gca tat gtt taagtgaata cgtttaagga gca
1206
Arg Ala Tyr Val
360

<210> 130
<211> 361
<212> PRT
<213> Corynebacterium glutamicum

<400> 130
Met Asn Leu Leu Thr Thr Lys Ile Asp Leu Asp Ala Ile Ala His Asn
1 5 10 15

Thr Arg Val Leu Lys Gln Met Ala Gly Pro Ala Lys Leu Met Ala Val
20 25 30

Val Lys Ala Asn Ala Tyr Asn His Gly Val Glu Lys Val Ala Pro Val
35 40 45

Ile Ala Ala His Gly Ala Asp Ala Phe Gly Val Ala Thr Leu Ala Glu
50 55 60

Ala Met Gln Leu Arg Asp Ile Gly Ile Ser Gln Glu Val Leu Cys Trp
65 70 75 80

Ile Trp Thr Pro Glu Gln Asp Phe Arg Ala Ala Ile Asp Arg Asn Ile
85 90 95

Asp Leu Ala Val Ile Ser Pro Ala His Ala Lys Ala Leu Ile Glu Thr
100 105 110

Asp Ala Glu His Ile Arg Val Ser Ile Lys Ile Asp Ser Gly Leu His
115 120 125

Arg Ser Gly Val Asp Glu Gln Glu Trp Glu Gly Val Phe Ser Ala Leu
130 135 140

Ala Ala Ala Pro His Ile Glu Val Thr Gly Met Phe Thr His Leu Ala
145 150 155 160

Cys Ala Asp Glu Pro Glu Asn Pro Glu Thr Asp Arg Gln Ile Ile Ala
165 170 175

Phe Arg Arg Ala Leu Ala Leu Ala Arg Lys His Gly Leu Glu Cys Pro
180 185 190

Val Asn His Val Cys Asn Ser Pro Ala Phe Leu Thr Arg Ser Asp Leu
195 200 205

His Met Glu Met Val Arg Pro Gly Leu Ala Phe Tyr Gly Leu Glu Pro
210 215 220

Val Ala Gly Leu Glu His Gly Leu Lys Pro Ala Met Thr Trp Glu Ala
225 230 235 240

Lys Val Ser Val Val Lys Gln Ile Glu Ala Gly Gln Gly Thr Ser Tyr
245 250 255

Gly Leu Thr Trp Arg Ala Glu Asp Arg Gly Phe Val Ala Val Val Pro

```
            260                 265                 270

Ala Gly Tyr Ala Asp Gly Met Pro Arg His Ala Gln Gly Lys Phe Ser
        275                 280                 285

Val Thr Ile Asp Gly Leu Asp Tyr Pro Gln Val Gly Arg Val Cys Met
    290                 295                 300

Asp Gln Phe Val Ile Ser Leu Gly Asp Asn Pro His Gly Val Glu Ala
305                 310                 315                 320

Gly Ala Lys Ala Val Ile Phe Gly Glu Asn Gly His Asp Ala Thr Asp
                325                 330                 335

Phe Ala Glu Arg Leu Asp Thr Ile Asn Tyr Glu Val Val Cys Arg Pro
            340                 345                 350

Thr Gly Arg Thr Val Arg Ala Tyr Val
        355                 360


<210> 131
<211> 1152
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1129)
<223> RXN00636

<400> 131
tcatgggatt cagcaaggcg gccacccgaa ccgtctttgg tggaggagta ggagcgatga 60

tcgatctggc ccgttcgaac ataaggaata ttcctactcc atg atg att gat aca    115
                                            Met Met Ile Asp Thr
                                             1               5

cct gct gtt ctc att gac cgc gag cgc tta act gcc aac att tcc agg    163
Pro Ala Val Leu Ile Asp Arg Glu Arg Leu Thr Ala Asn Ile Ser Arg
                10                  15                  20

atg gca gct cac gcc ggt gcc cat gag att gcc ctg cgt ccg cat gtg    211
Met Ala Ala His Ala Gly Ala His Glu Ile Ala Leu Arg Pro His Val
            25                  30                  35

aaa acg cac aaa atc att gaa att gcg cag atg cag gtc gac gcc ggt    259
Lys Thr His Lys Ile Ile Glu Ile Ala Gln Met Gln Val Asp Ala Gly
        40                  45                  50

gcc cga ggg atc acc tgc gca acc att ggc gag gcg gaa att ttt gcc    307
Ala Arg Gly Ile Thr Cys Ala Thr Ile Gly Glu Ala Glu Ile Phe Ala
    55                  60                  65

ggc gca ggt ttt acg gac atc ttt att gca tat ccg ctg tat cta acc    355
Gly Ala Gly Phe Thr Asp Ile Phe Ile Ala Tyr Pro Leu Tyr Leu Thr
70                  75                  80                  85

gat cat gca gtg caa cgc ctg aac gcg atc ccc gga gaa att tcc att    403
Asp His Ala Val Gln Arg Leu Asn Ala Ile Pro Gly Glu Ile Ser Ile
                90                  95                  100
```

ggc gtg gat tcg gta gag atg gca cag gcg acg gcg ggt ttg cgg gaa 451
Gly Val Asp Ser Val Glu Met Ala Gln Ala Thr Ala Gly Leu Arg Glu
105 110 115

gat atc aag gct ctg att gaa gtg gat tcg gga cat cgt aga agt gga 499
Asp Ile Lys Ala Leu Ile Glu Val Asp Ser Gly His Arg Arg Ser Gly
120 125 130

gtc acg gcg act gct tca gaa ttg agt cag atc cgc gag gcg ctg ggc 547
Val Thr Ala Thr Ala Ser Glu Leu Ser Gln Ile Arg Glu Ala Leu Gly
135 140 145

agc agg tat gca gga gtg ttt act ttt cct ggg cat tct tat ggc ccg 595
Ser Arg Tyr Ala Gly Val Phe Thr Phe Pro Gly His Ser Tyr Gly Pro
150 155 160 165

gga aat ggt gag cag gca gca gct gat gag ctt cag gct cta aac aac 643
Gly Asn Gly Glu Gln Ala Ala Ala Asp Glu Leu Gln Ala Leu Asn Asn
170 175 180

agc gtc cag cga ctt gct ggc ggc ctg act tct ggc ggt tcc tcg ccg 691
Ser Val Gln Arg Leu Ala Gly Gly Leu Thr Ser Gly Gly Ser Ser Pro
185 190 195

tct gcg cag ttt aca gac gca atc gat gag atg cga cca ggc gtg tat 739
Ser Ala Gln Phe Thr Asp Ala Ile Asp Glu Met Arg Pro Gly Val Tyr
200 205 210

gtg ttt aac gat tcc cag cag atc acc tcg gga gca tgc act gag aag 787
Val Phe Asn Asp Ser Gln Gln Ile Thr Ser Gly Ala Cys Thr Glu Lys
215 220 225

cag gtg gca atg acg gtg ctg tct act gtg gtc agc cga aat gtg tca 835
Gln Val Ala Met Thr Val Leu Ser Thr Val Val Ser Arg Asn Val Ser
230 235 240 245

gat cgt cgg atc att ttg gat gcg gga tcc aaa atc ctc agc act gat 883
Asp Arg Arg Ile Ile Leu Asp Ala Gly Ser Lys Ile Leu Ser Thr Asp
250 255 260

aaa cca gca tgg att gat ggc aat ggt ttt gtt ctg ggg aat cct gaa 931
Lys Pro Ala Trp Ile Asp Gly Asn Gly Phe Val Leu Gly Asn Pro Glu
265 270 275

gcc cga atc tct gct ttg tcg gag cat cac gca acc att ttc tgg cca 979
Ala Arg Ile Ser Ala Leu Ser Glu His His Ala Thr Ile Phe Trp Pro
280 285 290

gat aaa gtg cta ctt cca gta atc ggg gag cag ctc aac atc gtg ccc
1027
Asp Lys Val Leu Leu Pro Val Ile Gly Glu Gln Leu Asn Ile Val Pro
295 300 305

aac cat gcc tgc aac gtg att aat ttg gtg gat gag gtc tac gtt cgg
1075
Asn His Ala Cys Asn Val Ile Asn Leu Val Asp Glu Val Tyr Val Arg
310 315 320 325

gaa gcc gat ggc act ttc cgt acc tgg aag gta gtt gcc cgc ggc aga
1123

Glu Ala Asp Gly Thr Phe Arg Thr Trp Lys Val Val Ala Arg Gly Arg
330 335 340

aac aat tagggaaacc tcttgacctt cac
1152
Asn Asn

<210> 132
<211> 343
<212> PRT
<213> Corynebacterium glutamicum

<400> 132
Met Met Ile Asp Thr Pro Ala Val Leu Ile Asp Arg Glu Arg Leu Thr
1 5 10 15

Ala Asn Ile Ser Arg Met Ala Ala His Ala Gly Ala His Glu Ile Ala
20 25 30

Leu Arg Pro His Val Lys Thr His Lys Ile Ile Glu Ile Ala Gln Met
35 40 45

Gln Val Asp Ala Gly Ala Arg Gly Ile Thr Cys Ala Thr Ile Gly Glu
50 55 60

Ala Glu Ile Phe Ala Gly Ala Gly Phe Thr Asp Ile Phe Ile Ala Tyr
65 70 75 80

Pro Leu Tyr Leu Thr Asp His Ala Val Gln Arg Leu Asn Ala Ile Pro
85 90 95

Gly Glu Ile Ser Ile Gly Val Asp Ser Val Glu Met Ala Gln Ala Thr
100 105 110

Ala Gly Leu Arg Glu Asp Ile Lys Ala Leu Ile Glu Val Asp Ser Gly
115 120 125

His Arg Arg Ser Gly Val Thr Ala Thr Ala Ser Glu Leu Ser Gln Ile
130 135 140

Arg Glu Ala Leu Gly Ser Arg Tyr Ala Gly Val Phe Thr Phe Pro Gly
145 150 155 160

His Ser Tyr Gly Pro Gly Asn Gly Glu Gln Ala Ala Ala Asp Glu Leu
165 170 175

Gln Ala Leu Asn Asn Ser Val Gln Arg Leu Ala Gly Gly Leu Thr Ser
180 185 190

Gly Gly Ser Ser Pro Ser Ala Gln Phe Thr Asp Ala Ile Asp Glu Met
195 200 205

Arg Pro Gly Val Tyr Val Phe Asn Asp Ser Gln Gln Ile Thr Ser Gly
210 215 220

Ala Cys Thr Glu Lys Gln Val Ala Met Thr Val Leu Ser Thr Val Val
225 230 235 240

Ser Arg Asn Val Ser Asp Arg Arg Ile Ile Leu Asp Ala Gly Ser Lys

```
                245                     250                     255

Ile Leu Ser Thr Asp Lys Pro Ala Trp Ile Asp Gly Asn Gly Phe Val
            260                     265                     270

Leu Gly Asn Pro Glu Ala Arg Ile Ser Ala Leu Ser Glu His His Ala
        275                     280                     285

Thr Ile Phe Trp Pro Asp Lys Val Leu Leu Pro Val Ile Gly Glu Gln
    290                     295                     300

Leu Asn Ile Val Pro Asn His Ala Cys Asn Val Ile Asn Leu Val Asp
305                     310                     315                     320

Glu Val Tyr Val Arg Glu Ala Asp Gly Thr Phe Arg Thr Trp Lys Val
                325                     330                     335

Val Ala Arg Gly Arg Asn Asn
            340


<210> 133
<211> 879
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(856)
<223> RXA02536

<400> 133
aagaagtgat cacgcgaacc tgtgtataac ttgcctcaaa gcgcctaggc tgtggattat 60

gcgtattgcc ttgcttcaga tctcgacgaa ttccgataag atg gac aac ttc gcc    115
                                           Met Asp Asn Phe Ala
                                           1               5

ctg ctg cgt gat gct gct gaa aaa gct gcg gaa cag ggg gct cgg gtg    163
Leu Leu Arg Asp Ala Ala Glu Lys Ala Ala Glu Gln Gly Ala Arg Val
                10                  15                  20

ttg gtg ttt ccg gag gcg act tcg caa agc ttt ggt acg gga agg ctt    211
Leu Val Phe Pro Glu Ala Thr Ser Gln Ser Phe Gly Thr Gly Arg Leu
            25                  30                  35

gat act cag gcg gag gag ctc gat ggc gaa ttc tcc acc gcg gta cga    259
Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe Ser Thr Ala Val Arg
        40                  45                  50

aaa tta gcc gat gag ctg gac gtt gtc atc gtt gcg ggc atg ttc acc    307
Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val Ala Gly Met Phe Thr
    55                  60                  65

cct gct gac acc gtg cag cgc ggt gaa aaa acg atc tcg cgc gtc aac    355
Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr Ile Ser Arg Val Asn
70                  75                  80                  85

aac acc gtg ctg att agt ggc gct gga ttg cat cag gga tac aac aaa    403
Asn Thr Val Leu Ile Ser Gly Ala Gly Leu His Gln Gly Tyr Asn Lys
                90                  95                  100
```

```
att cac aca tat gac gcg ttc ggt tat agg gaa tcc gac act gtg aaa     451
Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu Ser Asp Thr Val Lys
            105                 110                 115

ccg ggc gat gag ctg gtt gta ttc gag gtc gac gat att aaa ttt ggt     499
Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp Asp Ile Lys Phe Gly
        120                 125                 130

gtg gcg aca tgc tac gat att cga ttc cca gaa cag ttc aaa gac ctc     547
Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu Gln Phe Lys Asp Leu
    135                 140                 145

gcc cgc aac ggt gca cag ata att gtg gtt ccc acg tcg tgg caa gac     595
Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro Thr Ser Trp Gln Asp
150                 155                 160                 165

ggt cct gga aaa tta gaa caa tgg gaa gtc ctc cct cgc gcg cgt gca     643
Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu Pro Arg Ala Arg Ala
                170                 175                 180

ctg gat tcc acc tgc tgg atc gta gcg tgt ggg caa gcg cga ctt cca     691
Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly Gln Ala Arg Leu Pro
            185                 190                 195

gaa gaa tta cgc gat gaa cga aaa ggc cct acg ggg att ggt cat tcc     739
Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr Gly Ile Gly His Ser
        200                 205                 210

atg gtg aca aac cca cac ggt gaa gta att gct agc gcg ggt tat gag     787
Met Val Thr Asn Pro His Gly Glu Val Ile Ala Ser Ala Gly Tyr Glu
    215                 220                 225

cca gaa atg ttg atc gcg gat att gat gtc agc ggt ttg gcc aaa att     835
Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser Gly Leu Ala Lys Ile
230                 235                 240                 245

cgg gag gca ttg cct gtt ctt taaccactgt ctaaggaatc act               879
Arg Glu Ala Leu Pro Val Leu
                250
```

<210> 134
<211> 252
<212> PRT
<213> Corynebacterium glutamicum

<400> 134

```
Met Asp Asn Phe Ala Leu Leu Arg Asp Ala Ala Glu Lys Ala Ala Glu
  1               5                  10                  15

Gln Gly Ala Arg Val Leu Val Phe Pro Glu Ala Thr Ser Gln Ser Phe
            20                  25                  30

Gly Thr Gly Arg Leu Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe
        35                  40                  45

Ser Thr Ala Val Arg Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val
    50                  55                  60

Ala Gly Met Phe Thr Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr
```

```
65                  70                  75                  80

Ile Ser Arg Val Asn Asn Thr Val Leu Ile Ser Gly Ala Gly Leu His
                85                  90                  95

Gln Gly Tyr Asn Lys Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu
            100                 105                 110

Ser Asp Thr Val Lys Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp
        115                 120                 125

Asp Ile Lys Phe Gly Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu
    130                 135                 140

Gln Phe Lys Asp Leu Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro
145                 150                 155                 160

Thr Ser Trp Gln Asp Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu
                165                 170                 175

Pro Arg Ala Arg Ala Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly
            180                 185                 190

Gln Ala Arg Leu Pro Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr
        195                 200                 205

Gly Ile Gly His Ser Met Val Thr Asn Pro His Gly Glu Val Ile Ala
    210                 215                 220

Ser Ala Gly Tyr Glu Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser
225                 230                 235                 240

Gly Leu Ala Lys Ile Arg Glu Ala Leu Pro Val Leu
                245                 250


<210> 135
<211> 1635
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1612)
<223> RXS00870

<400> 135
caagacggcg atgtcgccgc cgctgttgat accgcagcgc gacttgttca cacagatatt 60

caacaattca cttcgcagag catttaagga atttacacac atg tct gaa cca caa    115
                                           Met Ser Glu Pro Gln
                                           1               5

acc atc tcg cac tgg att gac ggc gcg att tcc cca tcc act tcc ggc    163
Thr Ile Ser His Trp Ile Asp Gly Ala Ile Ser Pro Ser Thr Ser Gly
                10                  15                  20

aag acc gct cct gtc tac aat cct gca act ggc cag gtc acc gcc aat    211
Lys Thr Ala Pro Val Tyr Asn Pro Ala Thr Gly Gln Val Thr Ala Asn
            25                  30                  35
```

gtt gcg ctg gct agc cag gaa gag atc gat gcc acc atc gct tct gcc 259
Val Ala Leu Ala Ser Gln Glu Glu Ile Asp Ala Thr Ile Ala Ser Ala
40 45 50

acc aag gct gct aag acg tgg ggc aac ctg tct atc gct aag cgc caa 307
Thr Lys Ala Ala Lys Thr Trp Gly Asn Leu Ser Ile Ala Lys Arg Gln
55 60 65

gct gtg ctt ttc aac ttc cgt gag ctg ctg aat gct cgc aag ggt gag 355
Ala Val Leu Phe Asn Phe Arg Glu Leu Leu Asn Ala Arg Lys Gly Glu
70 75 80 85

ctg gcg gag atc atc act gca gag cac ggc aag gtc ttg tcc gat gcc 403
Leu Ala Glu Ile Ile Thr Ala Glu His Gly Lys Val Leu Ser Asp Ala
90 95 100

atg ggt gaa atc ctg cgc ggc cag gaa gtc gtg gag ctt gct acc ggt 451
Met Gly Glu Ile Leu Arg Gly Gln Glu Val Val Glu Leu Ala Thr Gly
105 110 115

ttc cca cac ctg ctt aaa ggt gcg ttc aac gag aac gtc tcc acc ggc 499
Phe Pro His Leu Leu Lys Gly Ala Phe Asn Glu Asn Val Ser Thr Gly
120 125 130

att gat gtg tat tcc ttg aag cag cca ctg ggt gtt gtc ggt atc atc 547
Ile Asp Val Tyr Ser Leu Lys Gln Pro Leu Gly Val Val Gly Ile Ile
135 140 145

agc ccg ttc aac ttc cct gcg atg gtg ccg atg tgg ttt ttc cca atc 595
Ser Pro Phe Asn Phe Pro Ala Met Val Pro Met Trp Phe Phe Pro Ile
150 155 160 165

gca atc gct gca ggc aac gca gtt att ttg aag cct tca gag aag gat 643
Ala Ile Ala Ala Gly Asn Ala Val Ile Leu Lys Pro Ser Glu Lys Asp
170 175 180

cct tcg gca gcg ctg tgg atg gct cag atc tgg aag gaa gct ggt ctt 691
Pro Ser Ala Ala Leu Trp Met Ala Gln Ile Trp Lys Glu Ala Gly Leu
185 190 195

cca gac ggc gta ttc aac gtg ctc cag ggc gac aag ctg gct gtt gat 739
Pro Asp Gly Val Phe Asn Val Leu Gln Gly Asp Lys Leu Ala Val Asp
200 205 210

ggt ttg ctg aac agc cct gat gtc tct gcg att tcc ttc gtg ggt tcc 787
Gly Leu Leu Asn Ser Pro Asp Val Ser Ala Ile Ser Phe Val Gly Ser
215 220 225

acc cca atc gca aag tac atc tac gag act tcc gcg aag aac ggc aag 835
Thr Pro Ile Ala Lys Tyr Ile Tyr Glu Thr Ser Ala Lys Asn Gly Lys
230 235 240 245

cgc gtc cag gcg ttg ggc ggc gcg aag aac cac atg ctg gtg ctg cca 883
Arg Val Gln Ala Leu Gly Gly Ala Lys Asn His Met Leu Val Leu Pro
250 255 260

gat gct gat ctg gat ctg gtt gcc gat cag gca atc aac gca ggt tac 931
Asp Ala Asp Leu Asp Leu Val Ala Asp Gln Ala Ile Asn Ala Gly Tyr
265 270 275

ggc gct gcc ggt gag cgt tgc atg gct gtt tct gtg gtc ttg gct att 979

Gly Ala Ala Gly Glu Arg Cys Met Ala Val Ser Val Val Leu Ala Ile
280 285 290

gaa tct gtt gcc gac gag ctc att gag aag atc aag gag cgc atc gac
1027
Glu Ser Val Ala Asp Glu Leu Ile Glu Lys Ile Lys Glu Arg Ile Asp
295 300 305

acc ctg cgc atc ggc aac ggt gcc ggc gac gag cag ggc gag ccg cac
1075
Thr Leu Arg Ile Gly Asn Gly Ala Gly Asp Glu Gln Gly Glu Pro His
310 315 320 325

ctg ggc cca cta atc acc gac gtc cac cgc gac aag gtc gct tct tat
1123
Leu Gly Pro Leu Ile Thr Asp Val His Arg Asp Lys Val Ala Ser Tyr
330 335 340

gtc gac atc gct gag gcc gac ggc gcc aag atc atc gtg gac ggg cgt
1171
Val Asp Ile Ala Glu Ala Asp Gly Ala Lys Ile Ile Val Asp Gly Arg
345 350 355

aac tgc gcc gta gac ggg cac gag gag ggc ttc ttc ttc ggc cct acg
1219
Asn Cys Ala Val Asp Gly His Glu Glu Gly Phe Phe Phe Gly Pro Thr
360 365 370

ctt atc gac gac atc cca ctc acg ttc cgc gcc tac acc gaa gaa atc
1267
Leu Ile Asp Asp Ile Pro Leu Thr Phe Arg Ala Tyr Thr Glu Glu Ile
375 380 385

ttc ggc ccg gtc ctc tct gtc gtt cgt gtc gca tcc ttc gac gag gca
1315
Phe Gly Pro Val Leu Ser Val Val Arg Val Ala Ser Phe Asp Glu Ala
390 395 400 405

att gag ctg atc aac tcc ggt gaa ttc ggc aac gga acc gca atc ttc
1363
Ile Glu Leu Ile Asn Ser Gly Glu Phe Gly Asn Gly Thr Ala Ile Phe
410 415 420

acc aac gat ggt gga gcg gca cgc cgc ttc cag cat gag atc gaa gtg
1411
Thr Asn Asp Gly Gly Ala Ala Arg Arg Phe Gln His Glu Ile Glu Val
425 430 435

ggc atg atc ggc atc aac gta cca atc cca gtg cct gtt gcg tac cac
1459
Gly Met Ile Gly Ile Asn Val Pro Ile Pro Val Pro Val Ala Tyr His
440 445 450

tcc ttc ggt ggt tgg aag aac tcc ctc ttc ggt gac gcc aag gca tat
1507
Ser Phe Gly Gly Trp Lys Asn Ser Leu Phe Gly Asp Ala Lys Ala Tyr
455 460 465

ggc act caa ggt ttt gat ttc ttc acc agg gaa aag gcg atc acc agc
1555
Gly Thr Gln Gly Phe Asp Phe Phe Thr Arg Glu Lys Ala Ile Thr Ser

470 475 480 485

cgt tgg ctc gac cca gca acc cac ggt ggc att aac ctc ggt ttc cca
1603
Arg Trp Leu Asp Pro Ala Thr His Gly Gly Ile Asn Leu Gly Phe Pro
490 495 500

cag aac gat taattgaagg agagcacagg act
1635
Gln Asn Asp

<210> 136
<211> 504
<212> PRT
<213> Corynebacterium glutamicum

<400> 136
Met Ser Glu Pro Gln Thr Ile Ser His Trp Ile Asp Gly Ala Ile Ser
1 5 10 15

Pro Ser Thr Ser Gly Lys Thr Ala Pro Val Tyr Asn Pro Ala Thr Gly
20 25 30

Gln Val Thr Ala Asn Val Ala Leu Ala Ser Gln Glu Glu Ile Asp Ala
35 40 45

Thr Ile Ala Ser Ala Thr Lys Ala Ala Lys Thr Trp Gly Asn Leu Ser
50 55 60

Ile Ala Lys Arg Gln Ala Val Leu Phe Asn Phe Arg Glu Leu Leu Asn
65 70 75 80

Ala Arg Lys Gly Glu Leu Ala Glu Ile Ile Thr Ala Glu His Gly Lys
85 90 95

Val Leu Ser Asp Ala Met Gly Glu Ile Leu Arg Gly Gln Glu Val Val
100 105 110

Glu Leu Ala Thr Gly Phe Pro His Leu Leu Lys Gly Ala Phe Asn Glu
115 120 125

Asn Val Ser Thr Gly Ile Asp Val Tyr Ser Leu Lys Gln Pro Leu Gly
130 135 140

Val Val Gly Ile Ile Ser Pro Phe Asn Phe Pro Ala Met Val Pro Met
145 150 155 160

Trp Phe Phe Pro Ile Ala Ile Ala Ala Gly Asn Ala Val Ile Leu Lys
165 170 175

Pro Ser Glu Lys Asp Pro Ser Ala Ala Leu Trp Met Ala Gln Ile Trp
180 185 190

Lys Glu Ala Gly Leu Pro Asp Gly Val Phe Asn Val Leu Gln Gly Asp
195 200 205

Lys Leu Ala Val Asp Gly Leu Leu Asn Ser Pro Asp Val Ser Ala Ile
210 215 220

Ser Phe Val Gly Ser Thr Pro Ile Ala Lys Tyr Ile Tyr Glu Thr Ser
225 230 235 240

Ala Lys Asn Gly Lys Arg Val Gln Ala Leu Gly Gly Ala Lys Asn His
245 250 255

Met Leu Val Leu Pro Asp Ala Asp Leu Asp Leu Val Ala Asp Gln Ala
260 265 270

Ile Asn Ala Gly Tyr Gly Ala Ala Gly Glu Arg Cys Met Ala Val Ser
275 280 285

Val Val Leu Ala Ile Glu Ser Val Ala Asp Glu Leu Ile Glu Lys Ile
290 295 300

Lys Glu Arg Ile Asp Thr Leu Arg Ile Gly Asn Gly Ala Gly Asp Glu
305 310 315 320

Gln Gly Glu Pro His Leu Gly Pro Leu Ile Thr Asp Val His Arg Asp
325 330 335

Lys Val Ala Ser Tyr Val Asp Ile Ala Glu Ala Asp Gly Ala Lys Ile
340 345 350

Ile Val Asp Gly Arg Asn Cys Ala Val Asp Gly His Glu Glu Gly Phe
355 360 365

Phe Phe Gly Pro Thr Leu Ile Asp Asp Ile Pro Leu Thr Phe Arg Ala
370 375 380

Tyr Thr Glu Glu Ile Phe Gly Pro Val Leu Ser Val Val Arg Val Ala
385 390 395 400

Ser Phe Asp Glu Ala Ile Glu Leu Ile Asn Ser Gly Glu Phe Gly Asn
405 410 415

Gly Thr Ala Ile Phe Thr Asn Asp Gly Gly Ala Ala Arg Arg Phe Gln
420 425 430

His Glu Ile Glu Val Gly Met Ile Gly Ile Asn Val Pro Ile Pro Val
435 440 445

Pro Val Ala Tyr His Ser Phe Gly Gly Trp Lys Asn Ser Leu Phe Gly
450 455 460

Asp Ala Lys Ala Tyr Gly Thr Gln Gly Phe Asp Phe Phe Thr Arg Glu
465 470 475 480

Lys Ala Ile Thr Ser Arg Trp Leu Asp Pro Ala Thr His Gly Gly Ile
485 490 495

Asn Leu Gly Phe Pro Gln Asn Asp
500

<210> 137
<211> 531
<212> DNA
<213> Corynebacterium glutamicum

<220>

```
<221> CDS
<222> (101)..(508)
<223> RXS02299

<400> 137
acgcgggggt tgttgccgga tcgaaatatt cctttccttg tcatctcacg ctatgatttc 60

taaaacttgc aggacaaccc ccataaggac accacaggac atg ctg cgc acc atc   115
                                         Met Leu Arg Thr Ile
                                          1               5

ctc gga agt aag att cac cga gcc act gtc act caa gct gat cta gat   163
Leu Gly Ser Lys Ile His Arg Ala Thr Val Thr Gln Ala Asp Leu Asp
                10                  15                  20

tat gtt ggc tct gta acc atc gac gcc gac ctg gtt cac gcc gcc gga   211
Tyr Val Gly Ser Val Thr Ile Asp Ala Asp Leu Val His Ala Ala Gly
            25                  30                  35

ttg atc gaa ggc gaa aaa gtt gcc atc gta gac atc acc aac ggc gct   259
Leu Ile Glu Gly Glu Lys Val Ala Ile Val Asp Ile Thr Asn Gly Ala
        40                  45                  50

cgt ctg gaa act tat gtc att gtg ggc gac gcc gga acg ggc aat att   307
Arg Leu Glu Thr Tyr Val Ile Val Gly Asp Ala Gly Thr Gly Asn Ile
    55                  60                  65

tgc atc aat ggt gcc gct gca cac ctt att aat cct ggc gat ctt gtg   355
Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn Pro Gly Asp Leu Val
70                  75                  80                  85

atc atc atg agc tac ctt cag gca act gat gcg gaa gcc aag gcg tat   403
Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala Glu Ala Lys Ala Tyr
                90                  95                  100

gag cca aag att gtg cac gtg gac gcc gac aac cgc atc gtt gcg ctc   451
Glu Pro Lys Ile Val His Val Asp Ala Asp Asn Arg Ile Val Ala Leu
            105                 110                 115

ggc aac gat ctt gcg gaa gca cta cct gga tcc ggg ctt ttg acg tcg   499
Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser Gly Leu Leu Thr Ser
        120                 125                 130

aga agc att tagcgtttta gctcgccaat att                             531
Arg Ser Ile
    135


<210> 138
<211> 136
<212> PRT
<213> Corynebacterium glutamicum

<400> 138
Met Leu Arg Thr Ile Leu Gly Ser Lys Ile His Arg Ala Thr Val Thr
1               5                   10                  15

Gln Ala Asp Leu Asp Tyr Val Gly Ser Val Thr Ile Asp Ala Asp Leu
            20                  25                  30

Val His Ala Ala Gly Leu Ile Glu Gly Glu Lys Val Ala Ile Val Asp
```

35 40 45

Ile Thr Asn Gly Ala Arg Leu Glu Thr Tyr Val Ile Val Gly Asp Ala
50 55 60

Gly Thr Gly Asn Ile Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn
65 70 75 80

Pro Gly Asp Leu Val Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala
85 90 95

Glu Ala Lys Ala Tyr Glu Pro Lys Ile Val His Val Asp Ala Asp Asn
100 105 110

Arg Ile Val Ala Leu Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser
115 120 125

Gly Leu Leu Thr Ser Arg Ser Ile
130 135

<210> 139
<211> 1053
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1030)
<223> RXA01561

<400> 139
gtgcccagaa attctgcttg cactcaccca agccgtttag caaattgaac ctcacgttca 60

taataatgtt cattttcatc gagttctaga aaacacaggc atg ctc acc ctc aac 115
Met Leu Thr Leu Asn
1 5

gat gtc atc acc gcc caa caa cga acc gcc cct cat gtt cga cga acg 163
Asp Val Ile Thr Ala Gln Gln Arg Thr Ala Pro His Val Arg Arg Thr
10 15 20

cca ctt ttc gaa gca gac ccc atc gac ggc aca caa atc tgg atc aaa 211
Pro Leu Phe Glu Ala Asp Pro Ile Asp Gly Thr Gln Ile Trp Ile Lys
25 30 35

gca gag ttc ctc caa aag tgc ggc gtg ttc aaa acg cgt gga gca ttc 259
Ala Glu Phe Leu Gln Lys Cys Gly Val Phe Lys Thr Arg Gly Ala Phe
40 45 50

aac cgc cag ctc gca gct tcg gaa aac gga cta ctc gac cca acg gtt 307
Asn Arg Gln Leu Ala Ala Ser Glu Asn Gly Leu Leu Asp Pro Thr Val
55 60 65

ggc atc gtc gcg gca tca ggc gga aac gca gga ctc gca aat gct ttt 355
Gly Ile Val Ala Ala Ser Gly Gly Asn Ala Gly Leu Ala Asn Ala Phe
70 75 80 85

gcc gca gca tcc tta agc gtt ccc gcc acg gta ttg gtg ccc gaa act 403
Ala Ala Ala Ser Leu Ser Val Pro Ala Thr Val Leu Val Pro Glu Thr
90 95 100

```
gcc cca caa gta aaa gtt gat cgc ctc aag caa tac ggt gca acc gtg    451
Ala Pro Gln Val Lys Val Asp Arg Leu Lys Gln Tyr Gly Ala Thr Val
            105                 110                 115

caa caa atc gga tct gaa tat gcg gaa gca ttt gag gca gct caa acc    499
Gln Gln Ile Gly Ser Glu Tyr Ala Glu Ala Phe Glu Ala Ala Gln Thr
        120                 125                 130

ttt gag tcg gaa act ggt gct ctg ttt tgc cac gcc tac gac cag ccc    547
Phe Glu Ser Glu Thr Gly Ala Leu Phe Cys His Ala Tyr Asp Gln Pro
    135                 140                 145

gac atc gca gct gga gca ggc gtc att ggg cta gaa att gtc gaa gat    595
Asp Ile Ala Ala Gly Ala Gly Val Ile Gly Leu Glu Ile Val Glu Asp
150                 155                 160                 165

ctt ccc gac gtt gac acc atc gtg gtt gct gtc ggt ggc ggt gga ctc    643
Leu Pro Asp Val Asp Thr Ile Val Val Ala Val Gly Gly Gly Gly Leu
                170                 175                 180

tat gca gga atc gca gcc gtc gta gca gcc cac gac atc aaa gtg gtg    691
Tyr Ala Gly Ile Ala Ala Val Val Ala Ala His Asp Ile Lys Val Val
            185                 190                 195

gcc gtt gaa ccc tcc aaa att cca acc ctg cac aac tca ctc att gcc    739
Ala Val Glu Pro Ser Lys Ile Pro Thr Leu His Asn Ser Leu Ile Ala
        200                 205                 210

ggc caa cca gtc gat gtg aac gtt tct ggt atc gcg gca gat tct ttg    787
Gly Gln Pro Val Asp Val Asn Val Ser Gly Ile Ala Ala Asp Ser Leu
    215                 220                 225

ggg gct cgc caa att gga cga gaa gcc ttt gac atc gca act gcc cat    835
Gly Ala Arg Gln Ile Gly Arg Glu Ala Phe Asp Ile Ala Thr Ala His
230                 235                 240                 245

ccc cca ata ggc gtc cta gtg gac gat gaa gca atc atc gca gct cga    883
Pro Pro Ile Gly Val Leu Val Asp Asp Glu Ala Ile Ile Ala Ala Arg
                250                 255                 260

cgc cac ctc tgg gac aac tac cgc atc cct gcc gag cat ggc gct gcc    931
Arg His Leu Trp Asp Asn Tyr Arg Ile Pro Ala Glu His Gly Ala Ala
            265                 270                 275

gca gca ctc gcc tct ctt acc agt gga gca tac aaa cct gca gca gat    979
Ala Ala Leu Ala Ser Leu Thr Ser Gly Ala Tyr Lys Pro Ala Ala Asp
        280                 285                 290

gaa aaa gtg gca gtc att gtg tgc gga gcg aac act gac ctc aca aca
1027
Glu Lys Val Ala Val Ile Val Cys Gly Ala Asn Thr Asp Leu Thr Thr
    295                 300                 305

ctg tgatgtgatt tcaaacgatc aca
1053
Leu
310
```

<210> 140

<211> 310
<212> PRT
<213> Corynebacterium glutamicum

<400> 140
Met Leu Thr Leu Asn Asp Val Ile Thr Ala Gln Gln Arg Thr Ala Pro
1 5 10 15

His Val Arg Arg Thr Pro Leu Phe Glu Ala Asp Pro Ile Asp Gly Thr
20 25 30

Gln Ile Trp Ile Lys Ala Glu Phe Leu Gln Lys Cys Gly Val Phe Lys
35 40 45

Thr Arg Gly Ala Phe Asn Arg Gln Leu Ala Ala Ser Glu Asn Gly Leu
50 55 60

Leu Asp Pro Thr Val Gly Ile Val Ala Ala Ser Gly Gly Asn Ala Gly
65 70 75 80

Leu Ala Asn Ala Phe Ala Ala Ala Ser Leu Ser Val Pro Ala Thr Val
85 90 95

Leu Val Pro Glu Thr Ala Pro Gln Val Lys Val Asp Arg Leu Lys Gln
100 105 110

Tyr Gly Ala Thr Val Gln Gln Ile Gly Ser Glu Tyr Ala Glu Ala Phe
115 120 125

Glu Ala Ala Gln Thr Phe Glu Ser Glu Thr Gly Ala Leu Phe Cys His
130 135 140

Ala Tyr Asp Gln Pro Asp Ile Ala Ala Gly Ala Gly Val Ile Gly Leu
145 150 155 160

Glu Ile Val Glu Asp Leu Pro Asp Val Asp Thr Ile Val Val Ala Val
165 170 175

Gly Gly Gly Gly Leu Tyr Ala Gly Ile Ala Ala Val Val Ala Ala His
180 185 190

Asp Ile Lys Val Val Ala Val Glu Pro Ser Lys Ile Pro Thr Leu His
195 200 205

Asn Ser Leu Ile Ala Gly Gln Pro Val Asp Val Asn Val Ser Gly Ile
210 215 220

Ala Ala Asp Ser Leu Gly Ala Arg Gln Ile Gly Arg Glu Ala Phe Asp
225 230 235 240

Ile Ala Thr Ala His Pro Pro Ile Gly Val Leu Val Asp Asp Glu Ala
245 250 255

Ile Ile Ala Ala Arg Arg His Leu Trp Asp Asn Tyr Arg Ile Pro Ala
260 265 270

Glu His Gly Ala Ala Ala Ala Leu Ala Ser Leu Thr Ser Gly Ala Tyr
275 280 285

Lys Pro Ala Ala Asp Glu Lys Val Ala Val Ile Val Cys Gly Ala Asn
290 295 300

```
Thr Asp Leu Thr Thr Leu
305                 310


<210> 141
<211> 1470
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1447)
<223> RXA01850

<400> 141
ttcgtgcaac ttcagactct tacggaggcg atggaccaaa aacaactaca atcaagcaga 60

tcaccttgta caccaccaga gaaaaggccc accctcagcc atg gct atc agt gtt   115
                                           Met Ala Ile Ser Val
                                           1               5

gtt gat cta ttt agc atc ggt atc gga cca tca tcc tca cat acc gtc   163
Val Asp Leu Phe Ser Ile Gly Ile Gly Pro Ser Ser Ser His Thr Val
                10                  15                  20

ggc ccc atg aga gcc gcc ctc acg tat atc tct gaa ttt ccc agc tcg   211
Gly Pro Met Arg Ala Ala Leu Thr Tyr Ile Ser Glu Phe Pro Ser Ser
            25                  30                  35

cat gtc gat atc acg ttg cac gga tcc ctt gcc gcc acc ggt aaa ggc   259
His Val Asp Ile Thr Leu His Gly Ser Leu Ala Ala Thr Gly Lys Gly
        40                  45                  50

cac tgc act gac cgg gcg gta tta ctg ggt ctg gtg gga tgg gaa cca   307
His Cys Thr Asp Arg Ala Val Leu Leu Gly Leu Val Gly Trp Glu Pro
    55                  60                  65

acg ata gtt ccc att gat gct gca ccc tca ccc ggc gcg ccg att cct   355
Thr Ile Val Pro Ile Asp Ala Ala Pro Ser Pro Gly Ala Pro Ile Pro
70                  75                  80                  85

gcg aaa ggt tct gtg aac ggg cca aag gga acg gtg tcg tat tcc ctg   403
Ala Lys Gly Ser Val Asn Gly Pro Lys Gly Thr Val Ser Tyr Ser Leu
                90                  95                  100

acg ttt gat cct cat cct ctt cca gaa cac ccc aat gcc gtt acc ttt   451
Thr Phe Asp Pro His Pro Leu Pro Glu His Pro Asn Ala Val Thr Phe
            105                 110                 115

aaa gga tca acc aca agg act tat ttg tcg gtg ggt ggt ggg ttc att   499
Lys Gly Ser Thr Thr Arg Thr Tyr Leu Ser Val Gly Gly Gly Phe Ile
        120                 125                 130

atg acg ttg gag gat ttc cgg aag ctg gac gat atc gga tca ggt gtg   547
Met Thr Leu Glu Asp Phe Arg Lys Leu Asp Asp Ile Gly Ser Gly Val
    135                 140                 145

tca acc att cat cca gag gca gag gtg cct tgt cct ttt cag aag agt   595
Ser Thr Ile His Pro Glu Ala Glu Val Pro Cys Pro Phe Gln Lys Ser
150                 155                 160                 165
```

```
tcc caa tta ctc gca tat ggt cgc gat ttt gcg gag gtc atg aag gat    643
Ser Gln Leu Leu Ala Tyr Gly Arg Asp Phe Ala Glu Val Met Lys Asp
                170                 175                 180

aat gag cgc tta atc cac ggg gat ctt ggc aca gtg gat gcc cat ttg    691
Asn Glu Arg Leu Ile His Gly Asp Leu Gly Thr Val Asp Ala His Leu
            185                 190                 195

gat cga gtg tgg cag att atg cag gag tgc gtg gca caa ggc atc gca    739
Asp Arg Val Trp Gln Ile Met Gln Glu Cys Val Ala Gln Gly Ile Ala
        200                 205                 210

acg ccg ggg att tta ccg ggt ggg ttg aat gtg caa cgt cgg gcg ccg    787
Thr Pro Gly Ile Leu Pro Gly Gly Leu Asn Val Gln Arg Arg Ala Pro
    215                 220                 225

cag gta cac gcg ctg att agc aac ggg gat acg tgt gag ctg ggt gct    835
Gln Val His Ala Leu Ile Ser Asn Gly Asp Thr Cys Glu Leu Gly Ala
230                 235                 240                 245

gat ctt gat gct gtg gag tgg gtg aat ctg tac gcc ttg gcg gtg aat    883
Asp Leu Asp Ala Val Glu Trp Val Asn Leu Tyr Ala Leu Ala Val Asn
                250                 255                 260

gaa gaa aac gcc gct ggt ggt cgt gtg gtt act gct ccg act aat ggt    931
Glu Glu Asn Ala Ala Gly Gly Arg Val Val Thr Ala Pro Thr Asn Gly
            265                 270                 275

gct gcg ggg att att ccg gcg gtg atg cac tat gcg cgg gat ttt ttg    979
Ala Ala Gly Ile Ile Pro Ala Val Met His Tyr Ala Arg Asp Phe Leu
        280                 285                 290

aca ggt ttt ggg gcg gag cag gcg cgg acg ttt ttg tat acc gcg ggt
1027
Thr Gly Phe Gly Ala Glu Gln Ala Arg Thr Phe Leu Tyr Thr Ala Gly
    295                 300                 305

gcg gtg ggc atc atc att aag gaa aat gcc tcg atc tct ggc gcg gag
1075
Ala Val Gly Ile Ile Ile Lys Glu Asn Ala Ser Ile Ser Gly Ala Glu
310                 315                 320                 325

gtg ggg tgt cag ggt gag gtt ggt tca gcg tcc gcg atg gcg gct gcc
1123
Val Gly Cys Gln Gly Glu Val Gly Ser Ala Ser Ala Met Ala Ala Ala
                330                 335                 340

ggg ttg tgt gca gtc tta ggt ggt tct ccg caa cag gtg gaa aac gcc
1171
Gly Leu Cys Ala Val Leu Gly Gly Ser Pro Gln Gln Val Glu Asn Ala
            345                 350                 355

gcg gag att gcg ttg gag cac aat ttg gga ttg acg tgc gat ccg gtg
1219
Ala Glu Ile Ala Leu Glu His Asn Leu Gly Leu Thr Cys Asp Pro Val
        360                 365                 370

ggc ggg tta gtg cag att ccg tgt att gaa cgc aac gct att gct gcc
1267
Gly Gly Leu Val Gln Ile Pro Cys Ile Glu Arg Asn Ala Ile Ala Ala
```

375 380 385

atg aag tcc atc aat gcg gca agg ctt gcc cgg att ggt gat ggc aac
1315
Met Lys Ser Ile Asn Ala Ala Arg Leu Ala Arg Ile Gly Asp Gly Asn
390 395 400 405

aat cgc gtg agt ttg gat gat gtg gtg gtc acg atg gct gcc acc ggc
1363
Asn Arg Val Ser Leu Asp Asp Val Val Val Thr Met Ala Ala Thr Gly
410 415 420

cgg gac atg ctg acc aaa tat aag gaa acg tcc ctt ggt ggt ttg gca
1411
Arg Asp Met Leu Thr Lys Tyr Lys Glu Thr Ser Leu Gly Gly Leu Ala
425 430 435

acc acc ttg ggc ttc ccg gtg tcg atg acg gag tgt tagcggtacg
1457
Thr Thr Leu Gly Phe Pro Val Ser Met Thr Glu Cys
440 445

gctttaacac ggc
1470

<210> 142
<211> 449
<212> PRT
<213> Corynebacterium glutamicum

<400> 142
Met Ala Ile Ser Val Val Asp Leu Phe Ser Ile Gly Ile Gly Pro Ser
1 5 10 15

Ser Ser His Thr Val Gly Pro Met Arg Ala Ala Leu Thr Tyr Ile Ser
20 25 30

Glu Phe Pro Ser Ser His Val Asp Ile Thr Leu His Gly Ser Leu Ala
35 40 45

Ala Thr Gly Lys Gly His Cys Thr Asp Arg Ala Val Leu Leu Gly Leu
50 55 60

Val Gly Trp Glu Pro Thr Ile Val Pro Ile Asp Ala Ala Pro Ser Pro
65 70 75 80

Gly Ala Pro Ile Pro Ala Lys Gly Ser Val Asn Gly Pro Lys Gly Thr
85 90 95

Val Ser Tyr Ser Leu Thr Phe Asp Pro His Pro Leu Pro Glu His Pro
100 105 110

Asn Ala Val Thr Phe Lys Gly Ser Thr Thr Arg Thr Tyr Leu Ser Val
115 120 125

Gly Gly Gly Phe Ile Met Thr Leu Glu Asp Phe Arg Lys Leu Asp Asp
130 135 140

Ile Gly Ser Gly Val Ser Thr Ile His Pro Glu Ala Glu Val Pro Cys
145 150 155 160

Pro Phe Gln Lys Ser Ser Gln Leu Leu Ala Tyr Gly Arg Asp Phe Ala
165 170 175

Glu Val Met Lys Asp Asn Glu Arg Leu Ile His Gly Asp Leu Gly Thr
180 185 190

Val Asp Ala His Leu Asp Arg Val Trp Gln Ile Met Gln Glu Cys Val
195 200 205

Ala Gln Gly Ile Ala Thr Pro Gly Ile Leu Pro Gly Gly Leu Asn Val
210 215 220

Gln Arg Arg Ala Pro Gln Val His Ala Leu Ile Ser Asn Gly Asp Thr
225 230 235 240

Cys Glu Leu Gly Ala Asp Leu Asp Ala Val Glu Trp Val Asn Leu Tyr
245 250 255

Ala Leu Ala Val Asn Glu Glu Asn Ala Ala Gly Gly Arg Val Val Thr
260 265 270

Ala Pro Thr Asn Gly Ala Ala Gly Ile Ile Pro Ala Val Met His Tyr
275 280 285

Ala Arg Asp Phe Leu Thr Gly Phe Gly Ala Glu Gln Ala Arg Thr Phe
290 295 300

Leu Tyr Thr Ala Gly Ala Val Gly Ile Ile Ile Lys Glu Asn Ala Ser
305 310 315 320

Ile Ser Gly Ala Glu Val Gly Cys Gln Gly Glu Val Gly Ser Ala Ser
325 330 335

Ala Met Ala Ala Ala Gly Leu Cys Ala Val Leu Gly Gly Ser Pro Gln
340 345 350

Gln Val Glu Asn Ala Ala Glu Ile Ala Leu Glu His Asn Leu Gly Leu
355 360 365

Thr Cys Asp Pro Val Gly Gly Leu Val Gln Ile Pro Cys Ile Glu Arg
370 375 380

Asn Ala Ile Ala Ala Met Lys Ser Ile Asn Ala Ala Arg Leu Ala Arg
385 390 395 400

Ile Gly Asp Gly Asn Asn Arg Val Ser Leu Asp Asp Val Val Val Thr
405 410 415

Met Ala Ala Thr Gly Arg Asp Met Leu Thr Lys Tyr Lys Glu Thr Ser
420 425 430

Leu Gly Gly Leu Ala Thr Thr Leu Gly Phe Pro Val Ser Met Thr Glu
435 440 445

Cys

<210> 143
<211> 1425

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1402)
<223> RXA00580

<400> 143
ttttatatat gggtatcggc ggtctatgct tgtgggcgta cctgtcccgc gagtgaggtc 60

ttacgcgcgg gattcgtctt gtgaaaggtt agctgacctg atg acc gat gcc cac 115
Met Thr Asp Ala His
1 5

caa gcg gac gat gtc cgt tac cag cca ctg aac gag ctt gat cct gag 163
Gln Ala Asp Asp Val Arg Tyr Gln Pro Leu Asn Glu Leu Asp Pro Glu
10 15 20

gtg gct gct gcc atc gct ggg gaa ctt gcc cgt caa cgc gat aca tta 211
Val Ala Ala Ala Ile Ala Gly Glu Leu Ala Arg Gln Arg Asp Thr Leu
25 30 35

gag atg atc gcg tct gag aac ttc gtt ccc cgt tct gtt ttg cag gcg 259
Glu Met Ile Ala Ser Glu Asn Phe Val Pro Arg Ser Val Leu Gln Ala
40 45 50

cag ggt tct gtt ctt acc aat aag tat gcc gag ggt tac cct ggc cgc 307
Gln Gly Ser Val Leu Thr Asn Lys Tyr Ala Glu Gly Tyr Pro Gly Arg
55 60 65

cgt tac tac ggt ggt tgc gaa caa gtt gac atc att gag gat ctt gca 355
Arg Tyr Tyr Gly Gly Cys Glu Gln Val Asp Ile Ile Glu Asp Leu Ala
70 75 80 85

cgt gat cgt gcg aag gct ctc ttc ggt gca gag ttc gcc aat gtt cag 403
Arg Asp Arg Ala Lys Ala Leu Phe Gly Ala Glu Phe Ala Asn Val Gln
90 95 100

cct cac tct ggc gca cag gct aat gct gct gtg ctg atg act ttg gct 451
Pro His Ser Gly Ala Gln Ala Asn Ala Ala Val Leu Met Thr Leu Ala
105 110 115

gag cca ggc gac aag atc atg ggt ctg tct ttg gct cat ggt ggt cac 499
Glu Pro Gly Asp Lys Ile Met Gly Leu Ser Leu Ala His Gly Gly His
120 125 130

ttg acc cac gga atg aag ttg aac ttc tcc gga aag ctg tac gag gtt 547
Leu Thr His Gly Met Lys Leu Asn Phe Ser Gly Lys Leu Tyr Glu Val
135 140 145

gtt gcg tac ggt gtt gat cct gag acc atg cgt gtt gat atg gat cag 595
Val Ala Tyr Gly Val Asp Pro Glu Thr Met Arg Val Asp Met Asp Gln
150 155 160 165

gtt cgt gag att gct ctg aag gag cag cca aag gta att atc gct ggc 643
Val Arg Glu Ile Ala Leu Lys Glu Gln Pro Lys Val Ile Ile Ala Gly
170 175 180

tgg tct gca tac cct cgc cac ctt gat ttc gag gct ttc cag tct att 691
Trp Ser Ala Tyr Pro Arg His Leu Asp Phe Glu Ala Phe Gln Ser Ile

185 190 195

gct gcg gaa gtt ggc gcg aag ctg tgg gtc gat atg gct cac ttc gct 739
Ala Ala Glu Val Gly Ala Lys Leu Trp Val Asp Met Ala His Phe Ala
200 205 210

ggt ctt gtt gct gct ggt ttg cac cca agc cca gtt cct tac tct gat 787
Gly Leu Val Ala Ala Gly Leu His Pro Ser Pro Val Pro Tyr Ser Asp
215 220 225

gtt gtt tct tcc act gtc cac aag act ttg ggt gga cct cgt tcc ggc 835
Val Val Ser Ser Thr Val His Lys Thr Leu Gly Gly Pro Arg Ser Gly
230 235 240 245

atc att ctg gct aag cag gag tac gcg aag aag ctg aac tct tcc gta 883
Ile Ile Leu Ala Lys Gln Glu Tyr Ala Lys Lys Leu Asn Ser Ser Val
250 255 260

ttc cca ggt cag cag ggt ggt cct ttg atg cac gca gtt gct gcg aag 931
Phe Pro Gly Gln Gln Gly Gly Pro Leu Met His Ala Val Ala Ala Lys
265 270 275

gct act tct ttg aag att gct ggc act gag cag ttc cgt gac cgt cag 979
Ala Thr Ser Leu Lys Ile Ala Gly Thr Glu Gln Phe Arg Asp Arg Gln
280 285 290

gct cgc acg ttg gag ggt gct cgc att ctt gct gag cgt ctg act gct
1027
Ala Arg Thr Leu Glu Gly Ala Arg Ile Leu Ala Glu Arg Leu Thr Ala
295 300 305

tct gat gcg aag gcc gct ggc gtg gat gtc ttg acc ggt ggc act gat
1075
Ser Asp Ala Lys Ala Ala Gly Val Asp Val Leu Thr Gly Gly Thr Asp
310 315 320 325

gtg cac ttg gtt ttg gct gat ctg cgt aac tcc cag atg gat ggc cag
1123
Val His Leu Val Leu Ala Asp Leu Arg Asn Ser Gln Met Asp Gly Gln
330 335 340

cag gcg gaa gat ctg ctg cac gag gtt ggt atc act gtg aac cgt aac
1171
Gln Ala Glu Asp Leu Leu His Glu Val Gly Ile Thr Val Asn Arg Asn
345 350 355

gcg gtt cct ttc gat cct cgt cca cca atg gtt act tct ggt ctg cgt
1219
Ala Val Pro Phe Asp Pro Arg Pro Pro Met Val Thr Ser Gly Leu Arg
360 365 370

att ggt act cct gcg ctg gct acc cgt ggt ttc gat att cct gca ttc
1267
Ile Gly Thr Pro Ala Leu Ala Thr Arg Gly Phe Asp Ile Pro Ala Phe
375 380 385

act gag gtt gca gac atc att ggt act gct ttg gct aat ggt aag tcc
1315
Thr Glu Val Ala Asp Ile Ile Gly Thr Ala Leu Ala Asn Gly Lys Ser
390 395 400 405

gca gac att gag tct ctg cgt ggc cgt gta gca aag ctt gct gca gat
1363
Ala Asp Ile Glu Ser Leu Arg Gly Arg Val Ala Lys Leu Ala Ala Asp
410 415 420

tac cca ctg tat gag ggc ttg gaa gac tgg acc atc gtc taagtttttc
1412
Tyr Pro Leu Tyr Glu Gly Leu Glu Asp Trp Thr Ile Val
425 430

tttgagtttt cat
1425

<210> 144
<211> 434
<212> PRT
<213> Corynebacterium glutamicum

<400> 144
Met Thr Asp Ala His Gln Ala Asp Asp Val Arg Tyr Gln Pro Leu Asn
1 5 10 15

Glu Leu Asp Pro Glu Val Ala Ala Ala Ile Ala Gly Glu Leu Ala Arg
20 25 30

Gln Arg Asp Thr Leu Glu Met Ile Ala Ser Glu Asn Phe Val Pro Arg
35 40 45

Ser Val Leu Gln Ala Gln Gly Ser Val Leu Thr Asn Lys Tyr Ala Glu
50 55 60

Gly Tyr Pro Gly Arg Arg Tyr Tyr Gly Gly Cys Glu Gln Val Asp Ile
65 70 75 80

Ile Glu Asp Leu Ala Arg Asp Arg Ala Lys Ala Leu Phe Gly Ala Glu
85 90 95

Phe Ala Asn Val Gln Pro His Ser Gly Ala Gln Ala Asn Ala Ala Val
100 105 110

Leu Met Thr Leu Ala Glu Pro Gly Asp Lys Ile Met Gly Leu Ser Leu
115 120 125

Ala His Gly Gly His Leu Thr His Gly Met Lys Leu Asn Phe Ser Gly
130 135 140

Lys Leu Tyr Glu Val Val Ala Tyr Gly Val Asp Pro Glu Thr Met Arg
145 150 155 160

Val Asp Met Asp Gln Val Arg Glu Ile Ala Leu Lys Glu Gln Pro Lys
165 170 175

Val Ile Ile Ala Gly Trp Ser Ala Tyr Pro Arg His Leu Asp Phe Glu
180 185 190

Ala Phe Gln Ser Ile Ala Ala Glu Val Gly Ala Lys Leu Trp Val Asp
195 200 205

Met Ala His Phe Ala Gly Leu Val Ala Ala Gly Leu His Pro Ser Pro
210 215 220

Val Pro Tyr Ser Asp Val Val Ser Ser Thr Val His Lys Thr Leu Gly
225 230 235 240

Gly Pro Arg Ser Gly Ile Ile Leu Ala Lys Gln Glu Tyr Ala Lys Lys
245 250 255

Leu Asn Ser Ser Val Phe Pro Gly Gln Gln Gly Gly Pro Leu Met His
260 265 270

Ala Val Ala Ala Lys Ala Thr Ser Leu Lys Ile Ala Gly Thr Glu Gln
275 280 285

Phe Arg Asp Arg Gln Ala Arg Thr Leu Glu Gly Ala Arg Ile Leu Ala
290 295 300

Glu Arg Leu Thr Ala Ser Asp Ala Lys Ala Ala Gly Val Asp Val Leu
305 310 315 320

Thr Gly Gly Thr Asp Val His Leu Val Leu Ala Asp Leu Arg Asn Ser
325 330 335

Gln Met Asp Gly Gln Gln Ala Glu Asp Leu Leu His Glu Val Gly Ile
340 345 350

Thr Val Asn Arg Asn Ala Val Pro Phe Asp Pro Arg Pro Pro Met Val
355 360 365

Thr Ser Gly Leu Arg Ile Gly Thr Pro Ala Leu Ala Thr Arg Gly Phe
370 375 380

Asp Ile Pro Ala Phe Thr Glu Val Ala Asp Ile Ile Gly Thr Ala Leu
385 390 395 400

Ala Asn Gly Lys Ser Ala Asp Ile Glu Ser Leu Arg Gly Arg Val Ala
405 410 415

Lys Leu Ala Ala Asp Tyr Pro Leu Tyr Glu Gly Leu Glu Asp Trp Thr
420 425 430

Ile Val

<210> 145
<211> 401
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(378)
<223> RXA01821

<400> 145
cga aac agc caa ggc aaa tgg tgc cca agt acg cga tca cca aaa aat 48
Arg Asn Ser Gln Gly Lys Trp Cys Pro Ser Thr Arg Ser Pro Lys Asn
1 5 10 15

acc agc atc gaa gac aac ggc gat cac gta gtc atc caa gca ggc gaa 96
Thr Ser Ile Glu Asp Asn Gly Asp His Val Val Ile Gln Ala Gly Glu

20 25 30

gaa acc aca atc gtg gac cgc gtt atc gtc acc acc ggc agc tgg aca 144
Glu Thr Thr Ile Val Asp Arg Val Ile Val Thr Thr Gly Ser Trp Thr
35 40 45

agc gag ctc gtg ccc tcc atc gcg cca ctg ctt gaa gtg cga cgc cta 192
Ser Glu Leu Val Pro Ser Ile Ala Pro Leu Leu Glu Val Arg Arg Leu
50 55 60

gtg ctc acc tgg ttc ctg ccc aac aat cca gtg gac ttc caa ccg gaa 240
Val Leu Thr Trp Phe Leu Pro Asn Asn Pro Val Asp Phe Gln Pro Glu
65 70 75 80

aac ctg cca tgc ttc atc cgt gac cgt gat ggc ttc cac gta ttt gga 288
Asn Leu Pro Cys Phe Ile Arg Asp Arg Asp Gly Phe His Val Phe Gly
85 90 95

gca cca tgc gtc gat ggg tac agc atc aaa att gcc gga ttg gat gag 336
Ala Pro Cys Val Asp Gly Tyr Ser Ile Lys Ile Ala Gly Leu Asp Glu
100 105 110

tgg ggc gtt cca tta agc ctc gat cca ccg atg tgc cct cgg 378
Trp Gly Val Pro Leu Ser Leu Asp Pro Pro Met Cys Pro Arg
115 120 125

tgatgtcctg atcccggttc cgg 401

<210> 146
<211> 126
<212> PRT
<213> Corynebacterium glutamicum

<400> 146
Arg Asn Ser Gln Gly Lys Trp Cys Pro Ser Thr Arg Ser Pro Lys Asn
1 5 10 15

Thr Ser Ile Glu Asp Asn Gly Asp His Val Val Ile Gln Ala Gly Glu
20 25 30

Glu Thr Thr Ile Val Asp Arg Val Ile Val Thr Thr Gly Ser Trp Thr
35 40 45

Ser Glu Leu Val Pro Ser Ile Ala Pro Leu Leu Glu Val Arg Arg Leu
50 55 60

Val Leu Thr Trp Phe Leu Pro Asn Asn Pro Val Asp Phe Gln Pro Glu
65 70 75 80

Asn Leu Pro Cys Phe Ile Arg Asp Arg Asp Gly Phe His Val Phe Gly
85 90 95

Ala Pro Cys Val Asp Gly Tyr Ser Ile Lys Ile Ala Gly Leu Asp Glu
100 105 110

Trp Gly Val Pro Leu Ser Leu Asp Pro Pro Met Cys Pro Arg
115 120 125

<210> 147

<211> 488
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(478)
<223> RXN02263

<400> 147
cctgggcaac ccaagtgtat gaaaacgccc tggaaaaagg cgtcggcacc acattgaacc 60

tgtgggaatc acccgcactg gcttgagaga agaaacaaca atg aaa att gcg gta 115
Met Lys Ile Ala Val
1 5

atc ggc ctt gga tca acc ggc tcc atg gca ctg tgg cac tta agt aac 163
Ile Gly Leu Gly Ser Thr Gly Ser Met Ala Leu Trp His Leu Ser Asn
10 15 20

atc cca ggt gta gag gcc atc ggc ttt gaa caa ttc ggc atc tcc cat 211
Ile Pro Gly Val Glu Ala Ile Gly Phe Glu Gln Phe Gly Ile Ser His
25 30 35

ggc tac ggc gca ttc aca ggg gag tcc cga ctg ttt cgc atg gcc tac 259
Gly Tyr Gly Ala Phe Thr Gly Glu Ser Arg Leu Phe Arg Met Ala Tyr
40 45 50

cac gaa ggc agc acc tac gtt ccg ttg ctc aaa cgc gca cga gca cta 307
His Glu Gly Ser Thr Tyr Val Pro Leu Leu Lys Arg Ala Arg Ala Leu
55 60 65

tgg tca tca ctg agc gag att tcc gga cgc gaa ctc ttc cac aac ttc 355
Trp Ser Ser Leu Ser Glu Ile Ser Gly Arg Glu Leu Phe His Asn Phe
70 75 80 85

ggt gtc tta agc acc ggc aag gaa gac gaa gca ccc ttc caa cgc ctg 403
Gly Val Leu Ser Thr Gly Lys Glu Asp Glu Ala Pro Phe Gln Arg Leu
90 95 100

gtg gaa tca gtg gaa cgt tat gag ctg cca cat gaa cga ctt acc gcc 451
Val Glu Ser Val Glu Arg Tyr Glu Leu Pro His Glu Arg Leu Thr Ala
105 110 115

gcg cag atg cgc agc gtt acc cag gtc tagacttccg 488
Ala Gln Met Arg Ser Val Thr Gln Val
120 125

<210> 148
<211> 126
<212> PRT
<213> Corynebacterium glutamicum

<400> 148
Met Lys Ile Ala Val Ile Gly Leu Gly Ser Thr Gly Ser Met Ala Leu
1 5 10 15

Trp His Leu Ser Asn Ile Pro Gly Val Glu Ala Ile Gly Phe Glu Gln
20 25 30

```
Phe Gly Ile Ser His Gly Tyr Gly Ala Phe Thr Gly Glu Ser Arg Leu
        35                  40                  45

Phe Arg Met Ala Tyr His Glu Gly Ser Thr Tyr Val Pro Leu Leu Lys
    50                  55                  60

Arg Ala Arg Ala Leu Trp Ser Ser Leu Ser Glu Ile Ser Gly Arg Glu
65                  70                  75                  80

Leu Phe His Asn Phe Gly Val Leu Ser Thr Gly Lys Glu Asp Glu Ala
                85                  90                  95

Pro Phe Gln Arg Leu Val Glu Ser Val Glu Arg Tyr Glu Leu Pro His
            100                 105                 110

Glu Arg Leu Thr Ala Ala Gln Met Arg Ser Val Thr Gln Val
        115                 120                 125


<210> 149
<211> 460
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(460)
<223> FRXA02263

<400> 149
cctgggcaac ccaagtgtat gaaaacgccc tggaaaaagg cgtcggcacc acattgaacc 60

tgtgggaatc acccgcactg gcttgagaga agaaacaaca atg aaa att gcg gta    115
                                           Met Lys Ile Ala Val
                                           1               5

atc ggc ctt gga tca acc ggc tcc atg gca ctg tgg cac tta agt aac    163
Ile Gly Leu Gly Ser Thr Gly Ser Met Ala Leu Trp His Leu Ser Asn
                10                  15                  20

atc cca ggt gta gag gcc atc ggc ttt gaa caa ttc ggc atc tcc cat    211
Ile Pro Gly Val Glu Ala Ile Gly Phe Glu Gln Phe Gly Ile Ser His
            25                  30                  35

ggc tac ggc gca ttc aca ggg gag tcc cga ctg ttt cgc atg gcc tac    259
Gly Tyr Gly Ala Phe Thr Gly Glu Ser Arg Leu Phe Arg Met Ala Tyr
        40                  45                  50

cac gaa ggc agc acc tac gtt ccg ttg ctc aaa cgc gca cga gca cta    307
His Glu Gly Ser Thr Tyr Val Pro Leu Leu Lys Arg Ala Arg Ala Leu
    55                  60                  65

tgg tca tca ctg agc gag att tcc gga cgc gaa ctc ttc cac aac ttc    355
Trp Ser Ser Leu Ser Glu Ile Ser Gly Arg Glu Leu Phe His Asn Phe
70                  75                  80                  85

ggt gtc tta agc acc ggc aag gaa gac gaa gca ccc ttc caa cgc ctg    403
Gly Val Leu Ser Thr Gly Lys Glu Asp Glu Ala Pro Phe Gln Arg Leu
                90                  95                  100

gtg gaa tca gtg gaa cgt tat gag ctg cca cat gaa cga ctt acc gcc    451
```

Val Glu Ser Val Glu Arg Tyr Glu Leu Pro His Glu Arg Leu Thr Ala
105 110 115

gcg cag atg 460
Ala Gln Met
120

<210> 150
<211> 120
<212> PRT
<213> Corynebacterium glutamicum

<400> 150
Met Lys Ile Ala Val Ile Gly Leu Gly Ser Thr Gly Ser Met Ala Leu
1 5 10 15

Trp His Leu Ser Asn Ile Pro Gly Val Glu Ala Ile Gly Phe Glu Gln
20 25 30

Phe Gly Ile Ser His Gly Tyr Gly Ala Phe Thr Gly Glu Ser Arg Leu
35 40 45

Phe Arg Met Ala Tyr His Glu Gly Ser Thr Tyr Val Pro Leu Leu Lys
50 55 60

Arg Ala Arg Ala Leu Trp Ser Ser Leu Ser Glu Ile Ser Gly Arg Glu
65 70 75 80

Leu Phe His Asn Phe Gly Val Leu Ser Thr Gly Lys Glu Asp Glu Ala
85 90 95

Pro Phe Gln Arg Leu Val Glu Ser Val Glu Arg Tyr Glu Leu Pro His
100 105 110

Glu Arg Leu Thr Ala Ala Gln Met
115 120

<210> 151
<211> 1251
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1228)
<223> RXA02176

<400> 151
gggtgctagg aactgacagc ttcagggtta tagttgttgg gtcagatcgt taacgatccc 60

tggccctttt acttccaagc gcagaaagtt gcccgaagac atg acc gac ttc ccc 115
Met Thr Asp Phe Pro
1 5

acc ctg ccc tct gag ttc atc cct ggc gac ggc cgt ttc ggc tgc gga 163
Thr Leu Pro Ser Glu Phe Ile Pro Gly Asp Gly Arg Phe Gly Cys Gly
10 15 20

cct tcc aag gtt cga cca gaa cag att cag gct att gtc gac gga tcc 211

Pro Ser Lys Val Arg Pro Glu Gln Ile Gln Ala Ile Val Asp Gly Ser
25 30 35

gca tcc gtc atc ggt acc tca cac cgt cag ccg gca gta aaa aac gtc 259
Ala Ser Val Ile Gly Thr Ser His Arg Gln Pro Ala Val Lys Asn Val
40 45 50

gtg ggt tca atc cgc gag gga ctc tcc gac ctc ttc tcc ctt cca gaa 307
Val Gly Ser Ile Arg Glu Gly Leu Ser Asp Leu Phe Ser Leu Pro Glu
55 60 65

ggc tac gag atc atc ctt tcc cta ggt ggt gcg acc gca ttc tgg gat 355
Gly Tyr Glu Ile Ile Leu Ser Leu Gly Gly Ala Thr Ala Phe Trp Asp
70 75 80 85

gca gca acc ttc gga ctc att gaa aag aag tcc ggt cac ctt tct ttc 403
Ala Ala Thr Phe Gly Leu Ile Glu Lys Lys Ser Gly His Leu Ser Phe
90 95 100

ggt gag ttc tcc tcc aag ttc gca aag gct tct aag ctt gct cct tgg 451
Gly Glu Phe Ser Ser Lys Phe Ala Lys Ala Ser Lys Leu Ala Pro Trp
105 110 115

ctc gac gag cca gag atc gtc acc gca gaa acc ggt gac tct ccg gcc 499
Leu Asp Glu Pro Glu Ile Val Thr Ala Glu Thr Gly Asp Ser Pro Ala
120 125 130

cca cag gca ttc gaa ggc gcc gat gtt att gca tgg gca cac aac gaa 547
Pro Gln Ala Phe Glu Gly Ala Asp Val Ile Ala Trp Ala His Asn Glu
135 140 145

acc tcc act ggc gcc atg gtt cca gtt ctt cgc ccc gaa ggc tct gaa 595
Thr Ser Thr Gly Ala Met Val Pro Val Leu Arg Pro Glu Gly Ser Glu
150 155 160 165

ggc tcc ctg gtt gcc att gac gca acc tcc ggc gct ggt gga ctg cca 643
Gly Ser Leu Val Ala Ile Asp Ala Thr Ser Gly Ala Gly Gly Leu Pro
170 175 180

gta gac atc aag aac tcc gat gtt tac tac ttc tcc cca cag aag tgc 691
Val Asp Ile Lys Asn Ser Asp Val Tyr Tyr Phe Ser Pro Gln Lys Cys
185 190 195

ttc gca tcc gac ggt ggc ctg tgg ctt gca gcg atg agc cca gca gct 739
Phe Ala Ser Asp Gly Gly Leu Trp Leu Ala Ala Met Ser Pro Ala Ala
200 205 210

ctc gag cgc atc gag aag atc aac gct tcc gat cgc ttc atc cct gag 787
Leu Glu Arg Ile Glu Lys Ile Asn Ala Ser Asp Arg Phe Ile Pro Glu
215 220 225

ttc ctc aac ctg cag acc gca gtg gat aac tcc ctg aag aac cag acc 835
Phe Leu Asn Leu Gln Thr Ala Val Asp Asn Ser Leu Lys Asn Gln Thr
230 235 240 245

tac aac acc cca gct gtt gct acc ttg ctg atg ctg gac aac cag gtc 883
Tyr Asn Thr Pro Ala Val Ala Thr Leu Leu Met Leu Asp Asn Gln Val
250 255 260

aag tgg atg aac tcc aac ggc ggc ctg gat gga atg gtt gct cgc acc 931
Lys Trp Met Asn Ser Asn Gly Gly Leu Asp Gly Met Val Ala Arg Thr

265 270 275

aca gca agc tcc tcc gcc ctg tac aac tgg gct gag gct cgc gag gag 979
Thr Ala Ser Ser Ser Ala Leu Tyr Asn Trp Ala Glu Ala Arg Glu Glu
280 285 290

gca tcc cca tac gtg gca gat gca gct aag cgc tcc ctc gtt gtc ggc
1027
Ala Ser Pro Tyr Val Ala Asp Ala Ala Lys Arg Ser Leu Val Val Gly
295 300 305

acc atc gac ttc gat gac tcc atc gac gca gca gtg atc gct aag ata
1075
Thr Ile Asp Phe Asp Asp Ser Ile Asp Ala Ala Val Ile Ala Lys Ile
310 315 320 325

ctg cgc gca aac ggc atc ctg gac acc gag cct tac cgc aag ctg gga
1123
Leu Arg Ala Asn Gly Ile Leu Asp Thr Glu Pro Tyr Arg Lys Leu Gly
330 335 340

cgc aac cag ctg cgc atc ggt atg ttc cca gcg atc gat tcc acc gat
1171
Arg Asn Gln Leu Arg Ile Gly Met Phe Pro Ala Ile Asp Ser Thr Asp
345 350 355

gtg gaa aag ctc acc gga gca atc gac ttc atc ctc gat ggc ggt ttt
1219
Val Glu Lys Leu Thr Gly Ala Ile Asp Phe Ile Leu Asp Gly Gly Phe
360 365 370

gca agg aag taataccccc actttgaaaa aca
1251
Ala Arg Lys
375

<210> 152
<211> 376
<212> PRT
<213> Corynebacterium glutamicum

<400> 152
Met Thr Asp Phe Pro Thr Leu Pro Ser Glu Phe Ile Pro Gly Asp Gly
1 5 10 15

Arg Phe Gly Cys Gly Pro Ser Lys Val Arg Pro Glu Gln Ile Gln Ala
20 25 30

Ile Val Asp Gly Ser Ala Ser Val Ile Gly Thr Ser His Arg Gln Pro
35 40 45

Ala Val Lys Asn Val Val Gly Ser Ile Arg Glu Gly Leu Ser Asp Leu
50 55 60

Phe Ser Leu Pro Glu Gly Tyr Glu Ile Ile Leu Ser Leu Gly Gly Ala
65 70 75 80

Thr Ala Phe Trp Asp Ala Ala Thr Phe Gly Leu Ile Glu Lys Lys Ser
85 90 95

Gly His Leu Ser Phe Gly Glu Phe Ser Ser Lys Phe Ala Lys Ala Ser
100 105 110

Lys Leu Ala Pro Trp Leu Asp Glu Pro Glu Ile Val Thr Ala Glu Thr
115 120 125

Gly Asp Ser Pro Ala Pro Gln Ala Phe Glu Gly Ala Asp Val Ile Ala
130 135 140

Trp Ala His Asn Glu Thr Ser Thr Gly Ala Met Val Pro Val Leu Arg
145 150 155 160

Pro Glu Gly Ser Glu Gly Ser Leu Val Ala Ile Asp Ala Thr Ser Gly
165 170 175

Ala Gly Gly Leu Pro Val Asp Ile Lys Asn Ser Asp Val Tyr Tyr Phe
180 185 190

Ser Pro Gln Lys Cys Phe Ala Ser Asp Gly Gly Leu Trp Leu Ala Ala
195 200 205

Met Ser Pro Ala Ala Leu Glu Arg Ile Glu Lys Ile Asn Ala Ser Asp
210 215 220

Arg Phe Ile Pro Glu Phe Leu Asn Leu Gln Thr Ala Val Asp Asn Ser
225 230 235 240

Leu Lys Asn Gln Thr Tyr Asn Thr Pro Ala Val Ala Thr Leu Leu Met
245 250 255

Leu Asp Asn Gln Val Lys Trp Met Asn Ser Asn Gly Gly Leu Asp Gly
260 265 270

Met Val Ala Arg Thr Thr Ala Ser Ser Ser Ala Leu Tyr Asn Trp Ala
275 280 285

Glu Ala Arg Glu Glu Ala Ser Pro Tyr Val Ala Asp Ala Ala Lys Arg
290 295 300

Ser Leu Val Val Gly Thr Ile Asp Phe Asp Asp Ser Ile Asp Ala Ala
305 310 315 320

Val Ile Ala Lys Ile Leu Arg Ala Asn Gly Ile Leu Asp Thr Glu Pro
325 330 335

Tyr Arg Lys Leu Gly Arg Asn Gln Leu Arg Ile Gly Met Phe Pro Ala
340 345 350

Ile Asp Ser Thr Asp Val Glu Lys Leu Thr Gly Ala Ile Asp Phe Ile
355 360 365

Leu Asp Gly Gly Phe Ala Arg Lys
370 375

<210> 153
<211> 1422
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(1399)
<223> RXN02758

<400> 153
atacatctca cccaattccc cataactaga caattgccca gcaacgactg ataagtctcc 60

aatgtcgtgt tccgcgctca gacatgagac aattgttgcc gtg act gaa ctc atc 115
Val Thr Glu Leu Ile
1 5

cag aat gaa tcc caa gaa atc gct gag ctg gaa gcc ggc cag cag gtt 163
Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu Ala Gly Gln Gln Val
10 15 20

gca ttg cgt gaa ggt tat ctt cct gcg gtg atc aca gtg agc ggt aaa 211
Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile Thr Val Ser Gly Lys
25 30 35

gac cgc cca ggt gtg act gcc gcg ttc ttt agg gtc ttg tcc gct aat 259
Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg Val Leu Ser Ala Asn
40 45 50

cag gtt cag gtc ttg gac gtt gag cag tca atg ttc cgt ggc ttt ttg 307
Gln Val Gln Val Leu Asp Val Glu Gln Ser Met Phe Arg Gly Phe Leu
55 60 65

aac ttg gcg gcg ttt gtg ggt atc gca cct gag cgt gtc gag acc gtc 355
Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu Arg Val Glu Thr Val
70 75 80 85

acc aca ggc ctg act gac acc ctc aag gtg cat gga cag tcc gtg gtg 403
Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His Gly Gln Ser Val Val
90 95 100

gtg gag ctg cag gaa act gtg cag tcg tcc cgt cct cgt tct tcc cat 451
Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg Pro Arg Ser Ser His
105 110 115

gtt gtt gtg gtg ttg ggt gat ccg gtt gat gcg ttg gat att tcc cgc 499
Val Val Val Val Leu Gly Asp Pro Val Asp Ala Leu Asp Ile Ser Arg
120 125 130

att ggt cag acc ctg gcg gat tac gat gcc aac att gac acc att cgt 547
Ile Gly Gln Thr Leu Ala Asp Tyr Asp Ala Asn Ile Asp Thr Ile Arg
135 140 145

ggt att tcg gat tac cct gtg acc ggc ctg gag ctg aag gtg act gtg 595
Gly Ile Ser Asp Tyr Pro Val Thr Gly Leu Glu Leu Lys Val Thr Val
150 155 160 165

ccg gat gtc agc cct ggt ggt ggt gaa gcg atg cgt aag gcg ctt gct 643
Pro Asp Val Ser Pro Gly Gly Gly Glu Ala Met Arg Lys Ala Leu Ala
170 175 180

gct ctt acc tct gag ctg aat gtg gat att gcg att gag cgt tct ggt 691
Ala Leu Thr Ser Glu Leu Asn Val Asp Ile Ala Ile Glu Arg Ser Gly
185 190 195

ttg ctg cgt cgt tct aag cgt ctg gtg tgc ttc gat tgt gat tcc acg 739
Leu Leu Arg Arg Ser Lys Arg Leu Val Cys Phe Asp Cys Asp Ser Thr

```
        200                     205                     210

ttg atc act ggt gag gtc att gag atg ctg gcg gct cac gcg ggc aag    787
Leu Ile Thr Gly Glu Val Ile Glu Met Leu Ala Ala His Ala Gly Lys
    215                     220                     225

gaa gct gaa gtt gcg gca gtt act gag cgt gcg atg cgc ggt gag ctc    835
Glu Ala Glu Val Ala Ala Val Thr Glu Arg Ala Met Arg Gly Glu Leu
230                     235                     240                     245

gat ttc gag gag tct ctg cgt gag cgt gtg aag gcg ttg gct ggt ttg    883
Asp Phe Glu Glu Ser Leu Arg Glu Arg Val Lys Ala Leu Ala Gly Leu
                250                     255                     260

gat gcg tcg gtg atc gat gag gtc gct gcc gct att gag ctg acc cct    931
Asp Ala Ser Val Ile Asp Glu Val Ala Ala Ala Ile Glu Leu Thr Pro
            265                     270                     275

ggt gcg cgc acc acg atc cgt acg ctg aac cgc atg ggt tac cag acc    979
Gly Ala Arg Thr Thr Ile Arg Thr Leu Asn Arg Met Gly Tyr Gln Thr
        280                     285                     290

gct gtt gtt tcc ggt ggt ttc atc cag gtg ttg gaa ggt ttg gct gag
1027
Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu Glu Gly Leu Ala Glu
    295                     300                     305

gag ttg gag ttg gat tat gtc cgc gcc aac act ttg gaa atc gtt gat
1075
Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr Leu Glu Ile Val Asp
310                     315                     320                     325

ggc aag ctg acc ggc aac gtc acc gga aag atc gtt gac cgc gct gcg
1123
Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile Val Asp Arg Ala Ala
                330                     335                     340

aag gct gag ttc ctc cgt gag ttc gct gcg gat tct ggc ctg aag atg
1171
Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp Ser Gly Leu Lys Met
            345                     350                     355

tac cag act gtc gct gtc ggt gat ggc gct aat gac atc gat atg ctc
1219
Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn Asp Ile Asp Met Leu
        360                     365                     370

tcc gct gcg ggt ctg ggt gtt gct ttc aac gcg aag cct gcg ctg aag
1267
Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala Lys Pro Ala Leu Lys
    375                     380                     385

gag att gcg gat act tcc gtg aac cac cca ttc ctc gac gag gtt ttg
1315
Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe Leu Asp Glu Val Leu
390                     395                     400                     405

cac atc atg ggc att tcc cgc gac gag atc gat ctg gcg gat cag gaa
1363
His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp Leu Ala Asp Gln Glu
                410                     415                     420
```

gac ggc act ttc cac cgc gtt cca ttg acc aat gcc taaagattcg
1409
Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn Ala
425 430

tttctcgacg ccc
1422

<210> 154
<211> 433
<212> PRT
<213> Corynebacterium glutamicum

<400> 154
Val Thr Glu Leu Ile Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu
1 5 10 15

Ala Gly Gln Gln Val Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile
20 25 30

Thr Val Ser Gly Lys Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg
35 40 45

Val Leu Ser Ala Asn Gln Val Gln Val Leu Asp Val Glu Gln Ser Met
50 55 60

Phe Arg Gly Phe Leu Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu
65 70 75 80

Arg Val Glu Thr Val Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His
85 90 95

Gly Gln Ser Val Val Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg
100 105 110

Pro Arg Ser Ser His Val Val Val Val Leu Gly Asp Pro Val Asp Ala
115 120 125

Leu Asp Ile Ser Arg Ile Gly Gln Thr Leu Ala Asp Tyr Asp Ala Asn
130 135 140

Ile Asp Thr Ile Arg Gly Ile Ser Asp Tyr Pro Val Thr Gly Leu Glu
145 150 155 160

Leu Lys Val Thr Val Pro Asp Val Ser Pro Gly Gly Gly Glu Ala Met
165 170 175

Arg Lys Ala Leu Ala Ala Leu Thr Ser Glu Leu Asn Val Asp Ile Ala
180 185 190

Ile Glu Arg Ser Gly Leu Leu Arg Arg Ser Lys Arg Leu Val Cys Phe
195 200 205

Asp Cys Asp Ser Thr Leu Ile Thr Gly Glu Val Ile Glu Met Leu Ala
210 215 220

Ala His Ala Gly Lys Glu Ala Glu Val Ala Ala Val Thr Glu Arg Ala
225 230 235 240

```
Met Arg Gly Glu Leu Asp Phe Glu Glu Ser Leu Arg Glu Arg Val Lys
                245                 250                 255

Ala Leu Ala Gly Leu Asp Ala Ser Val Ile Asp Glu Val Ala Ala Ala
            260                 265                 270

Ile Glu Leu Thr Pro Gly Ala Arg Thr Thr Ile Arg Thr Leu Asn Arg
        275                 280                 285

Met Gly Tyr Gln Thr Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu
    290                 295                 300

Glu Gly Leu Ala Glu Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr
305                 310                 315                 320

Leu Glu Ile Val Asp Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile
                325                 330                 335

Val Asp Arg Ala Ala Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp
            340                 345                 350

Ser Gly Leu Lys Met Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn
        355                 360                 365

Asp Ile Asp Met Leu Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala
    370                 375                 380

Lys Pro Ala Leu Lys Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe
385                 390                 395                 400

Leu Asp Glu Val Leu His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp
                405                 410                 415

Leu Ala Asp Gln Glu Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn
            420                 425                 430

Ala


<210> 155
<211> 490
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(490)
<223> FRXA02479

<400> 155
atacatctca cccaattccc cataactaga caattgccca gcaacgactg ataagtctcc 60

aatgtcgtgt tccgcgctca gacatgagac aattgttgcc gtg act gaa ctc atc   115
                                          Val Thr Glu Leu Ile
                                          1               5

cag aat gaa tcc caa gaa atc gct gag ctg gaa gcc ggc cag cag gtt   163
Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu Ala Gly Gln Gln Val
                10                  15                  20
```

```
gca ttg cgt gaa ggt tat ctt cct gcg gtg atc aca gtg agc ggt aaa    211
Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile Thr Val Ser Gly Lys
            25                  30                  35

gac cgc cca ggt gtg act gcc gcg ttc ttt agg gtc ttg tcc gct aat    259
Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg Val Leu Ser Ala Asn
        40                  45                  50

cag gtt cag gtc ttg gac gtt gag cag tca atg ttc cgt ggc ttt ttg    307
Gln Val Gln Val Leu Asp Val Glu Gln Ser Met Phe Arg Gly Phe Leu
    55                  60                  65

aac ttg gcg gcg ttt gtg ggt atc gca cct gag cgt gtc gag acc gtc    355
Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu Arg Val Glu Thr Val
 70                  75                  80                  85

acc aca ggc ctg act gac acc ctc aag gtg cat gga cag tcc gtg gtg    403
Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His Gly Gln Ser Val Val
                90                  95                 100

gtg gag ctg cag gaa act gtg cag tcg tcc cgt cct cgt tct tcc cat    451
Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg Pro Arg Ser Ser His
            105                 110                 115

gtt gtt gtg gtg ttg ggt gat ccg gtt gat gcg ctg gat                490
Val Val Val Val Leu Gly Asp Pro Val Asp Ala Leu Asp
        120                 125                 130


<210> 156
<211> 130
<212> PRT
<213> Corynebacterium glutamicum

<400> 156
Val Thr Glu Leu Ile Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu
 1               5                  10                  15

Ala Gly Gln Gln Val Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile
            20                  25                  30

Thr Val Ser Gly Lys Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg
        35                  40                  45

Val Leu Ser Ala Asn Gln Val Gln Val Leu Asp Val Glu Gln Ser Met
    50                  55                  60

Phe Arg Gly Phe Leu Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu
65                  70                  75                  80

Arg Val Glu Thr Val Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His
                85                  90                  95

Gly Gln Ser Val Val Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg
            100                 105                 110

Pro Arg Ser Ser His Val Val Val Val Leu Gly Asp Pro Val Asp Ala
        115                 120                 125

Leu Asp
    130
```

```
<210> 157
<211> 558
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(535)
<223> FRXA02758

<400> 157
aaggcgttgg ctggtttgga tgcgtcggtg atcgatgagg tcgctgccgc tattgagctg 60

acccttggtg cgcgcaccac gatccgtacg gttgaaccgc atg ggt tac cag acc   115
                                           Met Gly Tyr Gln Thr
                                            1               5

gct gtt gtt tcc ggt ggt ttc atc cag gtg ttg gaa ggt ttg gct gag   163
Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu Glu Gly Leu Ala Glu
                10                  15                  20

gag ttg gag ttg gat tat gtc cgc gcc aac act ttg gaa atc gtt gat   211
Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr Leu Glu Ile Val Asp
            25                  30                  35

ggc aag ctg acc ggc aac gtc acc gga aag atc gtt gac cgc gct gcg   259
Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile Val Asp Arg Ala Ala
        40                  45                  50

aag gct gag ttc ctc cgt gag ttc gct gcg gat tct ggc ctg aag atg   307
Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp Ser Gly Leu Lys Met
    55                  60                  65

tac cag act gtc gct gtc ggt gat ggc gct aat gac atc gat atg ctc   355
Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn Asp Ile Asp Met Leu
70                  75                  80                  85

tcc gct gcg ggt ctg ggt gtt gct ttc aac gcg aag cct gcg ctg aag   403
Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala Lys Pro Ala Leu Lys
                90                  95                  100

gag att gcg gat act tcc gtg aac cac cca ttc ctc gac gag gtt ttg   451
Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe Leu Asp Glu Val Leu
            105                 110                 115

cac atc atg ggc att tcc cgc gac gag atc gat ctg gcg gat cag gaa   499
His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp Leu Ala Asp Gln Glu
        120                 125                 130

gac ggc act ttc cac cgc gtt cca ttg acc aat gcc taaagattcg        545
Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn Ala
    135                 140                 145

tttctcgacg ccc                                                    558

<210> 158
<211> 145
<212> PRT
```

<213> Corynebacterium glutamicum

<400> 158
Met Gly Tyr Gln Thr Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu
1 5 10 15

Glu Gly Leu Ala Glu Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr
20 25 30

Leu Glu Ile Val Asp Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile
35 40 45

Val Asp Arg Ala Ala Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp
50 55 60

Ser Gly Leu Lys Met Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn
65 70 75 80

Asp Ile Asp Met Leu Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala
85 90 95

Lys Pro Ala Leu Lys Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe
100 105 110

Leu Asp Glu Val Leu His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp
115 120 125

Leu Ala Asp Gln Glu Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn
130 135 140

Ala
145

<210> 159
<211> 205
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (72)..(182)
<223> FRXA02759

<400> 159
tcttacttct aagctgaatg tgatattgcg attaagcgtt ctggtttgct gcgtcgttct 60

aagcgtctgg tgtg ctt cga ttg tat ccc acg ttg atc act ggt gag gtc 110
Val Leu Arg Leu Tyr Pro Thr Leu Ile Thr Gly Glu Val
1 5 10

att gag atg ctg gcg gct cac gcg ggc aag gaa gct aaa gtt gcg gca 158
Ile Glu Met Leu Ala Ala His Ala Gly Lys Glu Ala Lys Val Ala Ala
15 20 25

gtt act gag cgt gcg atg cgc ggg tgagctcgat ttcgaggagt ctc 205
Val Thr Glu Arg Ala Met Arg Gly
30 35

<210> 160

<211> 37
<212> PRT
<213> Corynebacterium glutamicum

<400> 160
Val Leu Arg Leu Tyr Pro Thr Leu Ile Thr Gly Glu Val Ile Glu Met
1 5 10 15

Leu Ala Ala His Ala Gly Lys Glu Ala Lys Val Ala Ala Val Thr Glu
20 25 30

Arg Ala Met Arg Gly
35

<210> 161
<211> 1188
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1165)
<223> RXA02501

<400> 161
cgccccgaaa gctttaccat ggatacgata ctcaatggag atatccatta tcggtttggc 60

gtctgtgcgc tcatgaacca ggaaggtttt tgtttgtctc atg agc tct gaa gga 115
Met Ser Ser Glu Gly
1 5

aga aac cac aac tgg gac tac gcc gcc atc ggc acc cca gag gat ttc 163
Arg Asn His Asn Trp Asp Tyr Ala Ala Ile Gly Thr Pro Glu Asp Phe
10 15 20

ctc gcc agc tgg agc gca tcc cgc gga aat cta cga cgc ttt ttc gaa 211
Leu Ala Ser Trp Ser Ala Ser Arg Gly Asn Leu Arg Arg Phe Phe Glu
25 30 35

gac cac gca gcc gcc ccc ata aac gat gcc gcc cag cgc caa gca ggt 259
Asp His Ala Ala Ala Pro Ile Asn Asp Ala Ala Gln Arg Gln Ala Gly
40 45 50

gaa gcc gca gca acc caa gcc gtc gca gcg atc tac ggc atg gag ctc 307
Glu Ala Ala Ala Thr Gln Ala Val Ala Ala Ile Tyr Gly Met Glu Leu
55 60 65

aac gaa ttc aac gca ggt gtc gac gcc gtc gcc ggc gcc atc gaa tct 355
Asn Glu Phe Asn Ala Gly Val Asp Ala Val Ala Gly Ala Ile Glu Ser
70 75 80 85

gcc ggc gcc atc cac gtc agc atc ccc gat ccc gat gtc ccc caa gat 403
Ala Gly Ala Ile His Val Ser Ile Pro Asp Pro Asp Val Pro Gln Asp
90 95 100

gtc gga gcc gca gca ttt ttc gac gtc gac aac acc ctc atc caa ggc 451
Val Gly Ala Ala Ala Phe Phe Asp Val Asp Asn Thr Leu Ile Gln Gly
105 110 115

tcc tcc ctc atc gtt ttc gcc caa gga ctc ttc cgg aag aaa ttc ttc 499

Ser Ser Leu Ile Val Phe Ala Gln Gly Leu Phe Arg Lys Lys Phe Phe
120 125 130

acc atc aaa gaa atc ctc ccc gtg gtg tgg aaa caa gtg aaa ttc aaa 547
Thr Ile Lys Glu Ile Leu Pro Val Val Trp Lys Gln Val Lys Phe Lys
135 140 145

ctc acc ggc tcc gaa aac gcc gac gac gtc tcc cgc ggc cgc gaa caa 595
Leu Thr Gly Ser Glu Asn Ala Asp Asp Val Ser Arg Gly Arg Glu Gln
150 155 160 165

gcc ctc gaa ttc atc aaa ggc cgc ccc gtc caa gaa cta gtt gac ctc 643
Ala Leu Glu Phe Ile Lys Gly Arg Pro Val Gln Glu Leu Val Asp Leu
170 175 180

tgc gaa gaa atc gtc gac caa cgc atg gcc gac aaa atg tgg ccc ggc 691
Cys Glu Glu Ile Val Asp Gln Arg Met Ala Asp Lys Met Trp Pro Gly
185 190 195

acc aaa caa ctc gcc gac atg cac atc gcc gcc ggc cac caa gtc tgg 739
Thr Lys Gln Leu Ala Asp Met His Ile Ala Ala Gly His Gln Val Trp
200 205 210

ctc gtc tcc gca acc ccc gtc caa ctc gcc caa atc ctg gca caa cgc 787
Leu Val Ser Ala Thr Pro Val Gln Leu Ala Gln Ile Leu Ala Gln Arg
215 220 225

ctc ggc ttc acc gga gcg atc ggc aca gtc gca gaa gca aaa gat gga 835
Leu Gly Phe Thr Gly Ala Ile Gly Thr Val Ala Glu Ala Lys Asp Gly
230 235 240 245

gta ttc acc ggc cga ctc gtc ggc gac atc ctc cac gga ccc ggc aaa 883
Val Phe Thr Gly Arg Leu Val Gly Asp Ile Leu His Gly Pro Gly Lys
250 255 260

aga cac gca gtc gca gca ctc gca tcc atc gaa caa ctc gac ctc acc 931
Arg His Ala Val Ala Ala Leu Ala Ser Ile Glu Gln Leu Asp Leu Thr
265 270 275

cga tgc acc gcc tac tcc gac tcc atc aac gac ctc ccc atg ctc tcc 979
Arg Cys Thr Ala Tyr Ser Asp Ser Ile Asn Asp Leu Pro Met Leu Ser
280 285 290

atg gtc ggc acc gcc gtc gca gta aac ccc gac tcc aaa ctc cgc aaa
1027
Met Val Gly Thr Ala Val Ala Val Asn Pro Asp Ser Lys Leu Arg Lys
295 300 305

gaa gcc gaa acc cga ggc tgg gac gtc cgc gat ttc cga agc atc cgc
1075
Glu Ala Glu Thr Arg Gly Trp Asp Val Arg Asp Phe Arg Ser Ile Arg
310 315 320 325

aaa gcc acc cgc gaa tac gga atc ccc gcc ctg gtc acc gcc gca ttc
1123
Lys Ala Thr Arg Glu Tyr Gly Ile Pro Ala Leu Val Thr Ala Ala Phe
330 335 340

agt gtc gcc ggc tgg agt cta cgc cgc cga tgg aga aaa caa
1165
Ser Val Ala Gly Trp Ser Leu Arg Arg Arg Trp Arg Lys Gln

345 350 355

taacgcacag gagccgtttt aag
1188

<210> 162
<211> 355
<212> PRT
<213> Corynebacterium glutamicum

<400> 162
Met Ser Ser Glu Gly Arg Asn His Asn Trp Asp Tyr Ala Ala Ile Gly
1 5 10 15

Thr Pro Glu Asp Phe Leu Ala Ser Trp Ser Ala Ser Arg Gly Asn Leu
20 25 30

Arg Arg Phe Phe Glu Asp His Ala Ala Ala Pro Ile Asn Asp Ala Ala
35 40 45

Gln Arg Gln Ala Gly Glu Ala Ala Ala Thr Gln Ala Val Ala Ala Ile
50 55 60

Tyr Gly Met Glu Leu Asn Glu Phe Asn Ala Gly Val Asp Ala Val Ala
65 70 75 80

Gly Ala Ile Glu Ser Ala Gly Ala Ile His Val Ser Ile Pro Asp Pro
85 90 95

Asp Val Pro Gln Asp Val Gly Ala Ala Ala Phe Phe Asp Val Asp Asn
100 105 110

Thr Leu Ile Gln Gly Ser Ser Leu Ile Val Phe Ala Gln Gly Leu Phe
115 120 125

Arg Lys Lys Phe Phe Thr Ile Lys Glu Ile Leu Pro Val Val Trp Lys
130 135 140

Gln Val Lys Phe Lys Leu Thr Gly Ser Glu Asn Ala Asp Asp Val Ser
145 150 155 160

Arg Gly Arg Glu Gln Ala Leu Glu Phe Ile Lys Gly Arg Pro Val Gln
165 170 175

Glu Leu Val Asp Leu Cys Glu Glu Ile Val Asp Gln Arg Met Ala Asp
180 185 190

Lys Met Trp Pro Gly Thr Lys Gln Leu Ala Asp Met His Ile Ala Ala
195 200 205

Gly His Gln Val Trp Leu Val Ser Ala Thr Pro Val Gln Leu Ala Gln
210 215 220

Ile Leu Ala Gln Arg Leu Gly Phe Thr Gly Ala Ile Gly Thr Val Ala
225 230 235 240

Glu Ala Lys Asp Gly Val Phe Thr Gly Arg Leu Val Gly Asp Ile Leu
245 250 255

His Gly Pro Gly Lys Arg His Ala Val Ala Ala Leu Ala Ser Ile Glu

260 265 270

Gln Leu Asp Leu Thr Arg Cys Thr Ala Tyr Ser Asp Ser Ile Asn Asp
275 280 285

Leu Pro Met Leu Ser Met Val Gly Thr Ala Val Ala Val Asn Pro Asp
290 295 300

Ser Lys Leu Arg Lys Glu Ala Glu Thr Arg Gly Trp Asp Val Arg Asp
305 310 315 320

Phe Arg Ser Ile Arg Lys Ala Thr Arg Glu Tyr Gly Ile Pro Ala Leu
325 330 335

Val Thr Ala Ala Phe Ser Val Ala Gly Trp Ser Leu Arg Arg Arg Trp
340 345 350

Arg Lys Gln
355

<210> 163
<211> 558
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(535)
<223> RXN03105

<400> 163
ggttggggtc atcaaaggat gcggacatcg ctgtggggtt gtgtaataat tgcacctgtg 60

aggtgccttt ctggcaggtg aatcaggact ctaagcaagc ttg att ctt cca gtt 115
Leu Ile Leu Pro Val
1 5

cag gag ggc att tcc tat ttt ccc acg ccg tta cac ctg aat cac atc 163
Gln Glu Gly Ile Ser Tyr Phe Pro Thr Pro Leu His Leu Asn His Ile
10 15 20

ggt gga tcc agg tta agc gca cat gta gaa gat gaa gat ctc cgc ctc 211
Gly Gly Ser Arg Leu Ser Ala His Val Glu Asp Glu Asp Leu Arg Leu
25 30 35

gac cgg gac gca gtc tct gaa ttt ggt cgg aaa acc cac gaa ctc ttc 259
Asp Arg Asp Ala Val Ser Glu Phe Gly Arg Lys Thr His Glu Leu Phe
40 45 50

ccc ggg gtc aac cca gag ccc aac cgt ttc agc gtc cac tat gac acc 307
Pro Gly Val Asn Pro Glu Pro Asn Arg Phe Ser Val His Tyr Asp Thr
55 60 65

tac act gca gac aaa tct cca att atc gac gcg gtt gac aat gtc att 355
Tyr Thr Ala Asp Lys Ser Pro Ile Ile Asp Ala Val Asp Asn Val Ile
70 75 80 85

gtg ctc acc gga gga tcc gga cac gcc ttc aag ctc tct cca gct tat 403
Val Leu Thr Gly Gly Ser Gly His Ala Phe Lys Leu Ser Pro Ala Tyr
90 95 100

```
ggc gaa ctc gca gca caa cga gcg gtc gga aac acc tcg ccg ctg tac    451
Gly Glu Leu Ala Ala Gln Arg Ala Val Gly Asn Thr Ser Pro Leu Tyr
            105                 110                 115

agc gaa gac ttt cgg atc gcc tcg cat gaa cca atc aaa gag cgg tgc    499
Ser Glu Asp Phe Arg Ile Ala Ser His Glu Pro Ile Lys Glu Arg Cys
        120                 125                 130

acg tat aga aag cta acc ttt tta agt gcg cgg ttt tagggtgaga         545
Thr Tyr Arg Lys Leu Thr Phe Leu Ser Ala Arg Phe
    135                 140                 145

atctaacgct gag                                                     558
```

<210> 164
<211> 145
<212> PRT
<213> Corynebacterium glutamicum

<400> 164

```
Leu Ile Leu Pro Val Gln Glu Gly Ile Ser Tyr Phe Pro Thr Pro Leu
  1               5                  10                  15

His Leu Asn His Ile Gly Gly Ser Arg Leu Ser Ala His Val Glu Asp
             20                  25                  30

Glu Asp Leu Arg Leu Asp Arg Asp Ala Val Ser Glu Phe Gly Arg Lys
         35                  40                  45

Thr His Glu Leu Phe Pro Gly Val Asn Pro Glu Pro Asn Arg Phe Ser
     50                  55                  60

Val His Tyr Asp Thr Tyr Thr Ala Asp Lys Ser Pro Ile Ile Asp Ala
 65                  70                  75                  80

Val Asp Asn Val Ile Val Leu Thr Gly Gly Ser Gly His Ala Phe Lys
                 85                  90                  95

Leu Ser Pro Ala Tyr Gly Glu Leu Ala Ala Gln Arg Ala Val Gly Asn
            100                 105                 110

Thr Ser Pro Leu Tyr Ser Glu Asp Phe Arg Ile Ala Ser His Glu Pro
        115                 120                 125

Ile Lys Glu Arg Cys Thr Tyr Arg Lys Leu Thr Phe Leu Ser Ala Arg
    130                 135                 140

Phe
145
```

<210> 165
<211> 687
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (62)..(664)

<223> RXS01130

<400> 165
agttcgtggc ggatgctgtg aacgtttccg gtggtcgcgt gggcgaagag gttctgtgtg 60

gatg gat ctg gct cgc aag ctt ggt ctt ctt gct ggc aag ctt gtc gac 109
Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp
1 5 10 15

gcc gcc cca gtc tcc att gag gtt gag gct cga ggc gag ctt tct tcc 157
Ala Ala Pro Val Ser Ile Glu Val Glu Ala Arg Gly Glu Leu Ser Ser
20 25 30

gag cag gtc aat gca ctt ggt ttg tcc gct gtt cgt ggt ttg ttc tcc 205
Glu Gln Val Asn Ala Leu Gly Leu Ser Ala Val Arg Gly Leu Phe Ser
35 40 45

gga att atc gaa gag tcc gtt act ttc gtc aac gct cct cgc att gct 253
Gly Ile Ile Glu Glu Ser Val Thr Phe Val Asn Ala Pro Arg Ile Ala
50 55 60

gaa gag cgt ggc ctg gac atc tcc gtg aag acc aac tct gag tct gtt 301
Glu Glu Arg Gly Leu Asp Ile Ser Val Lys Thr Asn Ser Glu Ser Val
65 70 75 80

act cac cgt tcc gtc ctg cag gtc aag gtc att act ggc agc ggc gcg 349
Thr His Arg Ser Val Leu Gln Val Lys Val Ile Thr Gly Ser Gly Ala
85 90 95

agc gca act gtt gtt ggt gcc ctg act ggt ctt gag cgc gtt gag aag 397
Ser Ala Thr Val Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys
100 105 110

atc acc cgc atc aat ggc cgt ggc ctg gat ctg cgc gca gag ggt ctg 445
Ile Thr Arg Ile Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu
115 120 125

aac ctc ttc ctg cag tac act gac gct cct ggt gca ctg ggt acc gtt 493
Asn Leu Phe Leu Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val
130 135 140

ggt acc aag ctg ggt gct gct ggc atc aac atc gag gct gct gcg ttg 541
Gly Thr Lys Leu Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu
145 150 155 160

act cag gct gag aag ggt gac ggc gct gtc ctg atc ctg cgt gtt gag 589
Thr Gln Ala Glu Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu
165 170 175

tcc gct gtc tct gaa gag ctg gaa gct gaa atc aac gct gag ttg ggt 637
Ser Ala Val Ser Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly
180 185 190

gct act tcc ttc cag gtt gat ctt gac taattagaga tccatttgct 684
Ala Thr Ser Phe Gln Val Asp Leu Asp
195 200

tga 687

<210> 166

<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 166
Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp
1 5 10 15

Ala Ala Pro Val Ser Ile Glu Val Glu Ala Arg Gly Glu Leu Ser Ser
20 25 30

Glu Gln Val Asn Ala Leu Gly Leu Ser Ala Val Arg Gly Leu Phe Ser
35 40 45

Gly Ile Ile Glu Glu Ser Val Thr Phe Val Asn Ala Pro Arg Ile Ala
50 55 60

Glu Glu Arg Gly Leu Asp Ile Ser Val Lys Thr Asn Ser Glu Ser Val
65 70 75 80

Thr His Arg Ser Val Leu Gln Val Lys Val Ile Thr Gly Ser Gly Ala
85 90 95

Ser Ala Thr Val Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys
100 105 110

Ile Thr Arg Ile Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu
115 120 125

Asn Leu Phe Leu Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val
130 135 140

Gly Thr Lys Leu Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu
145 150 155 160

Thr Gln Ala Glu Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu
165 170 175

Ser Ala Val Ser Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly
180 185 190

Ala Thr Ser Phe Gln Val Asp Leu Asp
195 200

<210> 167
<211> 604
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(604)
<223> RXS03112

<400> 167
gtgagcacgc aatttctttg ctgctgtcta ctgctcgcca gatcctgctg ctgatgcgac 60

gctgcgtgag ggcgagtgga agcggtcttc tttcaacggt gtg gaa att ttc gga 115
Val Glu Ile Phe Gly
1 5

```
aaa act gtc ggt atc gtc ggt ttt ggc cac att ggt cag ttg ttt gct    163
Lys Thr Val Gly Ile Val Gly Phe Gly His Ile Gly Gln Leu Phe Ala
                10                  15                  20

cag cgt ctt gct gcg ttt gag acc acc att gtt gct tac gat cct tac    211
Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val Ala Tyr Asp Pro Tyr
            25                  30                  35

gct aac cct gct cgt gcg gct cag ctg aac gtt gag ttg gtt gag ttg    259
Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val Glu Leu Val Glu Leu
        40                  45                  50

gat gag ctg atg agc cgt tct gac ttt gtc acc att cac ctt cct aag    307
Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr Ile His Leu Pro Lys
    55                  60                  65

acc aag gaa act gct ggc atg ttt gat gcg cac ctc ctt gct aag tcc    355
Thr Lys Glu Thr Ala Gly Met Phe Asp Ala His Leu Leu Ala Lys Ser
70                  75                  80                  85

aag aag ggc cag atc atc atc aac gct gct cgt ggt ggc ctt gtt gat    403
Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg Gly Gly Leu Val Asp
                90                  95                  100

gag cag gct ttg gct gat gcg att gag tcc ggt cac att cgt ggc gct    451
Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly His Ile Arg Gly Ala
            105                 110                 115

ggt ttc gat gtg tac tcc acc gag cct tgc act gat tct cct ttg ttc    499
Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe
        120                 125                 130

aag ttg cct cag gtt gtt gtg act cct cac ttg ggt gct tct act gaa    547
Lys Leu Pro Gln Val Val Val Thr Pro His Leu Gly Ala Ser Thr Glu
    135                 140                 145

gag gct caa gat cgt gcg ggt act gac att gct gat tct gtg ctc aag    595
Glu Ala Gln Asp Arg Ala Gly Thr Asp Ile Ala Asp Ser Val Leu Lys
150                 155                 160                 165

gcg ctg gct                                                        604
Ala Leu Ala
```

```
<210> 168
<211> 168
<212> PRT
<213> Corynebacterium glutamicum

<400> 168
Val Glu Ile Phe Gly Lys Thr Val Gly Ile Val Gly Phe Gly His Ile
1               5                   10                  15

Gly Gln Leu Phe Ala Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val
            20                  25                  30

Ala Tyr Asp Pro Tyr Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val
        35                  40                  45
```